Network Decontamination using Cellular Automata

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Abstract

We consider the problem of decontaminating a network where all nodes are infected by a virus. The decontamination strategy is performed using a Cellular Automata (CA) model in which each node of the network is represented by the automata cell and thus, the network host status is also mapped to the CA state (contaminated, decontaminating, decontaminated). All hosts are assumed to be initially contaminated and the status of each cell is synchronously updated according to a set of local rules, based on the state of its neighbourhood. Our goal is to find the set of local rules that will accomplish the decontamination in an optimal way. The metrics used to define optimality is the minimization of three metrics: the maximum number of decontaminating cells at each step, the required value of the immunity time of each cell and the number of steps to complete the sanitization algorithm.

In our research, we explore the designing of these local decontamination rules by refining the concept of the neighbourhood radius of CA with the addition of two new dimensions: Visibility Hop and Contamination Distance. Additionally, a research tool that help us manage our study have been developed.

Ho anao

Tsy nitsahatra namporisika ahy

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Sincerely,
Livaniaina Hary Rakotomalala

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Chapter 1

Introduction

1.1. Problem Statement

Consider a network where sites (nodes) are processing some computations. In addition, sites can communicate with each other through links. A very realistic situation is that some sites might be contaminated, for example, by a virus. These infections could have been inserted locally in the network or by external network attacks. When infected these nodes usually behave incorrectly. Typically, antivirus programs are run at each infected network site for disinfection. However, there is no genuine guarantee that the clean site will not be re-infected again. To accentuate the issue, a network site cannot detect the presence of viruses within itself and therefore cannot curb the spread of viruses. This situation is exploited by some types of viruses which are capable of encouraging infected nodes to propagate the fault to neighbouring nodes. The evident solution to execute the antivirus against all existing hosts of the network is not an acceptable one because when active, it is assumed that the antiviral program will reduce or even stop local computation and therefore disrupt the entire network. In order to sanitize the network, a system must be capable of firstly, cleaning the infected hosts and secondly, counteracting the propagation of faults. Network Decontamination is the research of strategies for network sanitation by considering these previous two key points.

1.2. Network Decontamination

The Network Decontamination problem was first introduced in Speleology, where a maze of caves was infected by gas and needed to be decontaminated [Bre67]. In computer science, Network Decontamination is a field of study that addresses the problem of sanitizing a network which is contaminated by a virus. A virus is assumed to be a program that, when executed against a clean host, will make the host faulty. The faulty host then spreads the virus over the network using communication links. A network is considered contaminated by a virus when either one or more machine hosts are infected by a virus. Infected hosts expose faulty behaviors and can contaminate neighbouring hosts which

recursively affects the entire network. In the decontamination problem, it is generally assumed that the network is partially or fully contaminated. Our interest is to find an efficient strategy to correct every faulty node by executing an antivirus against contaminated hosts.

1.2.1. Decontamination by Mobile Agents

The most popular approach to sanitizing a distributed network is the use of Mobile Agents. Mobile Agents are extensively used in distributed systems to solve typical problems such as *Rendez-vous*, *Graph Exploration* and *Black Holes*. A listing of the use of Mobile Agents in Distributed systems is found in [KK07]. Mobile Agents can be defined as software entities with the capacity for motion inside a network and which can act on behalf of their user with some degree of autonomy in order to accomplish different computing tasks. Mobile Agents have been found to be useful in a number of network security applications including Network Decontamination. The nature of the network topology plays an important role in the efficiency of operations executed within the network by the sites and the Mobile Agents (see [FHL06], [FHL08] and [FHL07]).

1.2.2. Network Topology and Graph approach

The standard visual way to represent a network is by the means of a graph: hosts are represented by nodes, and the presence of edges between two nodes stipulates that there is a connection link between these two hosts. Researchers have shown tremendous interest in the debate over the best graph topology on which to model a network. Among the known topologies are *Ring*, *Tree*, *Rectangular Grids (or Mesh), Hypercube* and *Complete* graphs. Clearly, the choice of the topology has a direct impact on the efficiency of operations that will be executed under the network. For instance, an optimal decontamination strategy against a *Ring* network might not necessarily be efficient, nor even meaningful, for a *Complete* graph.

Most solutions for graph theory problems such as graph coloring, covering problems (e.g., Vertex cover), and route problems (e.g., Hamiltonian path, spanning tree) are frequently used as the backbone of solutions in distributed systems problems such as Voting, Leader Election, Broadcasting, or Routing. The Network Decontamination problem is related, under certain conditions, to that of the graph search ([Mes08]). Thus, several of the

techniques and models considered by researchers for the general graph search problems are quite useful in the study of the Network Decontamination problems when the network is modeled by a graph.

1.2.3. The Cellular Automaton approach

In our thesis, we take a tangent direction from the graph approach. Instead of having the external intervention of Mobile Agents cleaning the network, we put our focus on finding "local" strategies so that hosts can trigger and execute the decontamination themselves. The idea of using local approaches is known in distributed systems. Distributed and networked systems often employ *local majority* based rules to enhance reliability and fault-tolerance. Local voting schemes are used as decision tools in a variety of different applications, for example, agreement and consensus in distributed systems. Also, systems employing majority-based local voting schemes are known to have a higher level of resistance. (For instance, one can use a similar idea with respect to network contamination in which a clean cell is always immune to contamination as long as a majority of its neighbours are uncontaminated). More precisely, we want to build local rules that will be applied to each network site in a uniform way. To this end, we use a Cellular Automaton to model both the network and the operations that need to be performed. Invented by Ulam and Neumann in the 1950s, Cellular Automaton was originally used to study their joint work on liquid motion for self-organizing and reproducing behaviors [Neu51]. Our motivation is based on the fact that it is a discrete model known for its simplicity in integrating a locally based voting scheme, yet powerful enough to model any complex application. The study of its properties and its behavior has interested various disciplines as diverse as physics, biology, and theoretical computer science (e.g. [ADF07], [Kar05], [CD98], [LM10]).

1.3. Cellular Automata

1.3.1. Definition and structure

A Cellular Automaton (CA) consists of a regular grid of *cells*, each having a finite number of states (A formal definition of a CA can be consulted in *Chapter 3*). The grid can be in any finite number of dimensions but the most used in practical applications are the 1-dimensional and 2-dimensional ones (see Figure 1.1). For each cell, a set of cells, called

its *neighbourhood,* is defined relative to the specified cell. Neighbours are usually composed by a set of cells surrounding the centered cell itself within a specific integer distance called *radius*. An initial state is selected by assigning a state for each cell. A new *generation* is created at the next step according to a fixed *transition rule* that determines the new state of each cell in terms of the current state of the cell and the states of the cells in its neighbourhood. Typically, the rule for updating the states of cells is the same for each cell, does not change over time, and is applied to the whole grid simultaneously, which makes the execution of the state update in a *synchronous* fashion.

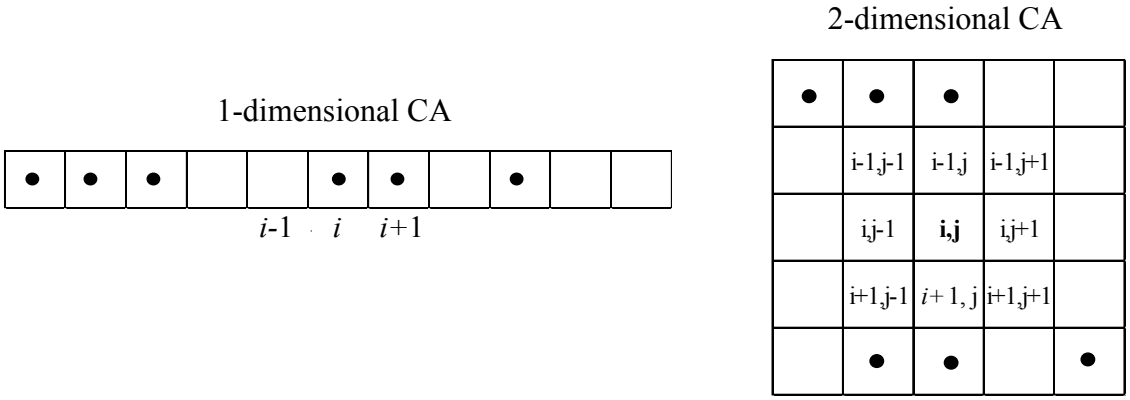


Figure 1.1: The native representation of a CA grid

The most elementary model of a CA is the 1-dimensional version (1D) (see Figure 1.1). Each site or cell in the lattice is in either the ON (a filled circle in the cell) or OFF (an empty cell) state. In the example illustrated here, the site *i*-1 is OFF and the sites *i* and *i*+1 are ON. Each cell can have two states; therefore, there are 2^3= 8 possible configurations of this neighborhood. For the CA to work, it is necessary to define what the state should be in the next generation. Consequently, there are 2^8 = 256 possible local rules with a wide range of behaviours and properties. The diversity of these simple rules alone has raised great interest and contributes to its popularity since its introduction.

1.3.2. Cellular Automata and network topology

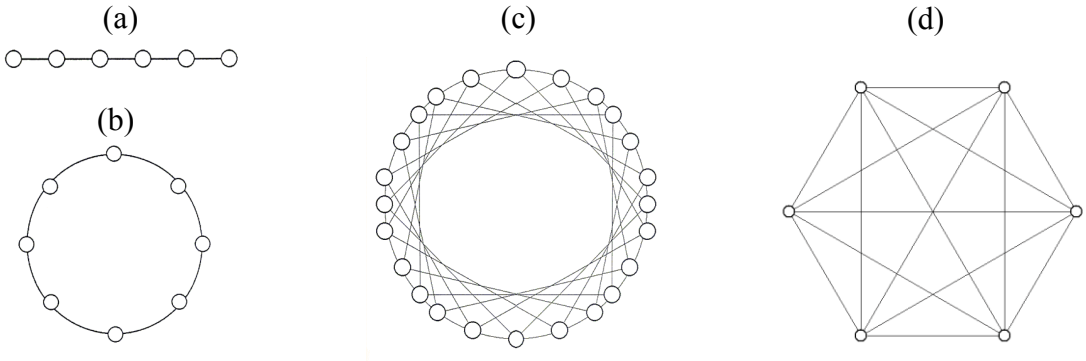


Figure 1.2: Sample of topologies that can be modeled by a 1-dimensional CA: *Chain*(a), *Ring*(b), C*hordal Ring* (c) and *Complete Graph* (d).

Network topology addresses how the various elements of a computer network are arranged and graphs are useful because they serve as mathematical models of network structures. The topological structure of a network can be depicted *physically* (how various component such as the location of the device or cables are placed); or *logically* (how the data flows within the network regardless of its physical design). In a CA, the physical topology of the network can be a *ring*, a *mesh* or *a torus* and the dataflow between the components which determines the logical topology of the network is addressed by the CA neighbourhood. Indeed, CA has ability to model some specific classes of network topologies. For instance, it is easy to see that a *chain* is naturally modeled by a 1-dimensional CA. To this end, the chain is only extrapolated by a single array (see Figure 1.2a). Chorded rings are also special type of 1-dimensional circular CA (see Figure 1.2c). A *chordal ring* $C(\{1,2,...,p,k\})$ of size n is a ring on n nodes $x_0, x_1, ..., x_{n-1}$ where each node x_i is connected to nodes $x_{(i+1) \bmod n} ... x_{(i+p) \bmod n}$ and $x_{(i+k) \bmod n}$. In a general aspect, a chordal ring can be considered as a k-neighbours 1-dimensional circular CA. Note that when $p = k = 1$, the *chordal* ring is a simple *Ring* (see Figure 1.2b) and becomes a *Complete graph* when $p = k = \left\lfloor \frac{n}{2} \right\rfloor$ (see Figure 1.2d).

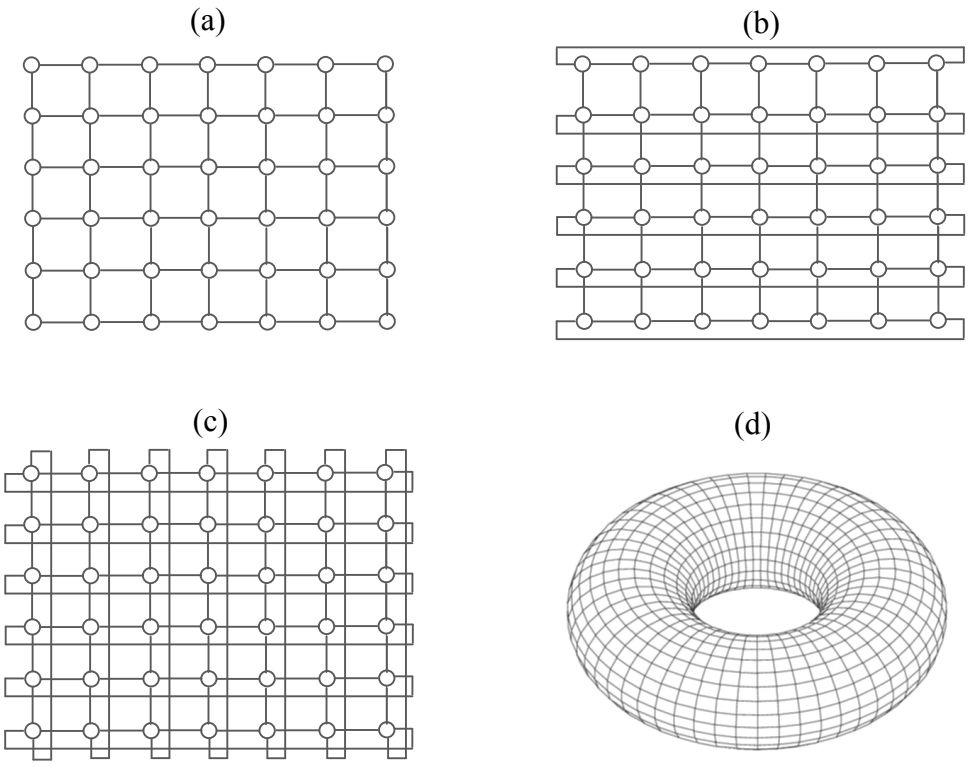


Figure 1.3: Sample of topologies that can be modeled by a 2-dimensional CA: *Rectangle Grid* (a), *Circular Grid* (b), *Torus* (2D view (c) and its 3D representation (d))

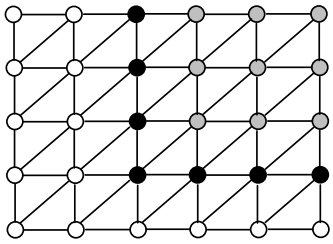
Additionally, *rectangle grid* (*mesh*) and possible variations can naturally be modeled by a 2-dimensional (2D) CA (Figure 1.3a). When making a circular connection between the various extremities of the 2D grid, the bi-dimensional CA with circular connections become a *Torus* (Figure 1.3c). In fact, a 2D CA can model any instance of a grid as long as the connections between elements follow a regular pattern that can be represented by the CA neighbourhood concept. A 2D CA can represent a grid network with larger connections between hosts in a larger neighbourhood defined in the CA. Figure 1.4 is an example of the modelling of a simple sub-network by a 2D CA. In this example, a cell has a maximum of six neighbours.

1.3.3. Decontamination using Cellular Automata

The use of a CA to perform the decontamination is possible under two conditions. The first hypothesis is that the network must be modeled by a CA. In the previous section, we

have shown some candidate topologies that satisfy this condition. The second condition concerns the state of the network sites that has to be mapped with the CA transition states. To this end, each CA's cell state is just set to one of these three states: *Contaminated* (the network site is infected by a virus), *Decontaminating* (The network site is executing the antiviral program) and *Decontaminated* (the virus has been removed from the network site and the site is currently clean). The decontamination goal is to study the building of transition rules that take as input a contaminated CA, and transfer each cell state from a faulty contaminated state into a decontaminating state so that each cell eventually becomes and remains decontaminated. An illustration of an execution is shown in Figure 1.4. Contaminated network sites (white cell) are represented by the number "1" in the CA while decontaminated cells are represented by "0" to represented the clean site (gray cell). When cells are in a decontaminating state, it is represented by a dot "•" within both the CA and the network graph representation.

Network using a graph representation



CA Representation

1	1	•	0	0	0
1	1	•	0	0	0
1	1	•	0	0	0
1	1	•	•	•	•
1	1	1	1	1	1

Figure 1.4: An example of a 2D grid network modeled by a Cellular Automaton

1.4. Motivation and Pertinence

In a world dominated by networking and its ramifications (Internet, social networks, distributed systems, distributed data, and cloud computing), networking reliability is crucial. Similar to software which cannot be bug free, any networking system cannot insure complete reliability. Indeed, network systems are now facing an increased number of attacks than they have faced in the past. The problem is that faulty network sites become vulnerable and can expose security holes. There are various types of breakdown including process deaths, machine crashes, and network failures. A great concern for fault tolerance and

security is how to devise strategies to correct the faulty behaviour at network sites and to control the propagation of faults. Thus, Network Decontamination has attracted many researchers in the past decade. They have approached the Network Decontamination problem from many angles including its empirical version of a fully contaminated network that needs a full decontamination.

1.5. Research Questions and Requirements

1.5.1. State of the art and challenges

The general result within the field of Network Decontamination using external approach is that the problem of determining the optimal number of mobile agents necessary to perform the decontamination in arbitrary topologies is NP-hard. To date, much research has been done on the study of the decontamination problem, especially in the theoretical field of fault tolerance within distributed systems theory. There are a considerable number of papers that have been published on the topic. Many researchers have studied the decontamination problem under different types of parameters; however, most have concentrated their efforts in the study of decontamination in topologies of graphs, such as *Trees*, *Rings*, *Tories*, and *Hypercubes*. There are a few papers in which the network is modelled by a CA.

With respect to pure CA theory, there are a number of papers devoted primarily to its structure and its properties. There are also a considerable number of applications that directly use CA as a backbone. That said, the amount of research that has been done regarding the use of CA in the field of Network Decontamination is still limited.

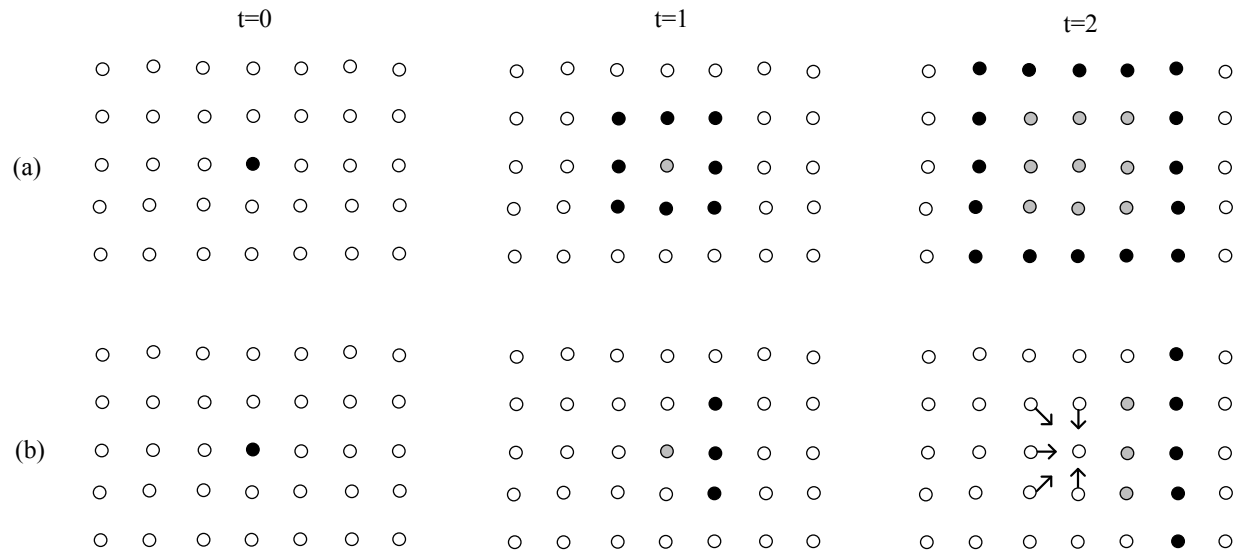


Figure 1.5: Two examples of attempted decontamination of a 2-dimensional CA

One trivial decontamination strategy using a CA is to initially run the antiviral program to one or multiple cells (*initiators*) of our CA and to propagate the decontamination strategy to all existing neighbours (Figure 1.5a). This strategy is simple because it just possesses two rules. The first rule suggests that any decontaminating cell gets decontaminated at the next stage. The second rule proposes that any contaminated state in contact with a decontaminating cell will also run the antiviral program in the next stage. With this solution, we can see that the CA eventually gets fully decontaminated. However, the fundamental issue with this solution is that the number of decontaminating cells considerably increases at each step and therefore is boundless. If one attempt to reduce the number of decontaminating cells at each step, a possible strategy would only propagate the decontamination from the initiator cells to a limited number of neighbours, for instance to the neighbours located on its right (as in Figure 1.5b). However, with this strategy, any decontaminated cell will get re-contaminated by its left neighbours. These examples show the nature of some problems that must be taken into account when building decontamination strategies.

1.5.2. Our research and contributions

Our research focuses on the Network Decontamination problem using the concept of CA. We propose optimal strategies to decontaminate a network using local rules by using a 2-dimensional CA as a model. Various basic algorithms using this type of model have been investigated in [Daa12]. In this thesis, we continue this line of research by studying new strategies under new assumptions. More precisely, we study the decontamination problem under two new dimensions arising from the concept of *radius* within CA. To this date, only direct neighbourhood (*radius*=1) have been considered. Therefore,

- a new model of accessing knowledge information, which we define as *Visibility Hop*, is proposed. This property allows a cell to oversee a larger neighbourhood.
- a new model of (re)infections, which we define as *Contamination Distance*, is also proposed. This property allows us to define which distant infected neighbours can contaminate cleaned cells.

We demonstrate that the addition of these parameters brings new dynamics to the decontamination process. The *Visibility Hop* allows us to discover new decontamination strategies. Moreover, the *Contamination Distance* allows us to differentiate the strategies to take under weaker or stronger conditions. Also fundamentally, a greater value assigned to these properties also implies that the graph topology covered by the CA is denser than a simple rectangle grid. These dynamics are seen in more details in Chapter 3.

Principally in this thesis, we developed several decontamination techniques under these parameters. Additionally, a research tool that help us manage our research have been developed.

1.6. Thesis Organization

This thesis is organized as follows.

In Chapter 2, we review the existing literature on the Network Decontamination problem. We also briefly present some related results on CA which are significant to our study.

Chapter 3 presents the model we will use in this thesis. We will also present the terminology and other formal characterization of the various entities used in our document.

In Chapter 4, we investigate the impact of the *Visibility Hop* and *Contamination Distance* against some basic known decontamination algorithms under a CA. We present the result of our initial studies against this new concept under the von Neumann and Moore neighbourhoods.

In Chapter 5, we present a new approach called Diagonal Flow and we show that the concept of Visibility can bring noticeable improvement against these schemes.

In Chapter 6, we present others schemes of decontaminating a CA by using a subdividing strategy similar to divide and conquer methods. We also show that the diagonal move presented in the previous chapter can serve as a base block in this strategy.

In Chapter 7, we present a research tool that we have implemented that aims to assist us in the study of Network Decontamination using CA.

In Chapter 8, we give a summary of the work accomplished so far and we present a non exhaustive list of possible future work.

Chapter 2

Literature Review

In this chapter, we give a survey of the known problems and results related to our work in this thesis. We briefly discuss the two different classifications of network decontamination with respect to the approach being internal or external. We review known results for each approach, especially when decontamination is performed by Mobile Agents. Then, we outline in detail the current known algorithms and results of internal decontamination using a CA as this is directly related to our study. We continue by enunciating some relevant properties of the theory of CA. We conclude the chapter by listing some various applications using CA.

2.1. Network Decontamination and approach classification

Network Decontamination is a widely studied problem in Computer Science. Network hosts or sites are assumed to be contaminated by malicious software and a *process* needs to be executed to clean the network. The process of decontamination is generally classified by two distinct aspects. Depending on whether the decontamination is carried out by the majority-voting mechanism already in place or by the use of a team of mobile agents, the decontamination process is called *internal* or *external*, respectively. The process is called internal due to the fact that the decontamination is processed by the sites themselves by using local rules and without any outside intervention. An example of an internal process is when the network is modeled by a CA and the local rules are composed of a set of transition rules in which each cell obeys in exactly the same fashion. The process is called external when the decontamination is processed by external entities to the system. An example of an external decontamination is the cleaning by means of *Mobile Agents*. [Flo09] presents a survey of the different methods of Network Decontamination with respect to these two different approaches. In this chapter, we give a survey of the most common problems and results related to our work in this thesis.

2.2. External Decontamination

2.2.1. Graph Search and the Search Number

The Network Decontamination problem is closely related to the graph search problem. The metaphorical rendition of the two concepts has been introduced by Breisch in [Bre67]. The problem was presented as follows. A person is lost in a totally dark cave and the goal is to find an efficient way to search and rescue the lost person. The author aims to find the minimum number of *searchers* required to explore the cave so that it is impossible to miss the victim. The analogy to the graph search problem is that the cave can be represented by a finite connected graph G so that rooms are represented by vertices and the passages by edges. The problem has been reformulated by other authors replacing the notion of the lost person with an intruder, motivated by the fact that in the new problem, there are assumptions that the intruder can have knowledge of the searchers' every move. Additionally, the intruder is arbitrarily fast, invisible to rescuers, and even tries to avoid meeting the searchers ([Par78], [Par76]). Theoretically, we are given a graph $G = (V, E)$ with contaminated edges and via a sequence of steps, one that uses searchers. The goal is to arrive at a situation where all edges of the graph are simultaneously clean. More precisely, the problem is to find the minimum number of searchers needed to clean the graph and to reach a final stage where all edges are simultaneously clean. A clean edge $e \in E$ is immune to recontamination on two conditions: either another searcher remains in a vertex adjacent to the edge, or all other edges incident to this vertex are clean. That is, e is re-contaminated if there exists a path P between e and a contaminated edge and there is no searcher residing in any node v for $\forall v \in P$. An edge $e = (x, y) \in E$ gets decontaminated if a searcher traverses it from x or y (or from y to x). Any decontamination strategy can be broken down into a sequence of 3 basic operations: the action of putting a searcher on a node v, the action of removing a searcher from a node v, and the action of making the searcher traverse an edge e. *Graph searching* is about finding a sequence composed of these three basic operations that results in all edges being simultaneously clean. In general, researchers are most interested in finding optimal search strategies and the minimization of the number of searchers used by a strategy. Assuming a search strategy exists, $s(G)$ is the smallest number of searchers for a graph G. Two results are important with respect to the search number. First, Meggido et al shows in

[MHG+88] that determining the search number of a graph is NP-hard. Second, LaPaugh [Lap93] has proven that for every G, there is always a monotone search strategy that uses $s(G)$ searchers. By definition, a search strategy is monotone if no recontamination ever occurs. Several techniques and models considered by researchers with respect to the graph search problem are useful in the study of the Network Decontamination problems.

2.2.2. Network Decontamination by Mobile Agents

The decontamination framework that has received great interest in recent years is Network Decontamination using mobile agents. In computer science, a mobile agent is a software entity that has the ability to move from node to node in a distributed system. Mobile agents have been used in solving many distributed systems problems because of their ease of use, their efficiency, and their fault-tolerance as explained in [KK07]. There are several papers on the use of mobile agents in distributed systems problems including graph *exploration, black hole search* and *rendez-vous*.

Decontamination by a mobile agent is considered an external decontamination because the cleaning process is performed by an entity which is external to the system. The decontamination process usually works in the same way. At any time, nodes can be *contaminated*, *clean*, or *guarded* (if they contain at least an agent). All nodes are initially contaminated except for one (the *homebase*) where a team of mobile agents is located. Agents can move in the network from a node to a neighbouring node, and a contaminated node is transformed into clean when an agent passes by the node. The goal is to reach a state in which all nodes are clean (or guarded). Mobile agents are self-contained programs that can move from a node to a neighbouring node to execute tasks independently of each other, or to cooperate to solve problems. The network is still seen as an environment where nodes represent hosts, edges represent connections between hosts, and we assume that the network is initially contaminated. The goal is to deploy a team of agents to decontaminate the network. An agent is a program that can migrate on the network. When an agent resides on a node, it can detect all intruders at the node and clean the node if it is contaminated. However, when a clean node has a contaminated neighbour, it becomes contaminated as well. It is assumed that the agents start from the same node (the homebase) and can move to neighbouring nodes. An important fact is that the problem of determining the optimal

number of agents necessary to perform the decontamination in arbitrary topologies is NP-hard. Several papers exist about the optimal strategy to clean a network using mobile agents under specific network topologies [FHL06], [LPS06], [LPS07], [FHL08], [FHL07].

In [FHL07], Flocchini et al consider the problem of decontaminating a network using a team of mobile agents. The agents can clean a node after the agent transits the node. When an agent transits a node, it can clean it, but when the node is left unguarded, it will be re-contaminated as soon as at least one of its neighbours is contaminated. The authors' focus is on asynchronous *chordal ring* networks with n nodes and chord lengths $d_1 = 1, d_2, ..., d_k$, and on *tori*. They also consider two variations of the model: one where an agent has only local knowledge, and the other in which it has "visibility". In other words, the agent can "see" the state of its neighbouring nodes. The main result is that, when the largest chord d_k is not too large, the number of agents necessary to perform the task in chordal rings does not depend on the size of the network but only on the length of the longest chord. The authors propose different algorithms for realizing the decontamination strategy. They also show a lower bound on the number of agents for the torus topology. For the complexity measures, they consider the number of moves and the time complexity of the decontamination algorithms showing that the visibility assumption allows for substantial decrease of both complexity measures. Another advantage of the *visibility model* is that agents move independently and autonomously without requiring any coordination, in other words, in an asynchronous way.

In [FHL08], the same authors studied the same decontamination idea but under the *Hypercube* topology. They introduced a new variation of the model used in [FHL07]. The variation was based on the capabilities of mobile agents in terms of *locality* (where agents can only access "local" information), *visibility* (where agents can "see" the state of their neighbours), *cloning* (where agents can create copies of themselves), and *synchronicity* (where agents can synchronize their actions). For each model, Flocchini et al designed a decontamination algorithm. For agents with locality, the decontaminating strategy is based on the use of a coordinator that serves as a leader for the other agents. The found strategy results in an optimal number of agents $\Theta\left(\frac{n}{\sqrt{\log n}}\right)$ and requires $O(n \log n)$ moves and $O(n \log n)$ time steps. For agents with visibility, with the assumption that the agents can move autonomously, the decontamination strategy is also achieved in an optimal

time complexity ($\log n$ time steps), but the number of agents increases to $\frac{n}{2}$. Finally, when the agents have the capability to clone combined with either visibility or synchronicity, the strategy reduces the move complexity, which becomes optimal, but at the expense of an increase in the number of agents.

One parameter that brings setbacks to any decontamination algorithm is the strong assumption that the host can be re-contaminated as soon as one of its neighbours is contaminated. In all the existing literature, it is usually assumed that the immunity level of a disinfected site is nil. Throughout the years researchers have attempted to weaken the hypothesis by introducing some forms of immunity after the node has been decontaminated. In [LPS06], the authors studied the Network Decontamination problem under a different model of recontamination. They consider the case when a disinfected vertex, after the cleaning agent has gone, will become re-contaminated, only if a *weak majority* of its neighbours are infected. Their work focuses on *tori* and *trees*. For these two types of graphs, they establish lower bounds on the number of moves performed by an optimal size time of agents. In addition, they design and present strategies for disinfecting *tori* and *trees* and prove that these strategies are optimal in terms of both team size (number of agents) and number of moves by the agents. The same idea of immunity is also used in [LPS07] with the authors focusing on *toroidal meshes*, graphs of vertex degree at most three (e.g., cubic graphs, binary trees), and of tree networks.

2.3. Internal Decontamination

When internal decontamination mechanisms are in place, a contaminated host can be decontaminated by itself with a pre-installed program, which is similar for each host in the network. These programs are typically based on local analysis by the host itself of the status of its neighbour. In other words, in a system with internal decontamination, all nodes are subject to a rule that is similarly applied to each node. Theoretically, this is similar to executing an existing Local-Majority mechanism. Peleg presents in [Pel02] a survey of some Local Majority Voting in graphs. The same concept has motivated researchers to use CA as the model to conduct some required decisions during the execution of the decontamination.

2.3.1. Decontamination using Cellular Automata

A Cellular Automaton consists of a grid of "cells" which are identical to each other and whose states are updated synchronously following a set of predefined rules. The rules applied to the cell itself are similar for each cell and are applied based on the state of a list of predefined neighbours. Due to that simplicity, CA have always been used to model discrete based systems, including Network Decontamination. In Network Decontamination using CAs, each cell has the possibility of having three states: *Contaminated*, *Decontaminated* and *Decontaminating*, respectively abbreviated and formally represented in the literature by the number 1, 0 and the dot "•".

2.3.2. 2D Cellular Automaton Neighbourhood

Two types of neighbourhood are omnipresent in the study of two-dimensional CAs: the von Neumann neighbourhood and the Moore neighbourhood (see Figure 2.1). Both neighbourhood have been named according to their authors, who were pioneers of the theory of CAs.

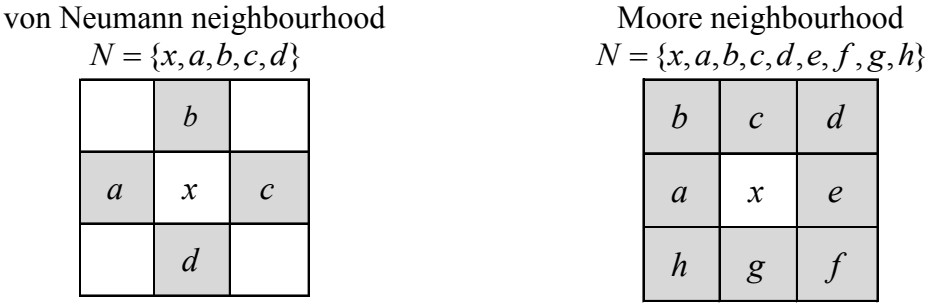


Figure 2.1: The omni standard neighbourhood: the *von Neumann* neighbourhood and the *Moore* neighbourhood.

2.3.2.1. The von Neumann neighbourhood

Assume the cell x is at coordinate (i, j) where the row index is i and j is the column index (see Figure 2.1). The von Neumann neighbourhood N consists of the output cell x and its four neighbouring cells a, b, c, d respectively at coordinate

$$(i, j-1), (i+1, j), (i, j+1), (i-1, j).$$

The usual notation seen in the literature is $N = \{x, a, b, c, d\}$

John von Neumann first used this neighbourhood to create a self-replicating machine named the *Universal Constructor*. The fundamental details of the machine were published in [Neu96]. von Neumann's design for a self-reproducing computer program is considered the world's first computer virus. The use of his neighbourhood and an extension of his *Universal Constructor* work have been extended in various applications. The most known CA application *Game of Life* uses the von Neumann neighbourhood [Gar70] and is the source of inspiration for many applications from different domain. For instance, the *Game of Life* CA is used in computer games for the generation of environments or in music for MIDI sequencing.

2.3.2.2. The Moore neighbourhood

Assume the cell x is at coordinate (i, j) where the row index is i and j is the column index (see Figure 2.1). The Moore neighbourhood N consists of the output cell x and its eight neighbouring cells, which consist of the neighbour cells in the von Neumann model plus the additional diagonal neighbours b, d, f, h respectively at coordinate

$$(i-1, j+1), (i+1, j+1), (i-1, j+1), (i-1, j-1)$$

The usual notation seen in the literature is $N = \{x, a, b, c, d, e, f, g, h\}$.

Edward F. Moore is the inventor of the Moore finite state machine (Moore FSM) and is considered an early pioneer of artificial life. He invented the Moore Neighbourhood in CA and his early work has contributed to some well-known theorems in CAs. One example is the *Garden of Eden* theorem in which the author proves that there exists a configuration that cannot appear on the lattice after one time step, regardless of the initial configuration (that is, it is a pattern that has no parents and thus can only occur at time t=0). The Moore neighbourhood has been used in the *Firing squad problem* in which the goal is to design a CA that starts with a single active cell and eventually reaches a state in which all cells are simultaneously active [MG68]. The Moore neighbourhood is currently used in various image editing software such as Adobe Photoshop as well as Macromedia's graphics software behind their image engine to manage the allocation of the boundary and edge of a digital image.

2.3.3. Basic Network Decontamination under CA

In this section, we review some results related to decontamination by 2-dimensional CA for which the global decontamination process is described by a set of CA local rules. The following results have been thoroughly developed in [Daa12]. Here we will only present and briefly discuss the local rules' results under the CA with a distinction made between the von Neumann and Moore neighbourhoods. We also make a distinction between the computational results based on a standard grid or circular topology since these types of neighbourhoods and topologies are the main cases we consider in this thesis.

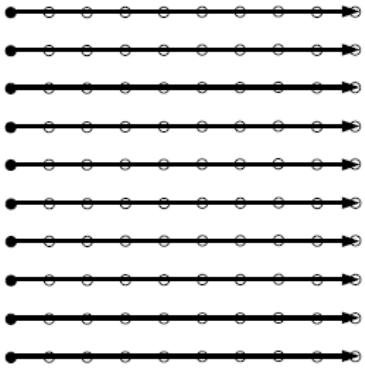
Model	Maximum Number of Decontaminating Cells k	Time Completion (Number of steps)
Basic CA with von Neumann or Moore neighbourhood	n	$\Theta(n)$
Circular CA with von Neumann or Moore neighbourhood	2n	$\Theta(n)$

Table 2.1: The computational results of the basic Network Decontamination of CAs under a von Neumann or Moore neighbourhood

Basic contamination algorithms presented in [Daa12] have used a common approach. They all obey a horizontal spread of the decontamination procedure, as opposed to the circular propagation from the center of the cellular automaton as depicted in Figure 2.4.

2.3.3.1. Horizontal flow under the von Neumann neighbourhood

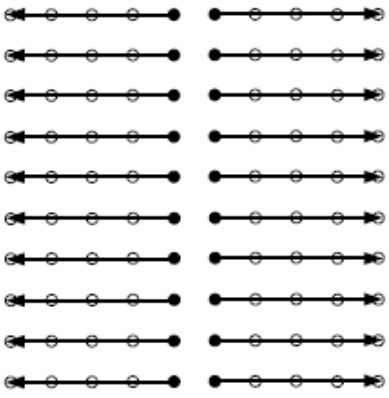
In finite two-dimensional CA under the von Neumann neighbourhood, optimal basic decontamination can be achieved using n simultaneously decontaminating cells. The process starts with n decontaminating cells aligned on one side (left) of the automata, and horizontally moving to the other side (right side). Through this process, all left cells that have been cleaned remain as such due to the protection of the current decontaminating cells on their right, preventing the left cells from being re-contaminated by the outer right cells still in a contaminated state. The process is represented in the Figure 2.2 below, displaying the set of local rules needed to perform these operations as well.



Configuration	Next State
$\{\bullet, *, *, *, *\}$	0
$\{1, \bullet, 0, 1, 1\}$	$\bullet$
$\{1, \bullet, 0, 0, 1\}$	$\bullet$
$\{1, \bullet, 1, 1, 1\}$	$\bullet$
$\{1, \bullet, 1, 1, 0\}$	$\bullet$
$\{1, \bullet, 1, 0, 1\}$	$\bullet$
$\{1, \bullet, 1, 0, 0\}$	$\bullet$

Figure 2.2: The process of decontaminating basic CAs under the von Neumann neighbourhood (source [Daa12])

In a circular CA, optimal basic decontamination can be achieved under the von Neumann neighbourhood using $2n$ simultaneously decontaminating cells. The process starts with 2 columns of n decontaminating cells aligned beside each other. The column of cells on the left side will be responsible for decontaminating the left half of the automata, and the right side of the column engages in the same operation against the right half of the CA. Each horizontal move produces a set of clean cells in the center of the CA, and the process will end when both columns encounter themselves after $\frac{n}{2}$ steps. Through this process, all cells that have been cleaned remain as such due to the protection of the current decontaminating cells that navigate either left to right or right to left. The process is depicted by the figure below and the set of local rules needed to perform these operations are also displayed.



Configuration	Next State
$\{\bullet, *, *, *, *\}$	0
$\{1, \bullet, 1, 1, 1\}$	$\bullet$
$\{1, 1, 1, \bullet, 1\}$	$\bullet$
$\{1, \bullet, 1, \bullet, 1\}$	$\bullet$

Figure 2.3: The process of decontaminating circular CAs under the von Neumann neighbourhood and its local rules (source [Daa12])

2.3.3.2. Horizontal flow under the Moore neighbourhood

Even if we increase the neighbourhood to include diagonal neighbours, (the Moore neighbourhood) we cannot obtain a better result than the von Neumann results. In fact, the lower bound on the number of simultaneously decontaminating cells is similar to the von Neumann neighbourhood both for finite and for circular CA.

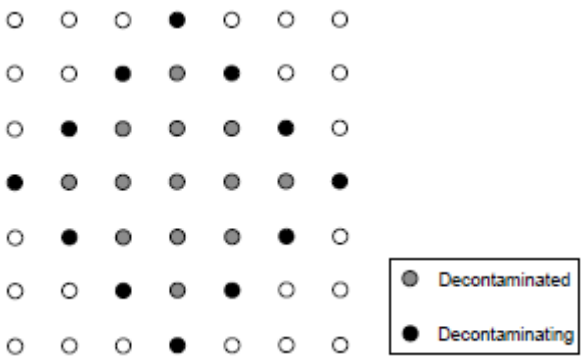


Figure 2.4: The circular propagation of an internal decontamination

2.3.4. Network Decontamination under CA with Time Immunity

The definition of Time Immunity is simple in Network Decontamination. With temporal decontamination, once a cell becomes decontaminated, it stays decontaminated for a certain amount of time ($t > 1$), called immunity time. Same as in the previous section, we review some results related to decontamination by 2D CA with Time Immunity systematically developed in [DFZ10]. In the following sub-sections, we present the global results with a distinction between the von Neumann and Moore neighbourhoods. The goal is to design a set of local rules in such a way that during the evolution of the CA, a decontaminated cell never comes into contact with a contaminated cell after its immunity time has expired.

2.3.4.1. Strategies under the von Neumann neighbourhood

Under the von Neumann neighbourhood, Figure 2.5 shows the strategy to perform the decontamination used by the algorithm. The author in [Daa12] distinguished three different scenarios for the value of the number of decontaminating cells k. For each value of k (k=1,

k=2 and *k*=4), the author propose a different strategy inspired by the same idea, to propagate a spiral flow going from the outer side of the CA into the central cell.

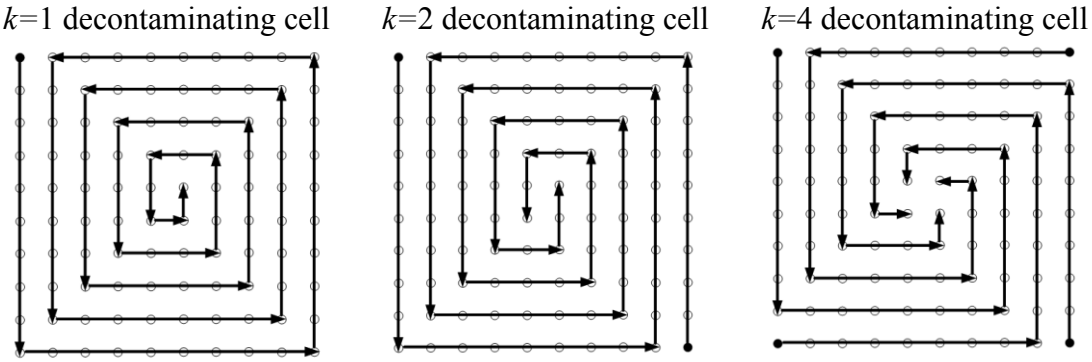


Figure 2.5: Propagation of *k* decontaminating cells with Temporal Immunity in CAs with von Neumann neighbourhood (source [DFZ10])

Various results are noted:

- with a single decontaminating cell per time unit, temporal decontamination is possible if and only if the immunity time $t \geq 4(n-1)-1$
- the case of using *k*=3 decontaminating cell is still an open problem; and
- with *k*=1, *k*=2 or *k*=4 decontaminating cells per time unit, temporal decontamination in a circular CA under the von Neumann neighbourhood is not feasible regardless of the immunity time.

A summary of the computational results under the von Neumann neighbourhood is presented in Table 2.2.

Model	Number of Decontaminating Cells k	Immunity time t
CAs with von Neumann	$k = 1,2,4$	$t \geq \frac{4}{k}(n-1)-1$ (optimal)
circular CAs with von Neumann	$k = 1,2,4$	$\varnothing$
circular CAs with von Neumann	$k < n$	$\varnothing$

Table 2.2: The computational results of the Network Decontamination under the von Neumann neighbourhood and with Time Immunity

2.3.4.2. Strategies under the Moore neighbourhood

Figure 2.6 depicts the strategy proposed by Daadaa et al during temporal decontamination under the Moore neighbourhood. With a single decontaminating cell (left image), the algorithm uses both a vertical and horizontal propagation resulting in a zig-zag propagation of the decontamination. The idea is to propagate the decontamination vertically to contaminated cells (a contaminated cell becomes decontaminating when its lower/upper neighbour, or both, are decontaminating) until they reach either another decontaminating cell or a clean one, in which case they propagate to the next column. The same approach is used when there are multiple initiators (right image).

single decontaminating cell multiple decontaminating cells

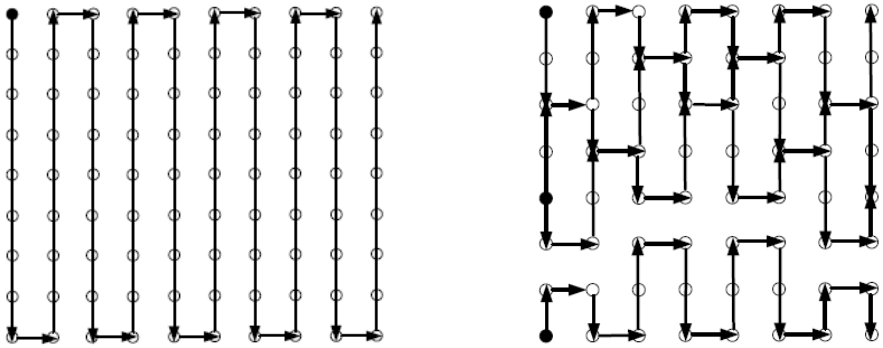


Figure 2.6: Propagation of decontaminating cells with Temporal Immunity in basic CAs under the Moore neighbourhood (source [DFZ10])

The strategy of the circular case is an extension of the finite case with a minor difference. In the circular case, initiators are placed equidistant on the first column at the maximum possible distance t where t is the immunity time. In the finite case, initiators can be placed on the first column as long as they at a distance greater than 1 from each other. The circular case strategy is shown in Figure 2.7. The author shows that with at least 2 decontaminating cells, it is possible to find a set of local rules if the immunity time is equal to a d_{max} value where d_{max} is the maximum distance between two consecutive decontaminating cells or between a decontaminating cell and a corner at a certain time.

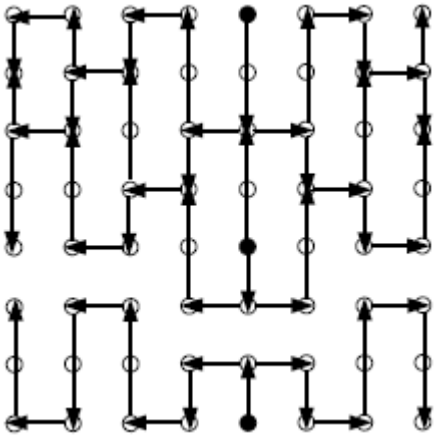


Figure 2.7: Propagation of decontaminating cells with Temporal Immunity in circular CAs under Moore neighbourhood (source [DFZ10])

Computational results using these previously shown strategies are summarized in Table 2.3 . We note that:

- with a single decontaminating cell per time unit, temporal decontamination is feasible if and only if the immunity time $t \geq 2n-1$; and
- when k>1, temporal decontamination can be achieved if $t \geq \left\lceil \frac{2n-1}{k} \right\rceil$

Model	Number of Decontaminating Cells k	Immunity time t
CAs with Moore	$k=1$	2n-1 (optimal)
CAs with Moore	k	$t \geq \left\lceil \frac{2n-1}{k} \right\rceil$
circular CAs with Moore	$k \geq 2$	$t=d_{max}$

Table 2.3: The computational results of the Network Decontamination under the Moore neighbourhood and with Time Immunity

2.4. Theory of Cellular Automata

2.4.1. Relevancy

From the days of von Neumann and Ulam who first proposed the concept of CA [Neu51], to the recent list of surveys ([Kar05], [Mit96]), the simple structure of CAs has

attracted researchers from various disciplines. It has been subjected to rigorous mathematical and physical analysis for the last fifty years and its application has been proposed in different branches of science –physical, biology, artificial intelligence, and social. A large number of research papers are published every year complemented by specialized conferences. Indeed, researchers from diverse domains have identified CA dynamics with problems in their own fields. For example, CAs have been used to model biological systems [Awa08]. They are used to model molecular systems in chemistry applications [Pac86]. In physics, CAs is used in various applications that cover the study of dynamical systems including the interaction of particles. In computer science, CAs have been employed to model the von Neumann (self-reproducing) machines [Neu96] and in parallel computing architecture [Wol88]. In social sciences, it is used to model social interaction and understand group formation. In the past few years, they have also been used to provide some base models in Network Decontamination problems [DFZ10], [DFZ11], [Qiu07].

Due to their relevancy, CAs have been studied for two important aspects, their computational complexity [LM08],[KVZ09],[Mit96],[LM10] and their dynamical behaviour [ADF07],[ADF09],[Sab08],[DLFM09].

2.4.2. Properties

In general, it is extremely difficult to determine the overall behavior of a CA by examining its local transition rules. The study of various properties of a CA are elaborated in [ADF07], [ADF09] and [Kar90]. In [Kar05], Karri presents a complete survey on various research focused on some theoretical aspects of CA. In particular, the article discusses classical and new results on some well-known properties of CAs including reversibility, conservation laws, and decidability questions. The article also discusses some universality and topological dynamics of CAs. An important result regarding reversibility is elaborated in [Kar90] by the same author. The problem of whether a given two- or higher-dimensional CA is reversible is shown by the author to be algorithmically un-decidable. (A CA is reversible if there exists another CA with both evolution functions inverse of each other. In other words, a CA has an inverse automata, that is, another CA that makes the system retrace its steps backwards in time). However, the same problem is known to be decidable for one-dimensional automata.

Another researcher who has also dedicated a considerable amount of research on CAs is Stephen Wolfram. The author has numerous papers, technical reports and books on CAs ([Wol02], [Wol94], [Wol84], [Wol88]). He offers a survey of CAs in contemporary use in his book "New Kind of Science" [Wol02], including the study of a 3D CA. Some of Wolfram's research is dedicated to the classification of CAs, proposing 4 different classes that can be divided depending on the behavior of their space-time diagram. The first class of CAs contains the automata that evolve to a unique and homogenous state after a finite transient. In this class, the randomness initiated in the initial pattern disappears. In the second class of CAs are those whose evolution leads to a set of separated simple but periodic and oscillating structures. In the third class are CAs whose evolution leads to chaotic (non periodic) space-time patterns and all initial patterns evolve in a pseudo-random manner. The last class contains CAs that evolve to more complex patterns with the formation of local structures that are able to survive for long periods of time.

2.4.3. Applications using Cellular Automata

CAs have been used in many different systems including Quantum Physics, Cryptography and Video Games. It is also used in various different fields of Computer Science such as Pattern recognition algorithms, parallel computing, image processing and more. Their utility in Network Decontamination is recent.

The most popular application using CAs is *Game of Life* invented by John Conway [Gar70]. It is a two-dimensional CA where each cell can take two values ("0" or "1", but we talk about "living" or "dead"), and where its future state is determined by its current status and the number of living among the eight cells that surround it. If the cell is alive and surrounded by two or three living cells, it remains alive for the next generation, otherwise it dies. If the cell is dead and surrounded by exactly three living cells, it reaches the next generation (see Figure 2.8)

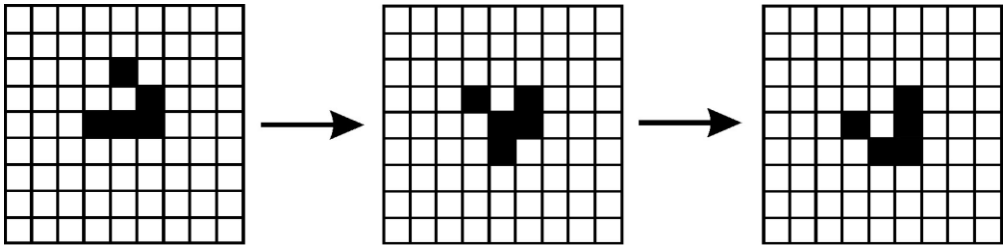


Figure 2.8: A partial execution of Conway's *Game of life*

Brian's Brain is a CA invented by Brian Silverman. It resembles the *Game of Life*, except that the cells have three states instead of just two states. The analogy to a brain is such that the cells are viewed as neurons with three states possible. First, they can be off but ready to fire. Second, they can be in a firing state, and third, they can be refractory after firing. The addition of the third state (refractory) dramatically changes the results comparison.There are numerous applications that also use CA as a backbone, such as *Langton's ant*, *Nobili CA*, and *Codd*'s CA. A survey of these existing applications can be retrieved in [Mit96] in which the author study their computational properties.

2.4.4. A selected review of simulation software

It is not very difficult to program the basic needs of a CA simulator and the web is full of achievements more or less successful. Here, we give a selective review of software that can simulate the execution of an arbitrary CA.

One influential tool that deals with CAs is Wolfram's *Mathematica* [WMS88]. The commercial software is now at its 9.0 version and is also available with a Student Edition. Note that the software is not only dedicated to CAs but to mathematics in general and there has a considerable repository of mathematical formulas. With respect its functionality, it contains a visualization tool to visualize any arbitrary CA. Creation of CAs and their rules are based on interaction with the software with a protocol similar to a programming language which might require some substantial user training.

JCASim[JCA00] is CA simulation system built in Java offered as a standalone application or as an applet. CAs data are specified in Java or in Compiler Description Language (CDL) and is interactive. It supports CAs of various dimensions (1D, 2D and 3D) and supports various neighbourhoods and boundary conditions. Original functionalities have

been based on the book "Simulation with CA" of J. R. Weimar published in 1998 and updated in 2002.

MCell [Mce99] was built in the late 90's by Wojtowicz. It offers simulation functionalities and a rich gallery of 300+ automata rules. Deployed as a Java applet or as a desktop application, it is open for extensions in which Programmers can add new rules by programming external Dlls.

Golly [Gol00] is an open source application that was originally built to explore Conway's game of life. It has received at least the contribution of several programmers and therefore contains a vast range of functionality. It can support up to 256 states and has most known CA in its libraries. One special functionality is its ability to plug in new rules from a rule table and a rule Tree algorithm. It also has advanced images handling as it can read common graphic formats (bmp, gif, tiff). It also possesses clipboard functionality for some copy/pasting functionality.

The web abounds much more simulation Cellular Automaton software than the ones listed in this section. Each software has its own scheme to present the simulation and often contains some functionality connected to a specific need of the author. Among others, *FiatLux* [Fia01] of Nazim Fates contains functionality from his research on the robustness of models whose aim is to study the synchronicity in the cell as well as the study of the grid topology. In this same line of thought, John Walker and Rudy Rucker have created *CelLab* [Cel88] for their experimentations related to graphics and design, and originally to complement functionalities required by the popular Autocad software, a computer-aided design (CAD / CAM) graphics program. The software mainly deals with 2D CAs and allows the user to explore it. Each user can design his own rule by writing short programs in Java and see the evolution on the screen. It contains considerable amount of functionalities including its ability to simulate heat flow, diffusion of gases, annealing of metal, chemical reactions and eco systems of artificial life, which have contributed to its popularity and often used as backbones of others simulation software.

Chapter 3

The Model

In this chapter, we are introducing the model used in our research. We start by enunciating a formal definition of a Cellular Automaton which we have briefly introduced in *Chapter 1* as a cellular space where cells change their state synchronously according to local rules. Then, we present the concise mapping from the network decontamination problem into the concept of a CA execution. We introduce two new concepts that complement the standard CA model: *Visibility Hop* and *Contamination Distance*. We give the impact of these two new notions on the two ubiquitous von Neumann and Moore neighbourhood. Then, we present the various assumptions considered in this thesis including the contamination model and the immunity model. We conclude the chapter by enunciating the notation used in the upcoming chapters, including a new visual notation of transition rules that intends to bring more clarity to the understanding of the rule's objective.

3.1. The Cellular Automaton model

Let us formally define a Cellular Automaton and its properties:

Definition 3.1. *Formally, a Cellular Automaton is a quadruple* (Z^d, S, N, f) *where*

- *d is its dimension so* Z^d *is its discrete space of dimension d;*
- S *is a finite set whose elements are the cell states;*
- $N \subseteq Z^d$ *is its neighbourhood;*
- $f : S^n \to S$ *is its local transition rule where n is the neighbourhood size.*

Definition 3.2. *A configuration* $c^t : Z^d \to S$ *is the attribution of a state to each cell of the CA at a specific time t.*

3.1.1. 2D CA as State space

Induced from *Definition 3.1.*, a two-dimension Cellular Automaton, simply abbreviated by 2D CA, is described by a quadruple (Z^2, S, N, f).

The future state of any cell x at time t+1 is generally induced by the state of the cells surrounding it at the previous time t. Formally, $S(x)$ at time $t+1$ is defined by a function on $N(x)$ at time t. The composition of $N(x)$ (and therefore its cardinality) relies on the cells which are visible to x. The use of a CA for solving the problem of decontamination of a network is motivated by two simple facts. First, the possible states of nodes in the network are represented by the transition states of the CA. Second, the algorithm for the Network Decontamination is defined by the collection of transition rules of the CA.

3.1.2. Network Host state as Transition State

In Network Decontamination using CAs, the state space of the CA has three states: *Contaminated*, *Decontaminating* and *Decontaminated*, respectively denoted in the current literature as 1 , • and 0. Thus, $S = \{0,1,\bullet\}$.

A host in the network that is infected by a virus is represented by a CA cell which is in the contaminated state. When the antivirus program is executed on the host, the cell is in a decontaminating state. When the antiviral program has been successfully executed, the CA is in a decontaminated state. The hypothesis is that every cell is considered *Contaminated* and the goal is to reach a state where all cells are simultaneously in a *Decontaminated* state. At time t=0, the given initial configuration is altered by the pre-selection of a finite list of cells that will be chosen to run the decontaminating program (and thus be in a *Decontaminating* state). Then, cell states are synchronously updated at each time step by the local transition rule applied to their neighbourhoods. Each cell is expected to transition from the contaminated state into decontaminating to be decontaminated and remain as such. A formal definition of the process is presented in the next subsection.

In our study, we will define a state called *absent*, which is not a transition state but rather a neighbouring state that denotes the absence of a neighbour. The neighbouring state *absent* has been introduced in our study for computational reasons and the definition is more meaningful when a cell within the grid can have its neighbour removed from the topology for investigation purposes. We mainly use the *absent* state when we investigate the removal/addition of a cell inside the CA that can affect the minimum number of decontaminating cells needed. This feature is implemented in our CA editor and simulator for network decontamination, as discussed in Chapter 7. However, the introduction of this

new state brings certain dilemmas to the state of the neighbouring cells that lie on the border of the CA. To be consistent with the definition, a cell on the border of the automata can see its outer neighbour as *absent* or *decontaminated*, the latter being the standard used in current literature. For instance, consider the top-left cell of a CA under the von Neumann neighbourhood, which does not have a left neighbour or a top neighbour. In current literature, the *absent* neighbour of cells on the border of the CA is considered a "decontaminated" cell, therefore, the cell sees both of its left and top neighbours as being in a "decontaminated" state rather than "absent" according to our definition. To solve the matter, unless it is explicitly specified, our effort will be focused first on the search for decontamination algorithms that do not differentiate the neighbouring state *absent* from the transition state *decontaminated*.

Regarding the terms used in the remainder of the thesis, we will use the term *dirty* and *contaminated* interchangeably to denote that the host is contaminated. We will also use the word *clean* to denote that the cell is in a *decontaminated* state.

3.1.3. Decontamination algorithms as Cellular Automaton Transition Rules

In Network Decontamination using a 2D CA, the configuration C is then the resulting map $c^t : \mathrm{Z}^2 \rightarrow \{0,1,\bullet\}$ at any time t.

At time t=0 of the process, every cell is considered "contaminated". The goal is to reach a state where all cells are simultaneously in a "decontaminated" state. Formally, given an initial configuration c^0 , that is a map $c^0 : \mathrm{Z}^2 \rightarrow \{0,1,\bullet\}$, cell states are synchronously updated at each time step by the local transition rule applied to their neighbourhood. Let $x_{i,j}^t$ denote the state of cell (i,j) at time t, and $N^t(i,j)$ the states of the neighbouring cells of (i,j). In the case of a von Neumann neighbourhood, $N^t(i,j) = x_{i-1,j}^t, x_{i,j+1}^t, x_{i+1,j}^t, x_{i,j-1}^t$ and the system behaviour can be described as follows:

1. $x_{i,j}^{t+1} = f(N^t(i,j))$
2. If $(x_{i-1,j}^t = 1) \vee (x_{i,j+1}^t = 1) \vee (x_{i+1,j}^t = 1) \vee (x_{i,j-1}^t = 1)$ then $x_{i,j}^{t+1} = 1$

The first point indicates the general law of a state change by following the local rule of the CA. The second point states that a node becomes contaminated if just one of the neighbouring cells is contaminated.

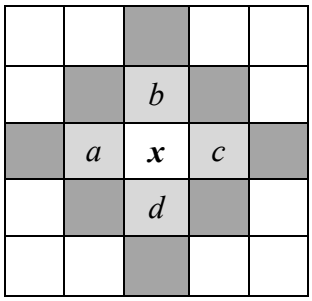
3.1.4. Conflicting rules and Non-determinism

In deterministic Cellular Automata, the update rules have no probabilistic component: for a given neighbourhood configuration, the updated cell state is always the same. In this thesis, only deterministic transition rules are considered and designed. Moreover, rules that conflicts are forbidden: two or several rules are in conflict when the updated cell state is different for the same neighbourhood configuration. That is, the previously defined $f : S^n \rightarrow S$ has to be a function.

3.2. New dimensions to the definition of a Cellular Automaton radius

Definition 3.3 *The radius r of a 2D CA is a positive integer* $(r \in N^*)$ *that designates the maximum distance between a cell and its neighbouring cells.*

The von Neumann neighbourhood when *r*=2



The Moore neighbourhood when *r*=2

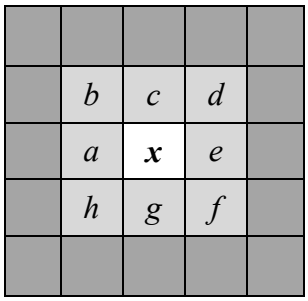


Figure 3.1: A representation of the von Neumann and Moore neighbourhood when the *radius* distance is equal to 2.

The Figure 3.1 highlights the neighbourhood of a cell under the von Neumann and Moore neighbourhood when *r*=2. The original neighbours located at *r*=1 are the ones having a label. New neighbours located at *r*=2 are highlighted in a dark gray background. These new neighbours are constructed recursively according to the definition of the original neighbourhood.

3.2.1. The Visibility Hop *Vh*

Definition 3.4 *In a finite 2D CA consisting of a model of neighbourhood N, the Visibility Hop Vh* ($Vh \in N^*$) *is a concept in which a cell "can see" the state of a neighbour if and only if the neighbouring cell is located within a radius* $r \leq Vh$.

In general, the current cell only "sees" the state of its direct neighbours which are located at radius 1. In our study, we will use the von Neumann and Moore neighbourhood schemes as a base on which to introduce this new metric. Of course, the concept of "seeing" the state of a larger surrounding induces that these states can now be inserted into transition rules. Our goal is to add this new dimension to the concept of neighbourhood in order to find new strategies of decontamination and to improve computational results with respect to some complexity measures that we introduce in upcoming sections of this chapter. The idea is to allow the current cell to have more knowledge about its surrounding neighbourhood of a predefined fixed radius distance denoted *Visibility Hop* at time *t*. We believe that that this knowledge can be used to make better decisions about what transition state the current cell needs to achieve at time t+1. Greater visibility is easily constructed by simple recursive transitivity of the neighbourhood at each cell with respect to Vh=1, that is, the cell sees its direct neighbour and the neighbours of each neighbour recursively.

Our goals are to investigate this new metric with respect to some existing decontamination algorithms and to develop new heuristics under this new scheme. One will note that the original von Neumann and Moore neighbourhoods can be seen as having a Visibility Hop distance equal to 1.

3.2.2. The Contamination Distance *Cd*

Definition 3.5 *In a finite 2D CA consisting of a model of neighbourhood N, the Contamination Distance Cd is a positive integer* ($Cd \in N^*$) *in which a clean cell gets contaminated at time t+1 if it was located at radius* $r \leq Cd$ *of a contaminated cell at time t.*

Generally, if a cell x is decontaminated at time t but is in direct contact with a contaminated cell y, then x will also be contaminated at time t+1. In [LPS06], a slight variation has been introduced where the cell only gets contaminated if the majority of its direct neighbours are contaminated. In both cases, it is worth mentioning that only direct

neighbours are considered to be a factor of re-contamination. Here in our research, like the Visibility Hop, we also point out the existence of a Contamination Distance in which a cell can be contaminated if its neighbour (at a radius distance *d* greater than 1) is contaminated.

3.2.3. Relationship between *Vh* and *Cd*

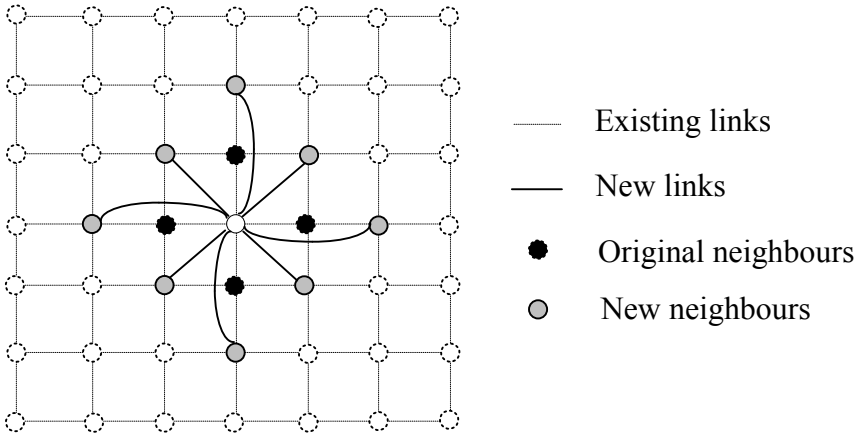


Figure 3.2: New edges inserted resulting to a new graph topology when *Vh*=2 under the von Neumann neighbourhood.

A greater visibility in the neighborhood could imply two things. First, if we assume that the central node can consult directly the state of the neighbours which are in a distant radius $r>1$, then this implies that a physical network connection exists between the central node and its new neighbours. Therefore, this implies that the CA no longer represents a normal grid but rather a new and denser network in which a cell can have more connections as stated by Figure 3.2. Thus, we face a new network topology. Secondly however, another hypothesis is that the network topology still is a grid but that greater visibility just insinuate that the central node possibly have knowledge of the state of its distant neighbors by the intermediary of nearest neighbors from successive and transitive communication. A direct consequence is that a *step of decontamination* becomes equivalent of a series of steps that are required for each cell to gather the states of all its distant neighbours. We note however that this situation can pose a problem because there is no genuine guarantee that the information that reaches the central node is not erroneous since the intermediate nodes might be contaminated and alter the data that they receive. Indeed, it is a very realistic assumption that some contaminated nodes may choose to taint the information, manner similar to Byzantine faults in a distributed network. Consequently, if this second case holds, our

assumption is that communicated data within the network are not altered even if they are originated from contaminated sites.

The addition of *Vh* and *Cd* also bring new dynamics to the decontamination process:

- Case $Vh = Cd$. This is the basic decontamination process in which there is no distinction between the definition of *Vh*, *Cd* and the radius *r*. A node sees a neighborhood of radius *r*, but can also be contaminated by these same neighbors.
- Case $Vh > Cd$. Even if every node has a larger visibility, only a specific set of nodes located in the surrounding area can only contaminate the central node.
- Case $Vh < Cd$. This is a stronger condition because even if a node sees just a smaller locality of neighborhood, they may still be contaminated by further distant nodes. Note that even under this case, we present in future Chapters that finding decontamination algorithms is still feasible.

3.3. Recontamination and Immunity model

3.3.1. The contamination model

Viruses and faults are usually spread within the network environment from an infected site to a neighbouring site. This process known as *network contamination* typically depends on the behaviour of the infected site. In the *full-spread* contamination model, a clean cell can be *contaminated or re-contaminated* at time *t* as soon as a single neighbour is contaminated at time *t*-1. This is also referred to in some literature as *contamination by contact*. Obviously, this assumption rule is a key factor in the complexity of the decontamination problem, and plays an important role in finding a good decontamination strategy. The full-spread contamination model has been used in [FHL08], [LP09], [BFFS02] and [FNS05]. On the other hand, different contamination models exist where the fault propagation is relaxed, such as in the *selective spread* model where faults only propagate to sites that are susceptible and only affect neighbouring nodes that are vulnerable. For instance, in [LPS06] and [KP00], the node is only vulnerable to contamination if a majority of its neighbors are faulty, or if *m* or more of its neighbours are infected, where $m \geq 1$ is a threshold parameter of the system [FLPS13]. These different contamination conditions are called *contamination rules*. This

idea which shows realistic practical assumptions has again been considered by researchers by Luccio et al in [LPS07]. In this thesis, we consider the full spread contamination model

3.3.2. The re-contamination model

A decontamination strategy is said to be "monotone" if, once a node becomes decontaminated, it does not become contaminated ever again. In most instances of the decontamination problem, it is known that optimal monotone strategies exist. In our study, we focus only on monotone strategies.

3.3.3. The immunity model

The definition of *Immunity* refers to the condition of a cell being *immune* from any re-contamination dictated by the contamination rules. The most natural form of immunity arises from the converse definition of the contamination rule itself. Like in [LPS06], [LPS07], and [KP00], the site is immune to contamination only when a minority of its neighbors are contaminated. We consider two forms of Immunity:

- *Processing Immunity*. It is assumed that a site processing an anti-virus program, in other words in a *decontaminating* state, is immune to re-contamination.
- *Temporal Immunity*. Another form of immunity has been introduced by Flocchini et al. in [FMS08] when authors studied strategies to decontaminate tree networks. A team of mobile agent is able to decontaminate any contaminated node it visits; once the cleaner leaves the node, the infected note is immune for $t \geq 0$ time units. In [Daa12] and [DFZ10], Daadaa et al. uses similar time based immunity called *temporal immunity* that we denote as *It*. According to Daadaa et al's definition, a clean cell always remains "clean" for a predefined time *It*=t (or a predefined number of steps in a synchronous system) regardless of the states of its neighbours. The formal definition of the decontamination process under some *Immunity* time is taken from [Daa12] (see below) and complements the formal definition of the decontamination process presented in previous section. Let $s_{i,j}^{t}$ be the immunity time of a decontaminated cell located at position (i, j) at time t. Again, taking the von Neumann neighbourhood definition as an example, the behaviour of the system from time t to time $t+1$ is described as:

1. $x_{i,j}^{t+1} = f(N^t(i,j))$

2. a) if $x_{i,j}^{t+1} = x_{i,j}^{t} = 0$. Let $s_{i,j}^{t} = It$

   b) if $s_{i,j}^{t} > 0$ then $s_{i,j}^{t+1} = It - 1$.

   c) if $s_{i,j}^{t} = 0$ and $((x_{i-1,j}^{t} = 1) \vee (x_{i,j+1}^{t} = 1) \vee (x_{i+1,j}^{t} = 1) \vee (x_{i,j-1}^{t} = 1)$ then $x_{i,j}^{t+1} = 1$.

The first point is similar to the case of a normal decontamination process without an immunity time, that is, the law of a state change following the local rule of the CA. The second point states the degradation of the decontamination state, that is, the node become less and less immune to contamination and eventually becomes contaminated if at least one of its neighbours is contaminated. One will note that a) and b) are the specifications added from the immunity-free decontamination process formalization.

In this thesis, we first investigate decontamination heuristics within the *full-spread* contamination model (a contaminated site will spread its virus to all its neighbors) and in which the immunity level of a decontaminated cell is nil (a cell is infected as soon as it is in contact with a contaminated cell). Second, we study a selective spread contamination model based on *temporal immunity* (as previously defined). We show that we can produce interesting decontamination algorithms that combine Time Immunity and the Visibility Hop/Contamination Distance just introduced in this research.

3.4. Terms and Notations

Throughout the thesis, we consider few abbreviations. The term *Cellular Automaton* is often abbreviated as CA and the plural term Cellular Automata as CAs. The Neighbour *Visibility Hop* is abbreviated as *Vh.* The *Contamination Distance* is abbreviated as *Cd.* The *Immunity Time* is abbreviated as *It*.

3.4.1. Transition state notation and representation in grayscale/color mode

	Traditional notation in current literature (e.g. for proofs)	Representation in figures using Grayscale mode	Representation in figures using Color mode
Contaminated	1	○	●
Decontaminating	●	●	●
Decontaminated	0	●	●
Generic	*		○
Absent	N/A	x	●

Table 3.1: Various notations of the transition state of a CA in current literature and in this thesis.

In this thesis, we intermittently use notation and representation as listed in Table 3.1 depending on its relevancy. The current literature generally uses grayscale mode to represent transition states. In this thesis, we add a representation of the neighbourhood in colour mode as these rules are provided by the research tool that we have implemented and presented in Chapter 7. Therefore, with respect to the various states of a cell in a CA, the following notations are used in this thesis.

- A *Contaminated* (also referred to as *Dirty*) state is denoted by the symbol 1 in theoretical explanations. Within a CA figure and some listings of decontamination rules, it will be represented by a circle with an empty background ○ in a grayscale mode or a red circle ● in a color mode.
- A *Decontaminated* (also referred to as *Clean*) state is denoted by the symbol 0 in theoretical explanations. Within a CA figure and some listings of decontamination rules (see upcoming sections), it will be represented by a circle with a grey background ● in grayscale mode or a green circle ● in a color mode.
- A *Decontaminating* state is denoted by a circle with a black background both in theoretical explanations and within a grayscale mode figure ●, but in a blue color ● in a color mode.
- A generic *arbitrary* state is denoted by * in theoretical explanations and in grayscale figures but as an empty circle in color mode.

- An *Absent* node is denoted by X in figures in grayscale mode and with a black circle ● in color mode.

A summary of these notations is listed in Table 3.1.

3.4.2. New Neighbourhood configuration notation

We reiterate that the *Neighbourhood Configuration* is denoted by $N = \{x, a, b, c, d\}$ and $N = \{x, a, b, c, d, e, f, g, h\}$ respectively under the von Neumann and Moore neighbourhoods when *Vh*=1. We intermittently call it *direct neighbourhood*.

In this thesis, we introduce a new notation when *Vh*>1. In the case of basic decontamination with *Vh*=1, each transition rule involves only 4 cells in the neighbourhood configuration under von Neumann neighbourhood and 8 cells under the Moore neighbourhood. With the introduction of the concept of *Vh*, the number of transition rules increases considerably. For instance, when *Vh*=2, 8 new cells are added to the von Neumann neighbourhood so each new rule has the possibility to contain up to 12 cells (Figure 3.1). In the case of the Moore neighbourhood, this addition is lined with 16 new cells and, consequently, a transition rule can involve up to 24 cells. The situation of substantial growth in the number of cells within the neighbourhood configuration may lead to confusion when using the traditional notation, that is,

- $N = \{x, a, b, c, d, ..., l\}$ under the von Neumann neighbourhood; and
- $N = \{x, a, b, c, d, e, f, g, h, ..., x\}$ for the Moore neighbourhood.

This could confuse the reader in understanding the logic behind the rule itself. This potential confusion prompted us to introduce a new notation of the configuration of the neighbourhood whose purpose is mainly to provide greater clarity about the neighbourhood configuration. This new notation is based on the "visual" configuration of the neighbouring cells involved within the rules. A sample of this notation is depicted in Figure 3.3. Another considerable advantage is to give the reader a faster understanding of the dynamics of the transition rule embedding the neighourhood (e.g. a left-to-right flow or a diagonal flow etc). We have two variations of the notations: the Grayscale mode and the Color mode. The latter mode were introduced as we used our research software tool (which we introduce in Chapter 7) to import transition rules.

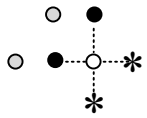
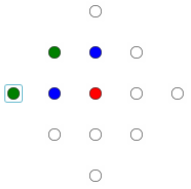
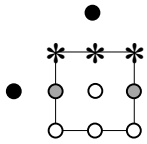
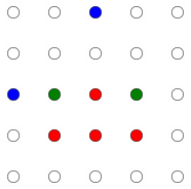
Neighbourhood	*Grayscale Mode*	*Color Mode*
Von Neumann	(a) 	(c) 
Moore	(b) 	(d) 

Figure 3.3: A sample of the new notation of a transition rule using a grayscale or color visual representation of the neighbourhood.

The grayscale mode also flags the reader by noticing that the configuration follows a von Neumann representation by having the concerned inner cell surrounded by a cross (see Figure 3.3*a*) and in the case of a Moore neighbourhood by a square (see Figure 3.3*b*). Within the notation, direct neighbours are always represented. (The neighbours of a visibility of 1 are the ones on the extremity of the cross in Figure 3.3a and the ones lying on the square in Figure 3.3b). In both notations, the neighbour's state of distance of 2 or greater is only represented if the state matters. In other words, we only write the cell state of the neighbour at distance greater than 1 if the state is other than generic, and missing cells can be of any state. For instance,

- Figure 3.3a stipulates that if at time t, the concerned contaminated cell has both of its left and top neighbours in a decontaminating state and its left and top neighbour of distance 2 in a decontaminated state then it transits to a decontaminating state at time t+1.
- Figure 3.3b stipulates that the concerned contaminated cell transits into a decontaminating state at time t+1 if at time t it respects the following conditions: its left and right neighbours are in a clean state; its bottom neighbour is in a dirty state; and both of its left and top neighbours of distance 2 in are in a decontaminating state, regardless of all its three direct top neighbours.

The colour mode includes all cells in the neighbourhood in which state obeys the configuration presented in Table 3.1.

3.5. Complexity measures

- *Maximum Decontaminating cells* and *Average Decontaminating cells***.** The first metric we will use to judge the optimality of the decontamination algorithm is the maximum number of decontaminating cells at any given time. The second metric is the average number of decontaminating cells at each step during the entire decontamination process.
- *Decontamination time***.** Since the decontamination is done synchronously among all cells, the time is expressed by the number of steps or the number of rounds that the cells run the local rules until the CA is fully decontaminated.
- *Immunity time.* The minimization of the value of the immunity time is also considered.

Chapter 4

Decontamination with Visibility Hop and Contamination Distance

In this chapter, we introduce the concepts of *Visibility Hop* and *Contamination Distance* by analyzing their effects on known basic decontamination algorithms. Our goal is to elaborate what the new concept of Visibility Hop brings to the network decontamination problem. For instance, we would like to know if changing the visibility of every node will relax or complicate the decontamination problem, and if so, under what conditions and which neighbourhood configuration. We look at known basic decontamination strategies for CAs and the impact of having a greater Visibility Hop. We consider the grid (or mesh) and its circular version when Vh=1, which is naturally described by a finite 2-dimensional three state CA. The topology inferred by the the 2-dimensional CA when Vh>1, as presented in Chapter 3, is also taken in consideration.

4.1. General Concept

Definition 4.1 *In a 2D CA, a Surface Block is a set of cells such that:*

1. *All cells have the same state*
2. *All cells of the surface block constitute a connected sub-graph of the CA (i.e. they are contiguous).*

Any Network Decontamination strategy without immunity conceptually splits the network topology in 3 distinctive surface blocks as depicted by the Figure 4.1 :

- the block set *C* which forms the contaminated cells;
- the block set *D* which forms the decontaminated cells; and
- the block set *T* which is a transition set between the contaminated state and the decontaminated state.

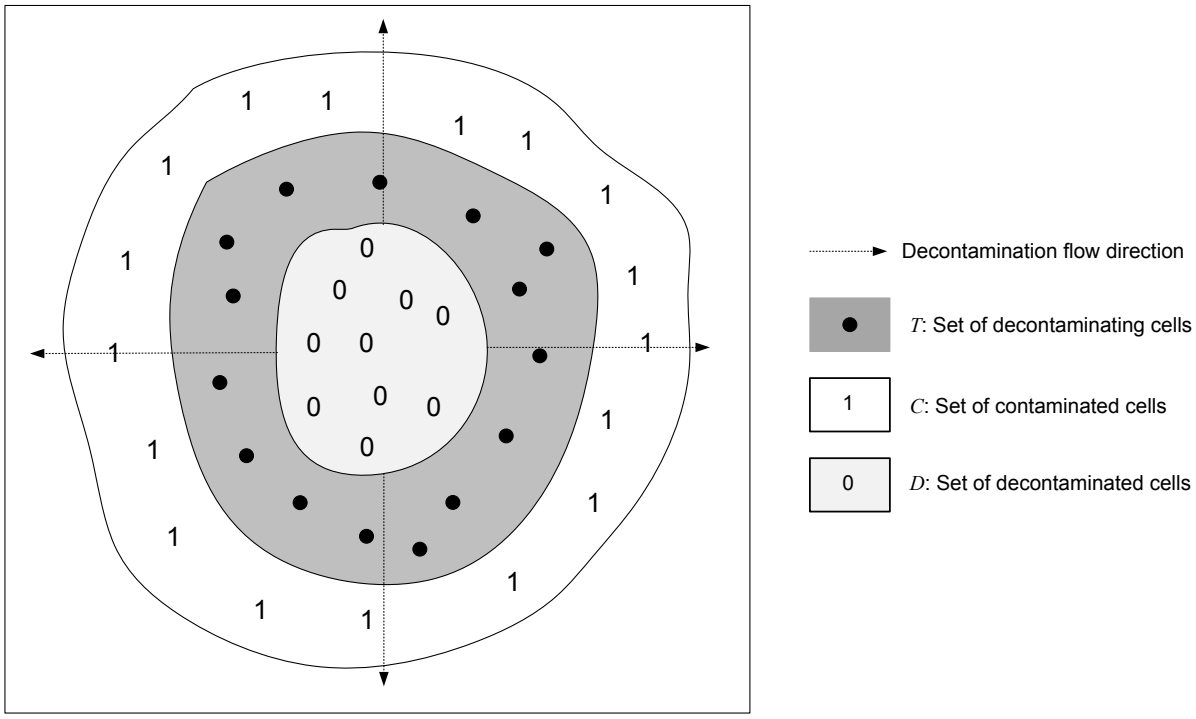


Figure 4.1: The decontamination block

The execution of the decontamination algorithm itself can be represented by the evolution of the cardinality of these three distinct sets. At time t=0 in the beginning of the process, the network configuration is represented by the full set C and both D and T are empty. At time t=1, when the algorithm starts, a few cells from C are chosen to compose the first elements of T. These chosen cells, called the initiators, are not arbitrarily but instead specifically chosen based on the decontamination flow generated by the decontamination strategy. Initiators are considered an integral part of the decontamination algorithm itself. At time t=2 and until the end of the process, local transition rules are applied to each cell. Since we only consider monotone decontamination algorithms, it is expected that the cardinality of C will decrease, while the cardinality of D will increase. The process ends when both T and C are empty and the network configuration is represented by the full set D.

According to our assessment criteria for the effectiveness of the algorithm, minimizing the time of decontamination is equivalent to finding the most efficient way to transit from the full set C to the full set D through the set T. Also, minimizing the number of decontaminating cells is similar to minimizing the cardinality of the set T at any time t

during the decontamination process. The efficiency of the strategy depends, among other factors, on:

- the decontamination flow;
- the ability to find the most efficient cut to propagate the flow;
- the choice of initiators that propagate the flow;
- the ability to control the size of T within the propagation flow; and
- the time taken by the whole decontamination process.

Let $G = (V, E)$ be a graph. Let us recall some standard graph definitions. The number of edges in a path between two vertices defines its length. The distance between two vertices x and y, denoted $d(x, y)$ is the length of the shortest path between x and y.

The distance between two disjoint sets of vertices A and B, denoted by $d(A, B)$ is defined as

$$d(A, B) = \min \{ d(x, y) : x \text{ is in } A \text{ and } y \text{ is in } B \}$$

A vertex separator S is a collection of vertices, the removal of which would disconnect the remaining graph. For instance, the set T is a vertex separator. The width of a vertex separator is defined as $d(A, B)$ -1, where A and B are two disjoint components when we remove the vertex separator from the graph.

Observation 4.1. *During the execution of a decontamination algorithm, at any time t and without immunity, if* $C \neq \emptyset$ *and* $D \neq \emptyset$ *then necessarily* $T \neq \emptyset$.

In other words C and D cannot share the same border when there is no Time Immunity, otherwise, cells in C will be contaminated by cells in D. This situation will induce the following observation on the width of T.

Observation 4.2. *During the execution of a decontamination algorithm and under the full-spread contamination rules, at any time t and without immunity, if* $C \neq \emptyset$ *and* $D \neq \emptyset$ *then necessarily the width of any block set T is, at least, Cd.*

Proof:

If the width of T is less than *Cd,* then cells in D can be reached by cells of C.

There are few more observations that can also be noted. The set *T* has more qualifications than a transition set between the contaminated state and the decontaminated state. Firstly, its key role is to serve as a "Protection" of the cells in *D* from being contaminated by cells from *C*. Secondly, the set *T* is not necessarily a closed and connected set only composed of decontaminating cells. Thirdly, the size and width of *T* can vary during the decontamination process.

Definition 4.2 *In network decontamination CA, a decontamination algorithm is qualified as "monotone" when the anti-virus is run only once at each node, that is, once a node is disinfected, we must guarantee that, regardless of its protection level, the node will stay clean forever.*

In Graph Search, LaPaugh [Lap93] has proven that for every graph *G*, there is always a monotone search strategy that uses $s(G)$ searchers.

Corollary 4.1 *When the number of decontaminating cells is fixed and constant (that is, the number does not change at each step of the decontamination), any monotone strategy is time-optimal.*

Proof: Assume the CA has *m* rows and *n* columns and the chosen number of decontaminating cells for each step is *c*. The disinfection process cannot be accomplished within a time $t < \frac{m * n}{c}$ otherwise a step of decontamination would have taken less than c decontaminating cells.

For all upcoming sections of this chapter, we revisit these basic decontamination algorithms known as the "left-to-right" or "horizontal flow" but under different *Visibility Hop* and *Contamination Distance* assumptions. Our basic question is whether a larger visibility will lead to better and more efficient strategies than the optimal ones for *Vh*=1. Also, we keep the same hypothesis regarding the immunity time being null (*It*=0). Since all these algorithms act in a horizontal flow, we only need the von Neumann neighbourhood to

achieve optimality. This is due to the fact that the needed neighbours are the ones located on the left or right of the concerned cell, and using the Moore neighbourhood will not add any efficiency to these algorithms.

4.2. Basic Visibility Hop *Vh*=1

4.2.1. Contamination distance *Cd*=1

In [Daa12], the problem of the case when there is no immunity (i.e., *It*=0), the Contamination Distance is 1 (i.e., *Cd*=1) and the Visibility Hop is 1 (i.e., *Vh*=1) is studied. It is proven that optimal basic decontamination can be achieved in a finite two-dimensional CA under the von Neumann neighbourhood using *n* simultaneously decontaminating cells. In the circular version of the CA, *2n* simultaneously decontaminating cells are required and the process is completed in $O(n)$ time. The same results are achieved under the Moore neighbourhood.

4.2.2. Contamination distance *Cd*=2

In this subsection, we present a stricter model than is presented in [Daa12]. We investigate the case when the Contamination Distance is greater than the Visibility Hop, that is *Vh*=1 and *Cd*>1. An execution of the algorithm is elaborated in the upcoming subsection, followed by the decontamination theorem and the proof.

4.2.2.1. Grid topology

The idea is to place the initial decontaminating cells in the first column (or the first 2 columns) of the CA (see Figure 4.2). At the initial stage, the first 2 columns are set to decontaminating, and then the decontaminating strategy begins. Decontaminating cells only become clean if, and only if, they are protected from the 2-hop contaminated neighbouring cells. Contaminated cells become decontaminating at time $t+1$ when their left neighbour cells were decontaminating at time t. Note that during the process, only a single column becomes decontaminated within a single unit of time. We can earn one unit of time at the end of the process (from t=4 to *t*=5 in Figure 4.2) because the last 2 columns can become simultaneously clean as every cell in the last column does not need to be protected from a contaminated neighbour on its right. To do so, we can add an extra rule to tackle the

configuration of the last decontaminating column. The effect of the local rules is a sequential decontamination of columns from left to right, where a decontaminated cell is obviously never in contact with a contaminated one. The CA is then fully decontaminated in *n* time units.

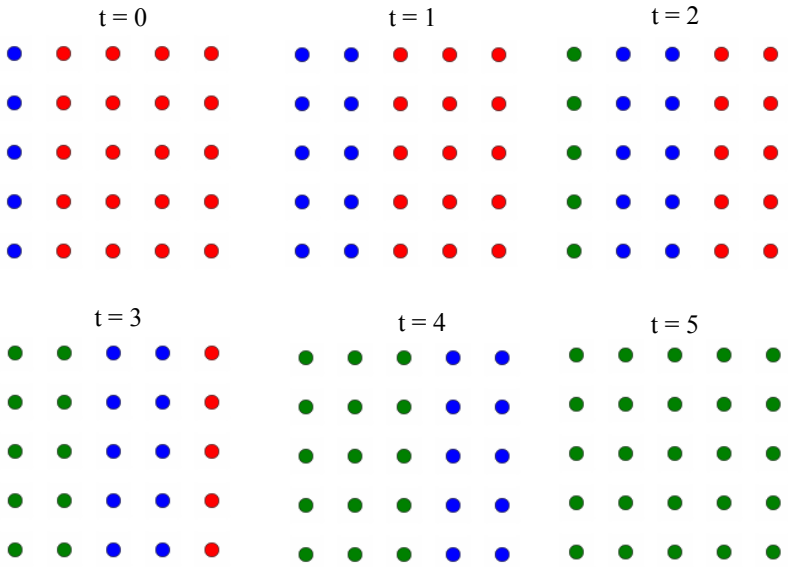


Figure 4.2: A sample execution of the left-to-right basic decontamination under the von Neumann neighbourhood in a finite CA when *Vh*=1 and *Cd*=2

Theorem 4.1. *Decontamination is achieved in a finite 2D CA of size* $n * m$ $(n \leq m)$ *under the von Neumann neighbourhood using a maximum of* $2n$ *simultaneously decontaminating cells when the Visibility Hop is 1, the Contamination Distance is 2 and the immunity time is null. Decontamination is achieved in at most m units time.*

Proof:

To prove that *2n* simultaneously decontaminating cells are sufficient, we need to prove that starting with *n* or *2n* decontaminating cells initially located in the first column, all cells will become decontaminated by the end of the process, and no cell will be re-contaminated. Therefore, we need to show that a set of rules that will perform the operation exists. Table 4.1 depicts this set of rules, inspired by the rules listed in Figure 2.2, in which each cell is analyzed from its location within the CA (if the cell is laying on the left, top, right, or bottom border or if the cell is an internal one). The first 6 rules denote the transition of a

decontaminating cell into a clean cell. Conversely, the last 6 rules denote the transition of a contaminated cell into a decontaminating one. Note in the rules R7, R8 and R9, these cells were decontaminating in the previous step but instead of becoming clean, they have to run the decontaminating process again to avoid being re-contaminated as their neighbours at distance 2 are still contaminated. Therefore, R7, R8, and R9 are the rules defining the set T. This is the key strategy to overcome the *Contamination Distance* greater than 1, implicitly simulating a temporal immunity of 1 unit of time.

#	Configuration	Next State	Notes
R1	{•,0,0,•,•}	0	clean if right neighbour is decontaminating
R2	{•,0,•,•,•}	0	Current middle-left decontaminating into a clean cell
R3	{•,0,•,•,0}	0	Current bottom-left decontaminating into a clean cell
R4	{•,•,0,0,•}	0	Last top-right cell decontaminating into a clean cell
R5	{•,•,•,0,•}	0	Last middle-right decontaminating into a clean cell
R6	{•,•,•,0,0}	0	Last bottom-right decontaminating into a clean cell
R7	{•,•,0,1,•}	•	
R8	{•,•,•,1,•}	•	
R9	{•,•,•,1,0}	•	
R10	{1,•,0,1,1}	•	
R11	{1,•,1,1,1}	•	
R12	{1,•,1,1,0}	•	
R13	{1,•,0,0,1}	•	Rightmost contaminated cells into Decontaminating
R14	{1,•,1,0,1}	•	
R15	{1,•,1,0,0}	•	

Table 4.1: Rule for Basic decontamination in Finite CA under the von Neumann neighbourhood when *Vh*=1 and *Cd*=2

A simpler list of rules is proposed in Table 4.2 in which the construction of rules is based on the propagation flow of the decontamination rather than its location within the CA. The difference between the two methods of constructing these rules is discussed in upcoming chapters.

#	Configuration	Next State	Notes
R1	{•,0,0,•,•}	0	clean if right neighbour is decontaminating
R2	{•,0,•,•,•}	0	clean if right neighbour is clean (last column on the CA)
R3	{1,•,1,0,0}	•	Propagation to the right.

Table 4.2: Alternative Rule for Basic decontamination in Finite CA under the von Neumann neighbourhood when *Vh*=1 and *Cd*=2

4.2.2.2. Circular grid topology

An execution of the algorithm is elaborated in this section, followed by the decontamination rules and the theorem proof.

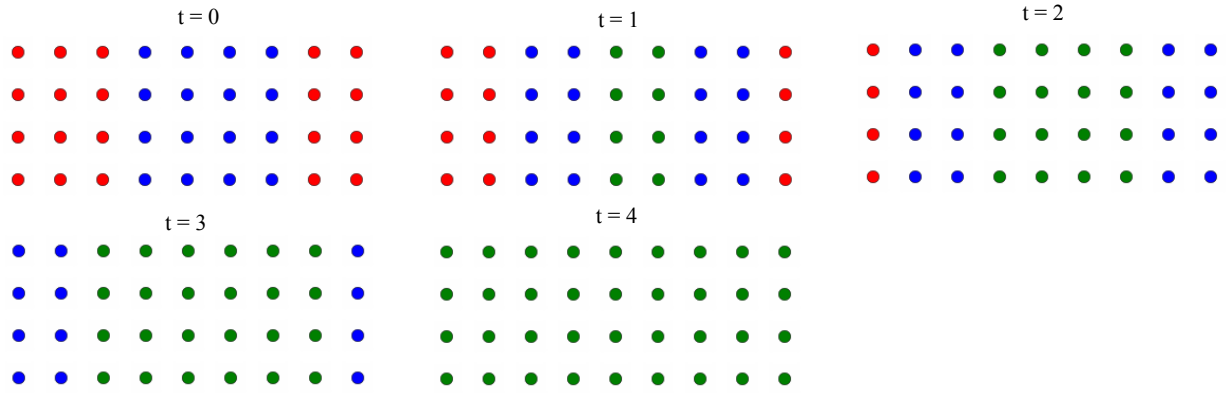


Figure 4.3: A sample execution of the left-to-right basic decontamination under the von Neumann neighbourhood in a circular CA when *Vh*=1 and *Cd*=2

The initial decontaminating cells are placed in any four consecutive columns of the CA and the cells obey the following simple rules.

- A decontaminating cell becomes decontaminated at time $t+1$
  - if both of its left and right neighbours are in a decontaminating state at time t, or
  - if one of its left or right neighbours is in a decontaminating state and the neighbour on the other side is in a decontaminated state at time t.
- A contaminated cell becomes decontaminating at time $t+1$ if it is in contact with a decontaminating state at time t

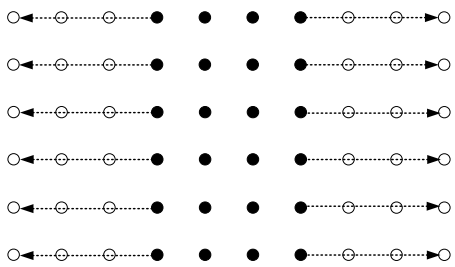


Figure 4.4: The propagation flow of the basic decontamination under the von Neumann neighbourhood in a circular CA

Theorem 4.2. *Decontamination can be achieved in a circular 2D CA of size* $n*m$ $(n \le m)$ *under the von Neumann neighbourhood using 4n simultaneous decontaminating cells when the Visibility Hop is 1, the Contamination Distance is 2 and the immunity time is null. Decontamination is achieved in at most* $\left\lceil \frac{m}{2} \right\rceil - 1$ *units time.*

Proof:

To prove that 4n simultaneous decontaminating cells are sufficient, we need to prove that a set of rules exists. These transition rules are shown in Table 4.3. At each step, two columns get decontaminated so the process should be completed in at most units of $\left\lceil \frac{m}{2} \right\rceil$ time. However the rule R1 allows the algorithm to save one step at the last stage of the process since the last four columns (if *n* is even) or the last three columns (if *n* is odd) gets simultaneously decontaminated.

#	Configuration	Next State	Notes
R1	{•,•,*,•,*}	0	Clean if both the left & right neighbour is decontaminating
R2	{•,0,*,•,*}	0	Clean if the left neighbour is clean & right neighbour is decontaminating
R3	{•,•,*,0, *}	0	Clean if the left neighbour is decontaminating & right neighbour is clean
R4	{1,•,*,*,*}	•	Propagation to the left
R5	{1,*,*,•,*}	•	Propagation to the right

Table 4.3: Rule for Basic decontamination in circular CA under the von Neumann neighbourhood when *Vh*=1 and *Cd*=2

4.3. The impact of a greater Visibility, case study of *Vh*=2

4.3.1. Contamination Distance *Cd*=1

4.3.1.1. Grid topology

Similar to the algorithm presented in [Daa12], the process starts by setting the cells of the first column as initiators. Then, the rules in Table 4.4 can be used to process the decontamination algorithms. The first observation is that the execution looks identical to the basic decontamination presented in [Daa12] and having the *Vh*>1 did not offer any improvement. Hence, we present the theorem below.

Theorem 4.3. *Optimal decontamination is achieved in m unit times, in a finite 2D CA of size* $n * m$ $(n \leq m)$ *under the von Neumann neighbourhood using n simultaneous decontaminating cells when the Visibility Hop is 2, the Contamination Distance is l and the immunity time is null.*

Proof:

The proof presented in [Daa12] shows that any decontamination strategies without immunity and with Contamination Distance 1 will require at least *n* simultaneously decontaminating cells. The same proof works independently of the visibility of every node. Therefore, the basic strategy presented in [Daa12] is optimal regardless of the visibility of every node.

#	Configuration	Next State	Notes
R1	{•,*,*,*,*}	0	Any decontaminating cell is clean in the next iteration
R2	{1,•,0,1,1}	•	
R3	{1,•,0,0,1}	•	
R4	{1,•,1,1,1}	•	
R5	{1,•,1,1,0}	•	
R6	{1,•,1,0,1}	•	
R7	{1,•,1,0,0}	•	

Table 4.4: Rule for Basic decontamination in Finite CA under the von Neumann neighbourhood when *Vh*=2 and *Cd*=1

4.3.1.2. Circular grid topology

For the circular case, the algorithm execution is exactly similar to the case *Vh*=1, *Cd*=1. The process starts by setting any two consecutive cells as *initiators* and propagates the decontamination in opposite directions in the CA (left to right and right to left).

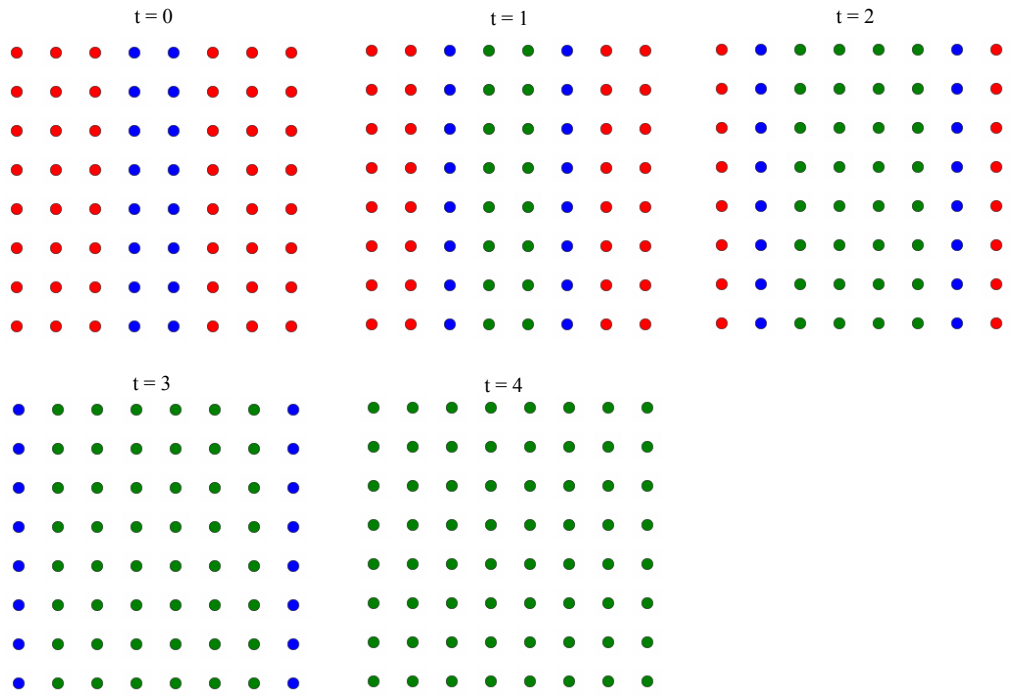


Figure 4.5: A sample execution of the left-to-right decontamination under the von Neumann neighbourhood in a circular CA when *Vh*=2 and *Cd*=1

Theorem 4.4. *Optimal decontamination can be achieved* in at most $\left\lceil \frac{m}{2} \right\rceil$ *units time in a circular 2D CA of size* $n * m$ $(n \leq m)$ *under the von Neumann neighbourhood using 2n simultaneous decontaminating cells when the Visibility Hop is 2, the Contamination Distance is 1 and the immunity time is null.*

Proof: The same induction proof for optimality for the case *Vh*=1, *Cd*=1 in [Daa12] holds here too, since it works independently of the visibility of every node. The transition rules of the decontamination are shown in Table 4.5.

#	Configuration	Next State	Notes
R1	{•,*,*,*,*}	0	Any decontaminating cell is clean in the next iteration
R2	{1,*,*,•,*}	•	Propagation to the left (decontaminating if right neighbour is decontaminating)
R3	{1,•,*,*,*}	•	Propagation to the right (decontaminating if left neighbour is decontaminating

Table 4.5: Rule for Basic decontamination in a circular and Finite CA under the von Neumann neighbourhood when *Vh*=2 and *Cd*=1

4.3.2. Contamination Distance *Cd*=2

4.3.2.1. Grid topology

The algorithm previously presented (*Cd*=2 and *Vh*=1) will still behave correctly if executed against a model of CA with greater visibility (i.e., when *Vh*>1), both in the case of a basic 2D mesh or the circular 2D mesh. Thus, the above mentioned examples of execution of the case *Vh*=1 and *Cd*=2 still hold for the case *Vh*=2 and *Cd*=2, and the same rules can still be applied to perform the decontamination. In fact, with a greater visibility, we will show that better results are achieved with respect to the time execution of the algorithm. Decontamination is achieved by setting all cells of the first 2 columns to decontaminating

and by applying the set of rules indicated in Table 4.6. Figure 4.6 shows the propagation of decontamination starting with decontaminating cells located in the two left most columns.

Theorem 4.5. *Decontamination is achieved in a finite 2D CA of size* $n*m$ $(n \leq m)$ *under the von Neumann neighbourhood using 2n simultaneously decontaminating cells when the Visibility Hop is 2, the Contamination Distance is 2 and the immunity time is null. Decontamination is achieved in at most* $\left\lceil \frac{m}{2} \right\rceil$ *units time.*

Proof:

In the case where *Vh=1*, even if we started the decontamination with the first two columns on the left, the algorithm would have faced two restrictions. The first restriction is that only a single column of cells could be decontaminating into the next step. The second restriction is that only a single column of cells in a decontaminating mode could be decontaminated. The other column of cells (the right column) would have to remain in a decontaminating state, otherwise, it would be re-contaminated in the next step as the column would be in contact with its right neighbour of distance 2. Generally, in any step of decontamination, if columns k and k+1 are decontaminating at time t, it means that at time t+1, the limitation is that a single decontaminating column could be decontaminated and only one contaminated column could be decontaminating. Thus, only the column k could be decontaminated. The column k+1 must remain in its decontaminating state and cannot be decontaminated, otherwise, it would be re-contaminated by the k+3 column (because that *Cd*=2).

The only way that the k+1 column changes its state into decontaminated is if the column k+3 could also change its state into a decontaminating mode, and therefore could protect the k+1 column. This is not feasible. It is impossible to find a rule that could change the states of the cells in column k+3 from contaminated to decontaminating because they are surrounded left and right by infected cells and the visibility is *Vh*=1. The column k+3 turns out to be identical to all remaining contaminated columns of the CA. A rule that would change the state of the column k+3 will also change the state of its other remaining contaminated cells.

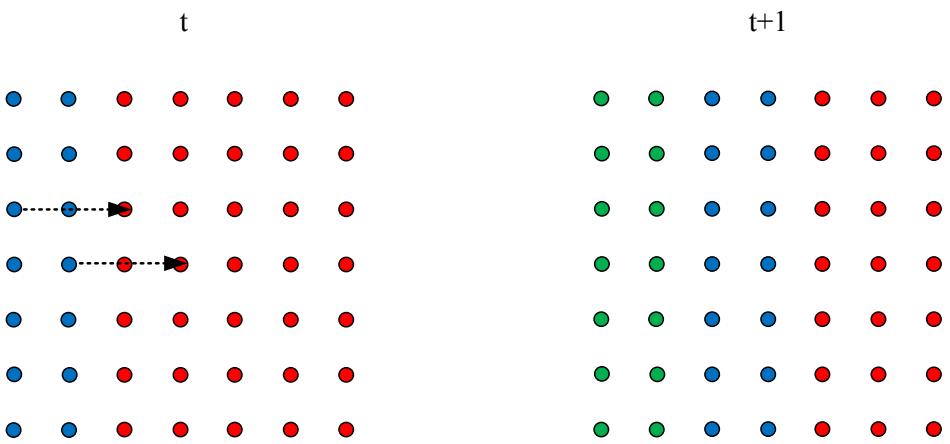


Figure 4.6: Propagation of a 2 by 2 column decontamination under the von Neumann neighbourhood when *Vh*=2 and *Cd*=2

However with visibility *Vh*=2, the *k*+3 column would be able to see the column *k*+1, which will differentiate the column *k*+3 from other contaminated columns of the CA. In this way, it is possible to find rules that can change its state. To perform the decontamination, each decontaminating cell at time *t* will become decontaminated at time *t*+1 (Rule R1 of Table 4.6). A contaminated cell becomes decontaminating at time *t*+1 if it notices that its left neighbour of distance 2 is decontaminating at time *t* (see Rule R2 of Table 4.6). According to this method, columns k and *k*+1 of the CA can change their state from decontaminating into decontaminated as they are protected at time *t*+1 by the two columns at indexes *k*+2 and *k*+3 being in a decontaminating mode. The reason is that the column *k*+2 would be in decontaminating mode at time *t*+1 as it sees its left neighbour of distance 2 (column k) in a decontaminating mode at time *t*. Respectively, the *k*+3 column will be in a decontaminating mode at time *t*+1 as it sees its left neighbour of distance 2 (column *k*+1) in a decontaminating mode at time *t*. Consequently, both columns k and *k*+1 are effectively protected from re-contamination since the closest contaminated column would be the *k*+4 column, which can reach at most the *k*+2 column but cannot reach the *k*+1 column as *Cd*=2. The CA is decontaminated in a two-by-two mode of decontaminated and decontaminating cells. Thus, if *m* is an even number, the decontamination is carried out in $\frac{m}{2}$ steps. If this size is odd, the decontamination time will therefore be $\left\lceil \frac{m}{2} \right\rceil$.

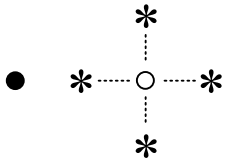
#	Configuration	Next State	Notes
R1			Any decontaminating cell will be decontaminated in the next step.
R2			A contaminated cell will be decontaminating at time t+1 if its left neighbour of distance 2 is decontaminating at time t.

Table 4.6: Rule for Basic Decontamination in Finite CA under the von Neumann neighbourhood when *Vh*=2 and Cd=2

4.3.2.2. Circular Grid topology

The initial decontaminating cells are placed in any four consecutive columns of the CA and the cells obey the following simple rules:

- a decontaminating cell becomes decontaminated at time t+1; and
- a contaminated cell becomes decontaminating at time t+1 if it is in contact (with respect to the visibility *Vh*=2) with a decontaminating state at time t.

.

Theorem 4.6. *Decontamination is achieved with a circular CA of size* $n * m\ (n \le m)$ *under the von Neumann neighbourhood using 4n simultaneous decontaminating cells if the Visibility Hop is 2, the Contamination Distance is 2 and the immunity time is null. Decontamination is achieved in at most* $\left\lceil \frac{m}{4} \right\rceil$ *units time.*

Proof:

The Table 4.7 shows the list of transition rules for the decontamination. Starting with 4 columns of decontaminating cells, the rules R3 and R4 will initiate 4 new columns at each step. Since the rule R1 will decontaminate each decontaminating cell at each step, it implies

that every successive 4 columns will get decontaminated at each step. Therefore, the decontamination is executed in $\left\lceil \frac{m}{4} \right\rceil$ units of time.

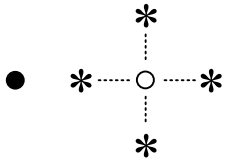
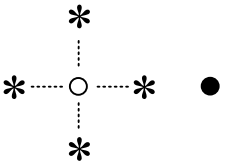
#	Configuration	Next State	Notes
R1			Any decontaminating cell will be decontaminated in the next step.
R2			A contaminated cell will be decontaminating at time t+1 if its left neighbour of distance 2 is decontaminating at time t.
R3			A contaminated cell will be decontaminating at time t+1 if its right neighbour of distance 2 is decontaminating at time t.

Table 4.7: Rule for Basic Decontamination in Finite CA under the von Neumann neighbourhood when *Vh*=2 and Cd=2

4.4. Summary

We started by enunciating the known results of decontaminating a CA under the von Neumann configuration. The optimal algorithm needs exactly *n* decontaminating cells and the required time of execution is linear based on the size of the CA. In the case of a circular CA, the optimal algorithm needs *2n* decontaminating cells and is performed in approximately half of the time. Then, we have shown that even with a strict model, in which we increase the Contamination Distance to *Cd*=2, it is still possible to execute the decontamination with a visibility *Vh*=1. In that configuration, the algorithm needs at least *2n* decontaminating cells with a normal CA and *n* time units of execution. Thanks to the use of *Visibility Hop*, it is possible to decrease the execution time. A summary of results established in this chapter is listed in the following table.

Neighbourhood Type	Topology	*Vh*	*Cd*	Number of Initiators	Maximum decontaminating cells	Time	Reference
von Neumann	CA	1	1	n	n	m	[Daa12]
von Neumann	Circular CA	1	1	n	$2n$	$\left\lceil \frac{m}{2} \right\rceil$	[Daa12]
von Neumann	CA	1	2	n	$2n$	m	Theorem 4.1
				$2n$	$2n$	$m-1$	
von Neumann	Circular CA	1	2	$2n$	$4n$	$\left\lceil \frac{m}{2} \right\rceil$	Theorem 4.2
				3n or $4n$	$4n$	$\left\lceil \frac{m}{2} \right\rceil - 1$	
von Neumann	CA	≥ 2	1	n	n	m	Theorem 4.3
von Neumann	Circular CA	≥ 2	1	$2n$	$2n$	At most $\left\lceil \frac{m}{2} \right\rceil$	Theorem 4.4
von Neumann	CA	2	2	$2n$	$2n$	$\left\lceil \frac{m}{2} \right\rceil$	Theorem 4.5
von Neumann	Circular CA	2	2	$4n$	$4n$	$\left\lceil \frac{m}{4} \right\rceil$	Theorem 4.6

Table 4.8: Summary of the basic decontamination results for a $n*m$ $(n \leq m)$ CA under the topology, Visibility Hop and Contamination Distance parameters.

In this chapter, we only concentrated on the von Neumann neighbourhood because all transition rules can be expressed with its cells, and because using the Moore neighbourhood would not increase the efficiency of these algorithms. We also analyzed the horizontal flow algorithm with specific values of *Vh* and *Cd*. We could have generalized the same algorithm for different values of *Cd* and *Vh,* however, this generalization will be introduced and studied in the next chapter. To avoid repeating the same ideas, we decided to introduce the generalization for more sophisticated algorithm.

Chapter 5

Diagonal Flow

In previous chapters, we focused on either the horizontal or the vertical cuts of our CA. The flow of decontamination was performed in a vertical way. In this chapter, we focus on a new way to cut the CA. Rather than doing it in a vertical (column by column) or horizontal (line by line), the decontamination is still in a straight line but following a diagonal pattern.

5.1. Motivation

In the previous chapter, we noted that decontamination was performed according to a horizontal flow. The success of this algorithm rests on the basic fact that the decontamination flow is cutting the CA in a vertical manner from both opposite borders of the CA. Cutting the CA following a straight line always guarantees the protection of cells already decontaminated. Moreover, a crucial condition is that the number of decontaminating cells is always bound to a constant number. Consider Figure 5.1. If a strategy offers a flow of decontamination from an internal cell, it is very likely that the same strategy will have some difficulty minimizing the size of T cells because its cardinality will increase over time. It is trivial that as the size of the square (in Figure 5.1a) or rhombus (Figure 5.1b) increases, it is necessary to increase the number of decontaminating cells that are required to protect already cleaned cells. The idea behind the decontamination using diagonal flow is based on the same motivation as the vertical flow.

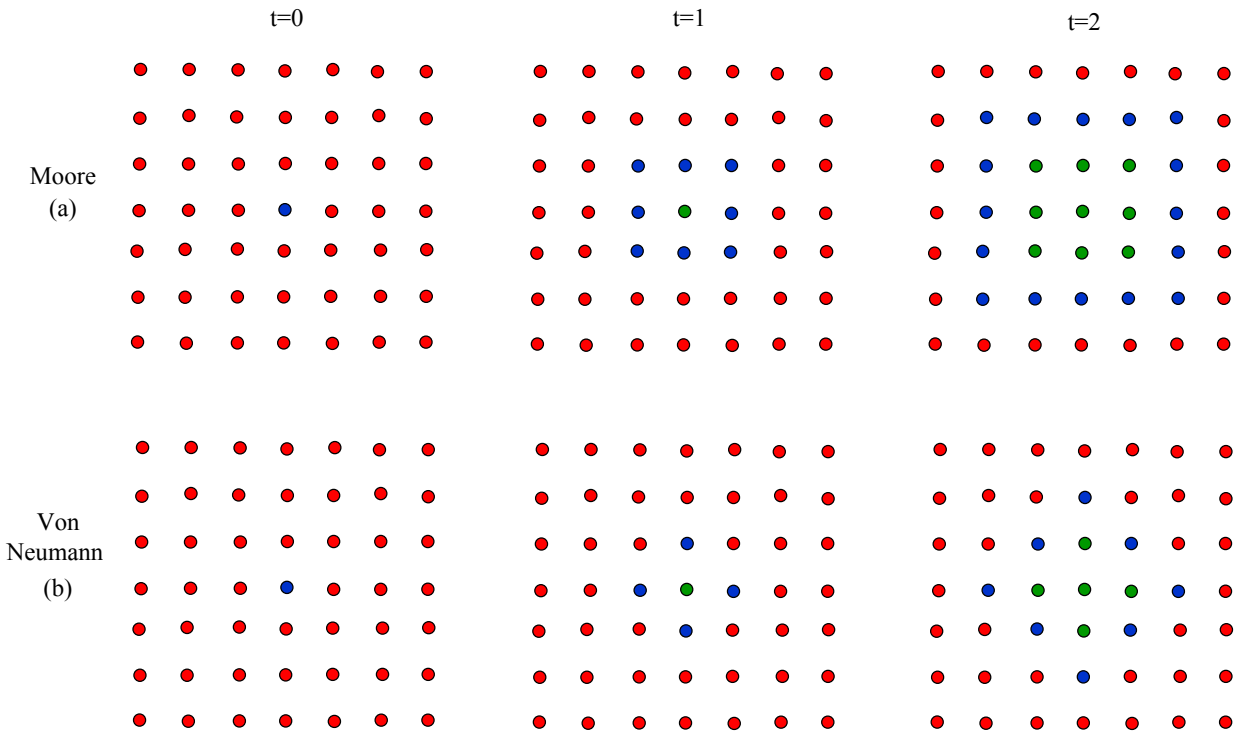


Figure 5.1: A basic propagation of a decontamination approach initiated by an inner cell showing a bound-less number of decontaminating cells

We also see in the previous chapter that one of the consequences of the sequential decontamination in a vertical mode is that the block set of decontaminating cells T must absolutely contain, at a minimum, all the cells within the same column and as many columns as the value of Cd. However, when using diagonal flow, we will show in the upcoming sections that it is possible to use less than n decontaminating cells for some steps. We are also interested in the diagonal approach as it presents a base for a "divide and conquer" strategy that we will investigate in detail in the upcoming chapters.

5.2. Basic Case of Visibility Vh=1

In this section, we show that with a visibility of 1, it is possible to find some decontamination algorithms using a diagonal flow under the von Neumann neighbourhood configuration.

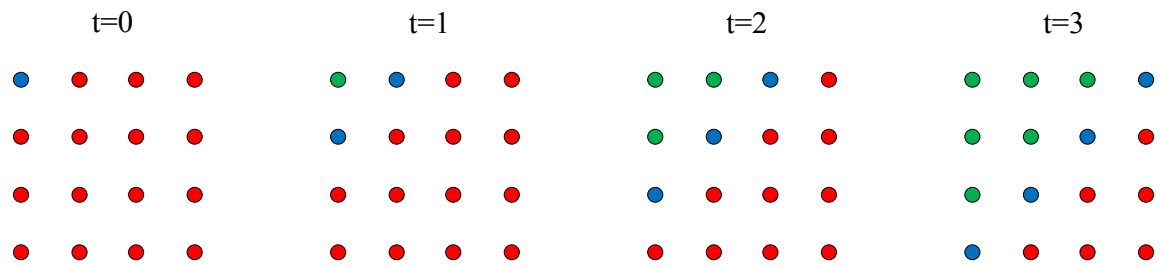


Figure 5.2: Propagation of the basic diagonal move under the von Neumann neighbourhood when *Vh*=1 and *Cd*=1

5.2.1. Contamination Distance *Cd*=1

The idea is to initiate the algorithm from a cell located on a corner of our CA (Figure 5.2). This chosen cell can be from any corner, but in our example, the selected cell is the one located on the first column and the first row (top left corner of our CA). Each cell becomes decontaminated at time $t+1$ after being in a decontaminating state at time t. The intention of the algorithm is to create a diagonal decontamination flow from the top-left cell to the bottom-right cell. In the next step, at time $t=2$, the algorithm is run by propagating decontaminating cells in the direction of the diagonal, which in our case is the two neighbour cells of the initial cell. The process continues to eventually reach the full diagonal (here $t=4$) and then a reverse symmetric execution happens until reaching the full decontamination. With this pattern, the CA will be properly decontaminated. We formulate the following theorem:

Theorem 5.1. *Decontamination using diagonal flow can be achieved with a CA of size* $n * m\ (n \leq m)$ *under the von Neumann neighbourhood if the Visibility Hop Vh =1 and the Contamination Distance Cd=1 by using at most n decontaminating cells at any time t. The decontamination process is performed using* $(m+n-1)$ *steps.*

Proof:

To prove that at most n simultaneously decontaminating cells are sufficient, we need to prove that starting with *1* decontaminating cell initially located in the left corner, all cells will become decontaminated by the end of the process, and no cell will be re-contaminated. That is, that once decontaminated, every cells stays decontaminated until the end of the

process, when all cells are decontaminated. Therefore, we need to show that such a set of rules that will perform the operation exists. Table 5.1 lists the needed rules to perform the decontamination.

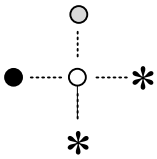
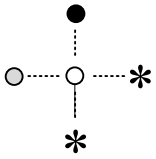
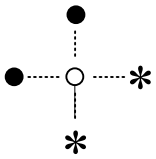
#	Configuration	Next State	Notes
R1			Any decontaminating cell will be decontaminated in the next step.
R2			Cell located on the top horizontal border of the CA
R3			Cell located on the left vertical border of the CA
R4			Internal Cell Cell laying on the Right vertical border Cell laying on the bottom horizontal border

Table 5.1: Rules for decontamination in Finite CA using basic diagonal move under the von Neumann neighbourhood when *Vh*=1 and *Cd*=1

5.2.2. Generalization of an arbitrary distance *Cd*=k

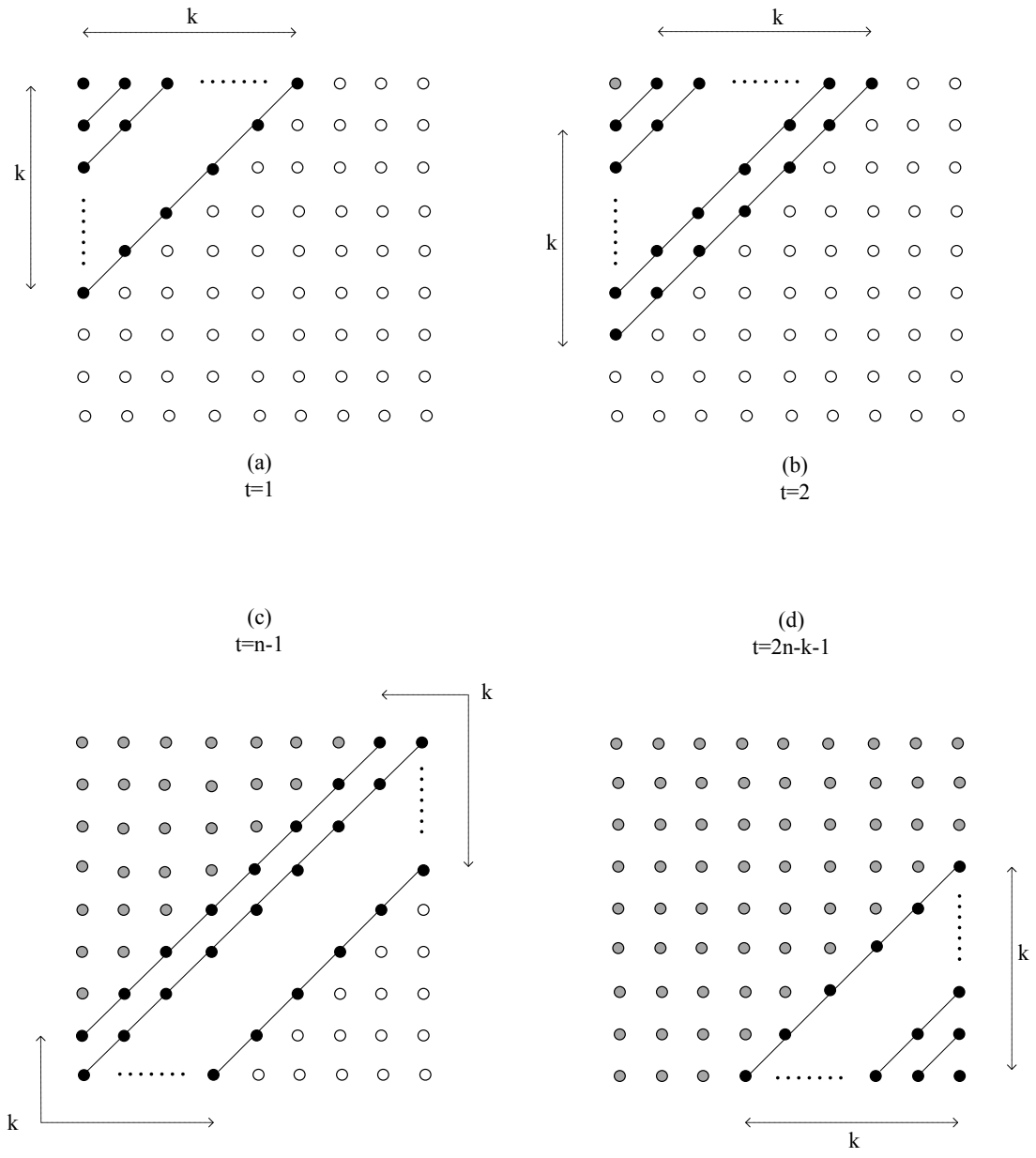


Figure 5.3: Propagation of the basic diagonal move under the von Neumann neighbourhood when *Vh*=1 and *Cd*=k

A generalization of the diagonal strategy under the von Neumann neighbourhood at various times during the decontamination process, when *Vh*=1 and for an arbitrary *Cd*, is depicted in Figure 5.3. We note that during the entire process, *Cd* is always equal to *k* and only a single diagonal gets decontaminated at each step.

Similar to the case of *Cd*=1, the idea is to initiate the algorithm from a group of cells located in a corner of our CA (Figure 5.3a). These chosen cells can be from any corner, but in our strategy, selected cells are the triangle of cells delimited by the first *k* columns and *k* rows (top left corner of our CA). The intention of the algorithm is to create a diagonal decontamination flow from the top-left cell to bottom-right cell by propagating decontaminating cells in the direction of the diagonal. At time *t*=2, only the top-left cell gets decontaminated and the next diagonal containing the border cell *k*+1 becomes decontaminating (Figure 5.3b). The process continues to eventually reach the full diagonal and then a reverse symmetric execution happens until full decontamination is reached. With this pattern, the CA will be properly decontaminated.

Beforehand, let us computes the size $D_k(n,m)$ of the first *k* diagonals in a $n*m$ rectangular grid with the hypothesis that $(n \le m)$.

Lemma 5.1. Let $D_k(n,m)$ be the size of the first *k* diagonals in a $n*m$ rectangle grid $(n \le m)$. Since there are $n+m-1$ diagonals in the grid, then obviously $k \le m+n-1$. Thus,

$$D_k(n,m) = \frac{k(k+1)}{2} \qquad \text{if } k \le n$$

$$D_k(n,m) = \frac{n(n+1)}{2} + (k-n)n \qquad \text{if } n < k \le m$$

$$D_k(n,m) = \frac{n(n+1)}{2} + (k-n)n + \left(\sum_{i=1}^{k-m}(n-i)\right) \qquad \text{if } m < k \le m+n-1$$

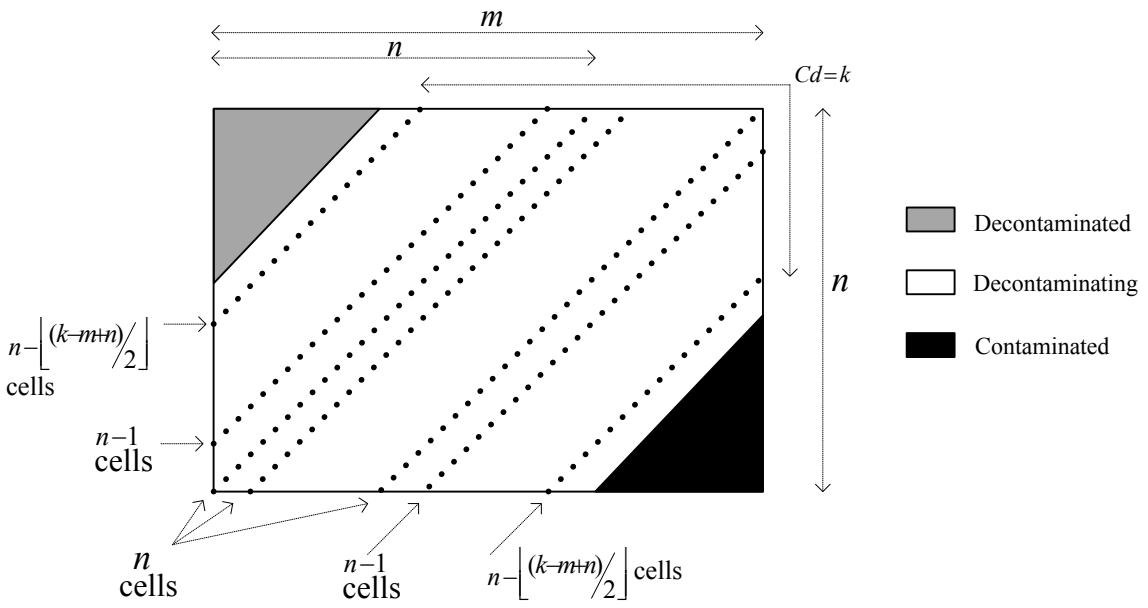


Figure 5.4: Maximum Number of Decontaminating cells in a diagonal move within the von Neumann Neighbourhood when *Vh*=1 and *Cd*=k

Theorem 5.2. *Decontamination using diagonal flow can be achieved with a CA of size* $n*m\ (n \le m)$ *under the von Neumann neighbourhood for a given Contamination Distance Cd=k if the visibility Vh =1 by using at most*

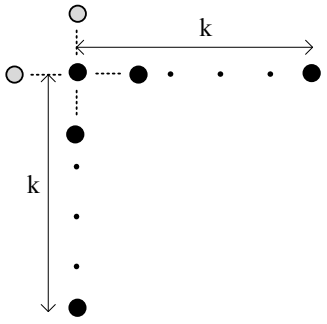
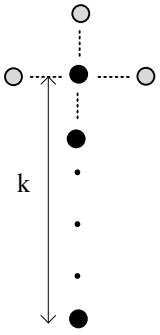
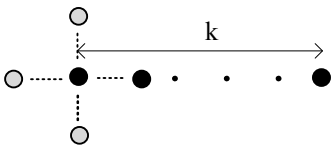
- $(m-n+1)n+2*\left(\sum_{i=1}^{\lfloor (k-m+n)/2 \rfloor}(n-i)\right)$ *decontaminating cells if* $(m-n)<k$ *; and*
- $k*n$ *decontaminating cells otherwise.*

The decontamination process starts with $D_k(n,m)$ *diagonals and is completed using* $n+m-1$ *steps.*

Proof:

To prove that it is feasible, we need to show that such a set of rules that will perform the operation exists. Table 5.2 shows these rules.

Figure 5.4 shows why at most $(m-n+1)n+2*\left(\sum_{i=1}^{\lfloor (k-m+n)/2 \rfloor}(n-i)\right)$ decontaminating cells are required when $(m-n)<k$. It is easy to see that if $Cd=k\geq(m-n)$ then k consecutive diagonals of size n are needed. It is too simply the maximum size of k consecutive diagonals in a $n*m$ $(n\leq m)$ rectangular grid. Also since each diagonal gets decontaminated one at a time, $n+m-1$ steps are required to perform the operation since there are $(2n-1)+(m-n)=n+m-1$ diagonals of the CA being involved.

#	**Configuration**	**Next State**	**Notes**
R1			
R2			Cell laying on the vertical right border (including top right corner but excluding bottom right corner)
R3			Cell laying on the bottom border (including bottom left corner but excluding bottom right corner)
			Last cell during decontamination (Bottom

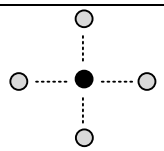
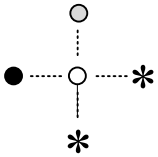
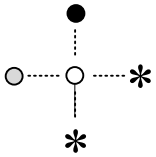
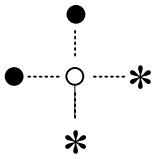
R4		●	Right corner)
R5		●	Cell located on the top horizontal border of the CA
R6		●	Cell located on the left vertical border of the CA
R7		●	Internal Cell Cell laying on the Right vertical border Cell laying on the bottom horizontal border

Table 5.2: Rules for Basic Decontamination in Finite CA using diagonal move under the von Neumann neighbourhood when Vh=1 and for an arbitrary Cd=k

5.3. The impact of a greater Visibility ($Vh \geq 2$) on Diagonal Moves

In this section, we show that with a visibility $Vh \geq 2$, it is possible to improve the execution time of the strategy using a diagonal flow under the von Neumann neighbourhood configuration.

5.3.1. Contamination Distance Cd=1

The decontamination rules for Cd=1 and Vh=1 (Table 5.1) also hold when Vh=2 and the process is even identical for a visibility $Vh \geq 2$. Since we still want to minimize the number of decontaminating cells, only a single decontaminating diagonal is sufficient at each step even if more diagonals can be processed because of a greater visibility.

5.3.2. Contamination Distance *Cd*=2

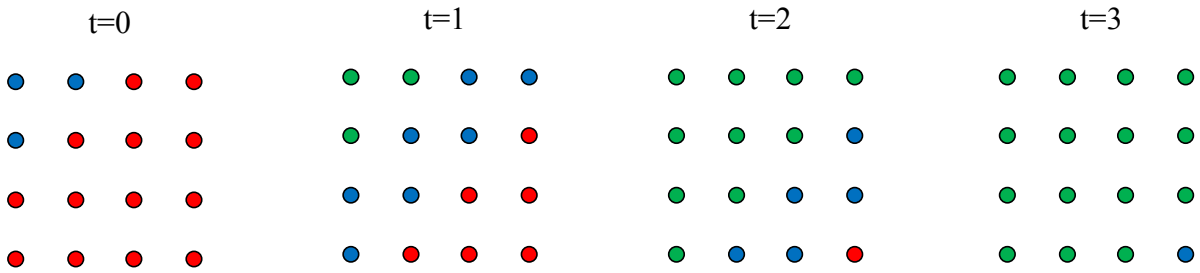


Figure 5.5: Propagation of the diagonal move under the von Neumann neighbourhood when $Vh \geq 2$ and *Cd*=2

The idea is to initiate the algorithm by two diagonals located in a corner of our CA (Figure 5.5). These chosen cells can be from any corner but in our execution sample, the selected cells are the first two diagonals from the top left. The algorithm is intended to create a diagonal decontamination flow from the top-left cell to the bottom-right cell. However, in opposition to the case of *Cd*=2 and *Vh*=1 where a decontaminating cell at time *t* becomes decontaminated in step *t*+2, here every cell gets decontaminated at time *t*. This is a notable improvement since all decontaminating diagonals all get decontaminated at once. In the next step, at time *t*=2, the algorithm is run by propagating decontaminating cells in the direction of the diagonal, which in our case are the next two neighbour cells of the first diagonal initiators. The process continues to eventually reach the last diagonal (the bottom right corner of the CA). With this pattern, the CA will be properly decontaminated. We state the following theorem:

Theorem 5.3. *Decontamination using diagonal flow can be achieved with a CA of size* $n * m$ $(n \leq m)$ *under the von Neumann neighbourhood for a given Contamination Distance Cd=2 if the visibility Vh=2 by using at most* $2n$ *decontaminating cells at any time t. The decontamination process is performed using* $\left\lceil \frac{n+m-1}{2} \right\rceil$ *steps.*

Proof:

To prove that it is feasible, we need to show that such a set of rules that will perform the operation exists. Table 5.2 and Table 5.4 show two alternatives. Since at most two diagonals can be in a decontaminating state, the cardinality of T is at most $2n$ which the maximum size of two consecutive diagonals. Note that for a square CA (that is, $m = n$), at most $n + (n-1) = 2n - 1$ decontaminating cells are required. With respect to the decontamination time, two diagonals get decontaminated at each step (except perhaps the last diagonal represented by a single cell). Since there are $(2n-1) + (m-n) = n + m - 1$ diagonals, the decontamination time is $\left\lceil \frac{n+m-1}{2} \right\rceil$ steps.

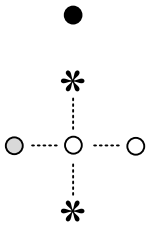
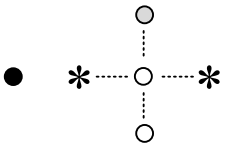
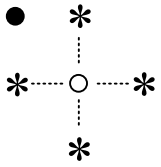
#	Configuration	Next State	Notes
R1			Any decontaminating cell will be decontaminated in the next step.
R2			Cell laying on the vertical left border
R3			Cell laying on the horizontal top border
R4			Internal cell Cell laying on the vertical right border Cell laying on the horizontal bottom border

Table 5.3: Rules for Basic Decontamination in Finite CA using diagonal move under the von Neumann neighbourhood when *Vh*=2 and *Cd*=2

A more simplistic rule is proposed in Table 5.4. We note that there are some situations where some cell's transition states can be eligible through both R2 and R3, but in these cases, the automata is still deterministic since the resulting state (decontaminating) is identical.

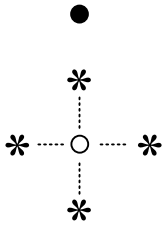
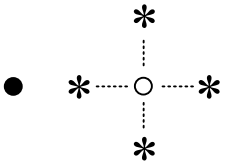
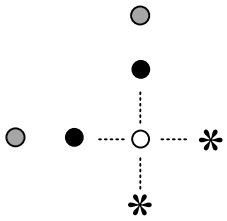
#	Configuration	Next State	Notes
R1			Any decontaminating cell will be decontaminated in the next step.
R2			
R3			
R4			Only to trigger the decontamination for the cell located on the second line & second column

Table 5.4: Another possible set of rules for Basic Decontamination in Finite CA using diagonal move under the von Neumann neighbourhood when *Vh*=2 and *Cd*=2

5.4. Generalization for an arbitrary *Cd* and *Vh*

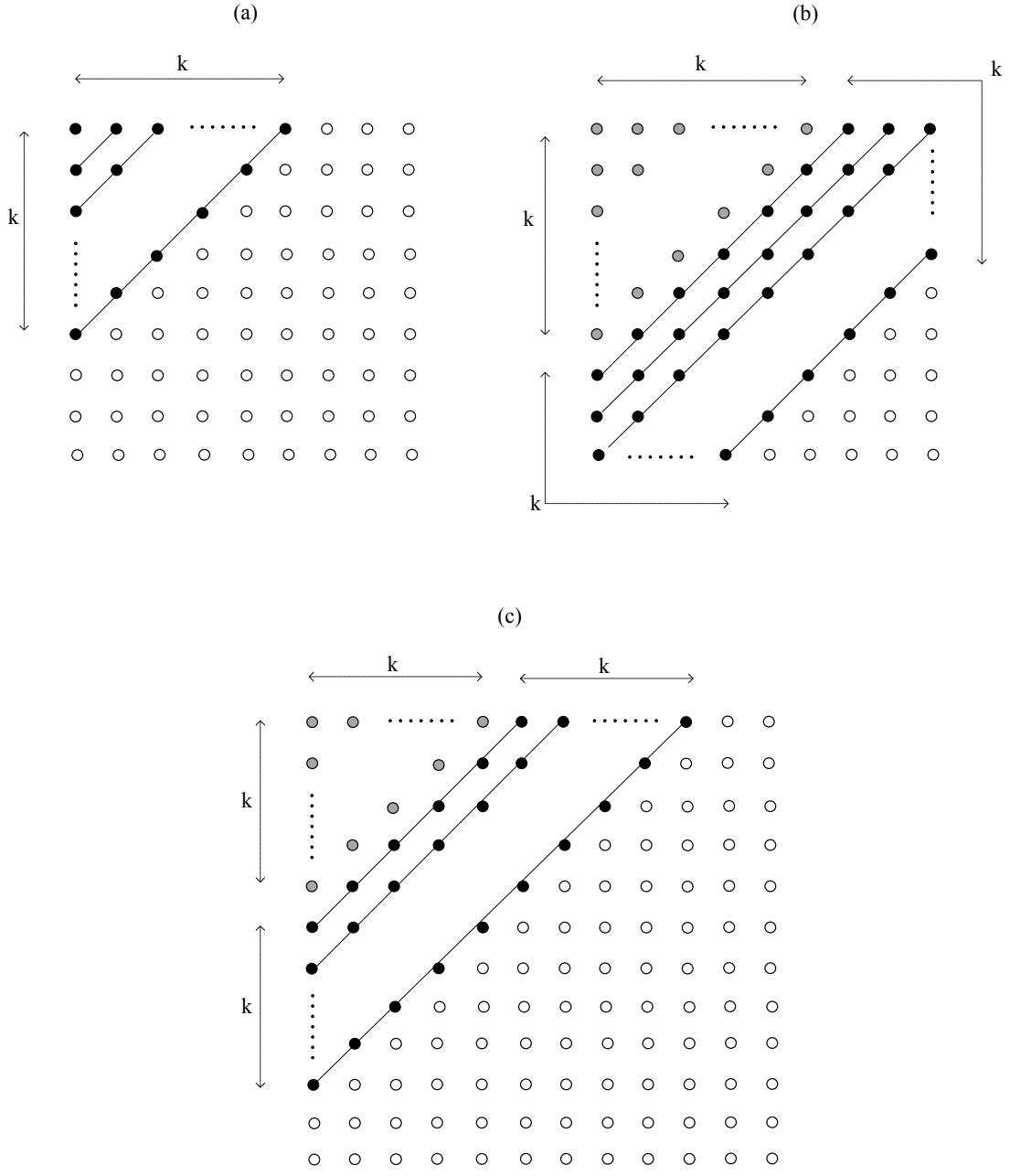


Figure 5.6: Propagation of the diagonal move under the von Neumann neighbourhood when *Vh*=*Cd*=k

In an attempt to generalize the diagonal strategy for any given *Cd*=*k* and any arbitrary *Vh*=*j*, we first look at the case of *k*=*j* and let us use Figure 5.3 as a reference. Because *Cd*=k, we first note that during the entire process, the width of the set of decontaminating cells *T* is

always equal to k as it serves as a shield to protect the cells which have already been decontaminated (Figure 5.3b and Figure 5.3c). Our second note is that because $Vh=k$, a new set of k contaminated diagonals can be set to a decontaminating state at each next step. For instance, the snapshots of the CA in Figure 5.3a is at time $t=1$ and in Figure 5.3b at time $t=2$. The rule to perform this transition is simple because each contaminated cell just needs to move into a decontaminating state if it sees a decontaminating neighbour at a distance $\leq k$. Similar to the proof of Theorem 5.2, we see that the strategy is using at most $(m-n+1)n+2*\left(\sum_{i=1}^{\lfloor (k-m+n)/2 \rfloor}(n-i)\right)$ decontaminating cells if $(m-n)<k$ and $k*n$ otherwise**,** at any time t. Also, the decontamination process is performed using $\left\lceil \frac{n+m-1}{k} \right\rceil$ steps. Two facts emerge from this observation.

1. If $Cd=k$, a cut of width k is always needed during the whole process of decontamination.
2. The visibility Vh will (independently of Cd) decide the velocity of the strategy.

As a generalization of the entire diagonal process, we state the following theorem:

Theorem 5.4. *Decontamination using diagonal flow can be achieved with a CA of size* $n*m$ $(n \leq m)$ *under the von Neumann neighbourhood for a given Contamination Distance* $Cd=k$ *and an arbitrary* $Vh=j$ *by using at most* $(m-n+1)n+2*\left(\sum_{i=1}^{\lfloor (k-m+n)/2 \rfloor}(n-i)\right)$ *decontaminating cells at any time t if* $(m-n)<k$ *; and* $k*n$ *decontaminating cells otherwise. The decontamination process starts with* $D_k(n,m)$ *diagonals and is completed using* $\left\lceil \frac{n+m-1}{\min\{j,k\}} \right\rceil$ *steps.*

Proof:

Without loss of generality, we assume $n \leq m$ and we start the process from the top left corner of the CA. To simplify the proof, we assume the CA is rotated in such a way that the vertical border height is *n* and the horizontal border width is *m*.

The process starts by choosing $D_k(n,m)$ initiators which are composed by the first k diagonals from the top left corner, note *T*. At each iteration, the set *T* is recreated by three rules

1. A subset of *T*, say *D*, composed by the first *j* diagonals from the top left (that is, a cut of width j) is removed from *T* and gets decontaminated.
2. The remaining set of diagonals, that is T/D of width $k-j$ remains in a decontaminating state and therefore stays in *T*.
3. The next *j* contaminated diagonals of the CA located right after *T* go to a decontaminating state and these new cells are added to the set *T*.

With respect to the maximum number of decontaminating cell and the number of initiators, the proof is identical to the one of Theorem 5.2. which is completed with Lemma 5.1.
When *Vh*<*Cd*, the process can only execute *Vh*=j diagonals at a time. Otherwise, when *Vh*>*Cd*, the process execute a minimum of *Cd*=*k* up to a maximum of *Vh*=j diagonals at a time. In this case, since we want to minimize the cardinality of *T*, we choose to process *Cd*=*k* diagonals. Therefore, the execution time of the algorithm is $\left\lceil \frac{n+m-1}{\min\{j,k\}} \right\rceil$.

5.5. Summary

In this chapter, we studied a new decontamination strategy that is based on a diagonal flow. Note, that we put the focus on von Neumann neighbourhood because all transition rules can be expressed with its cells. We also analyzed the diagonal flow algorithm with specific values of *Vh* and *Cd*. We completed the chapter by giving a generalization of the decontamination strategy using diagonal flow for any arbitrary value of *Cd* and *Vh*. A summary of results established in this chapter is listed in Table 5.5.

The Diagonal Move approach is an improvement over the horizontal flow algorithm presented in Chapter 4 with respect to the average number of decontaminating cells. Take for instance the special case of the square grid (m=n) during the basic setup of Vh=1 and Cd=1, the horizontal flow has an average use of $\frac{n^2}{n} = n$ decontaminating cells at each step compared to only $\frac{n^2}{2n-1}$ decontaminating cells for the diagonal move. With respect to the general case of an arbitrary Vh and Cd, the horizontal flow always processes a constant number of k=Cd set of diagonals (in which each diagonal contains n cells) at each step. Therefore, the average number of decontaminating cells at each step is k*n. However for the diagonal move, the same k*n decontaminating cells only appears in the decontamination process $\left\lceil \frac{m-n+1}{k} \right\rceil$ times. In the rest of the process, the diagonal moves considerably use less than k*n decontaminating cells.

N* Type	*Vh*	*Cd*	Number of Initiators	Max D*ing cells	Time	Ref.
VN	1	1	1	n	$2n$	Th. 5.1
VN	1	k	$D_k(m,n)$	$(m-n+1)n+2*\left(\sum_{i=1}^{\lfloor (k-m+n)/2 \rfloor}(n-i)\right)$ if $(m-n)<k$ $k*n$, if $(m-n)\geq k$	$n+m-1$	Th 5.2
VN	2	2	3	$2n$, if $m\neq n$ $2n-1$, if $m=n$	$\left\lceil \frac{n+m-1}{2} \right\rceil$	Th 5.3
VN	j	k	$D_k(m,n)$	$(m-n+1)n+2*\left(\sum_{i=1}^{\lfloor (k-m+n)/2 \rfloor}(n-i)\right)$ if $(m-n)<k$ $k*n$, if $(m-n)\geq k$	$\left\lceil \frac{n+m-1}{\min\{j,k\}} \right\rceil$	Th 5.4

Table 5.5: Summary of decontamination results of an $n*m$ ($n \leq m$) CA using Diagonal move strategies.

Chapter 6

Subdividing Strategies

In this chapter, we focus our research on a new approach which consists of investigating multiple cuts across various locations of the CA,. The idea is relatively similar to the widely known divide and conquer approach because the aim is to divide a large problem into several sub-problems and apply the same solution to these partitioned sub-problems. However, in our case, the base decontamination strategy needs a slight modification when applied to the various subdivisions. We show in every case that the base algorithm will always require some update in order to work on the divided substructure. Our goals are to show that we can perform such a strategy (the basic algorithm and the subdivision) and show that the Visibility Hop and Time immunity become important factors with respect to the feasibility of the strategy. We investigate the design of the basic algorithms and the different methods of building the algorithms against the subdivided structures.

6.1. Motivation

In Chapter 4, we focused on horizontal flow algorithms that went from left to right. In Chapter 5, we proposed algorithms with diagonal flow. In the previous two chapters, we concentrated our efforts on algorithms that split our CA with straight cuts. We also noted that each of these algorithms have constant and unidirectional flows (left to right, outside to inside). The disadvantage of this flow is the execution time of decontamination that becomes linear with respect to the size of the CA. The motivation for finding a divide and conquer strategy is to improve the execution time of the decontamination while still having a constant and limited number of decontaminating cells. To do so, we aim to find cuts to the CA that produces some subsets and to execute some specific strategies against these subsets.

In this chapter, we propose three different subdividing strategies: The Road Traffic approach, the Diagonal snake approach and a subdividing strategy based on the diagonal move approach used in Chapter 5. For each of three approaches, we consider the $n*n$ grid topology rather than the $n*m$ version for the benefits of more comprehensible statistics

formulas (with respect to the maximum number of decontaminating cells, the value of the immunity and the completion time) and avoid complex metrics which can divert the reader from the goal of giving attention to the subdivision technique. In addition, the algorithm behaves in an exact manner for both topologies.

6.2. Road Traffic Approach

6.2.1. Base Idea

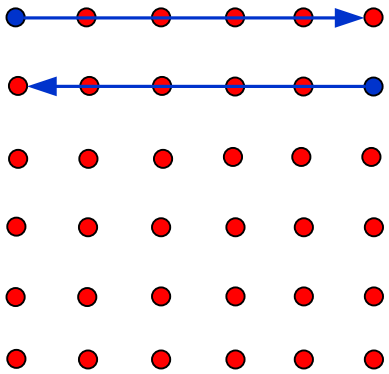


Figure 6.1: The road traffic approach

The main goal is to be able to perform the decontamination using only 2 decontaminating cells. The basic idea is to choose two diametrically opposed initiators. The first one is on the left border of the CA and the other one on the right border. The two cells are located on two consecutive rows. The idea is for the left cell to create a decontamination flow to the right and conversely, the right cell to cause a flow of decontamination to the left. This concept is depicted in Figure 6.1. In this entire strategy, we focus on the Contamination Distance *Cd*=1.

Theorem 6.1. *Decontamination using the road traffic approach can only be achieved in a 2D CA of size n*n under the von Neumann neighbourhood if the immunity time is at least n.*

Proof:

Since all cells laying on one complete row of the CA (n cells) are transitioned into a decontaminated state, all these cells are subjected to recontamination as they are all in contact with a contaminated cell. It takes at least n steps for the next row to protect the current row.

6.2.2. Sample Execution

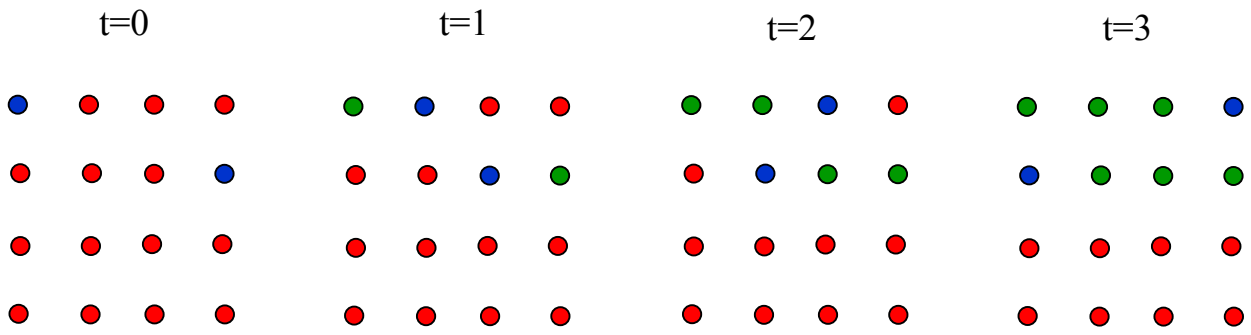


Figure 6.2: Propagation of the road traffic approach under the von Neumann neighbourhood

At the initial stage t=0, one chooses two initiators to start the algorithm. In the first row, the left border cell will cause its right neighbour to run the decontamination operation. In the second row, the right border cell will also cause his left neighbour to be in a decontaminating state. The process continues until it reaches the end of the first stage where each flow reaches the other column's extremity (here when t=3).

6.2.3. The pattern retrieval

At the end of the first stage, the CA will process two consecutive rows in which its extremity is in decontaminating state (see Figure 6.3a). The next step is to jump to the next two lines in order to re-execute the same process. Two choices are possible as depicted by Figure 6.3b and Figure 6.3c. The first choice offers the same configuration as the initial stage (t=0) in which all flow directions are exactly the same. The second choice however offers the opposite direction than the initial stage. The feasibility of both situations is studied

in the following subsections. The decontaminating rules with respect to the path of Figure 6.3b are noted in Table 6.1, while the decontamination rules for the path in Figure 6.3c are listed in Table 6.2.

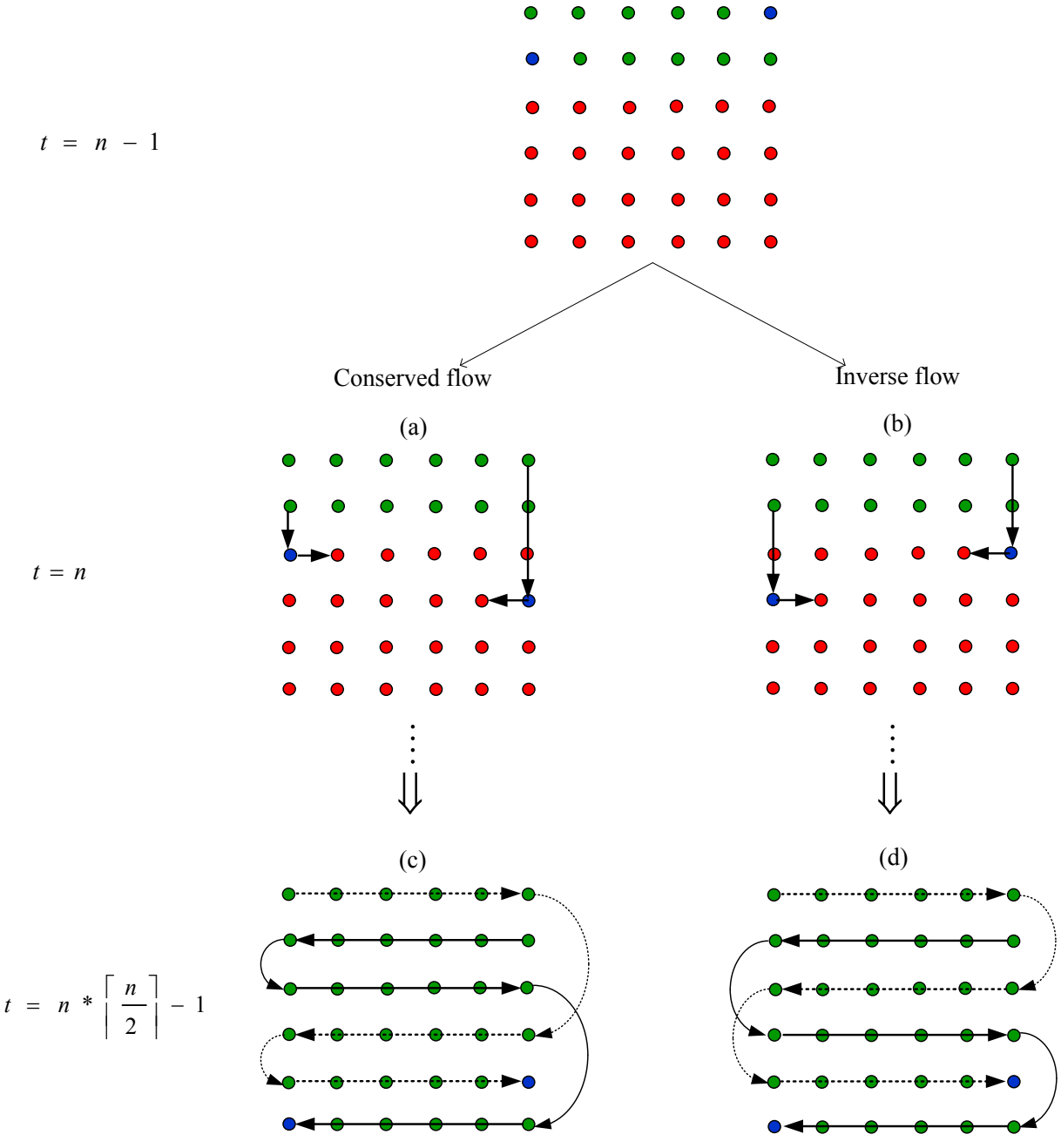


Figure 6.3: The two different possibilities of finding the initial case in the Road Traffic approach

Theorem 6.2. *Decontamination using the road traffic approach using exactly 2 decontaminating cells can only be achieved in a 2D CA of size* $n * m\ (n \leq m)$ *under a neighbourhood of visibility* $Vh > 1$.

Proof:

We will show that it is not possible to find the same road traffic pattern and resume the decontamination in the third and fourth row of the CA unless *Vh* is at least 2. We assume that *n* is even and without loss of generality, the same proof stands even if *n* is odd.

- In the first option for finding the initial pattern represented by the branch in Figure 6.3b, it is clear that the cell on the right border (4th row) has the same characteristics as the remaining cells on the same border but in lower rows (the direct neighbourhood configurations are identical). The only difference is that the cell sees a decontaminating cell at a distance of 3. This implies that the only rule that can trigger the cell's transition into a decontamination state is if it has a visibility *Vh*=3
- In the second option for finding the initial pattern represented by the branch in Figure 6.3c, it is clear that both the cell on the left border (4^{th} row) and the right border (3^{rd} row) have the same characteristics as the remaining cells on the same border but in lower rows (the direct neighbourhood configurations are identical). The only difference is that both cells see a decontaminating cell at a distance of 2. This implies that the only rule that can trigger its transition into a decontamination state is if the cell has a visibility *Vh*=2

We will show in the next sub-sections that there are two different solutions to retrieve the road traffic pattern if the visibility is greater than 1. The first solution is an exact pattern of the initial configuration with respect to the directions of the flow and requires a Visibility Hop of *Vh*=3. The second solution however, retrieves a symmetric configuration of the initial pattern with a visibility of *Vh*=2 only (resulting in an inverse flow).

6.2.3.1. The pattern retrieval with conserved decontamination flow

We show that decontamination using the road traffic algorithm is feasible under a von Neumann neighbourhood of $Vh = 3$ when following the retrieval pattern depicted in Figure 6.3a.

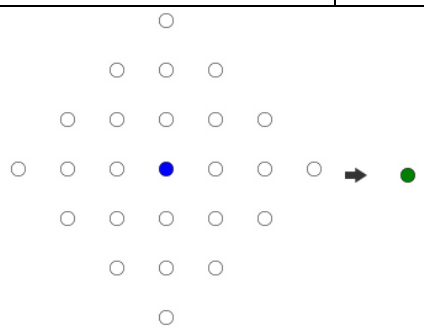
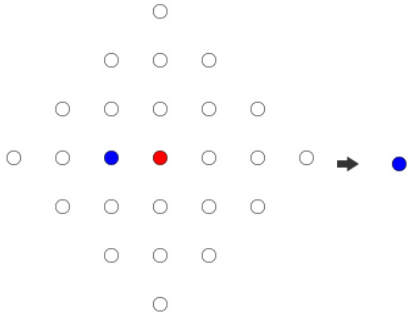
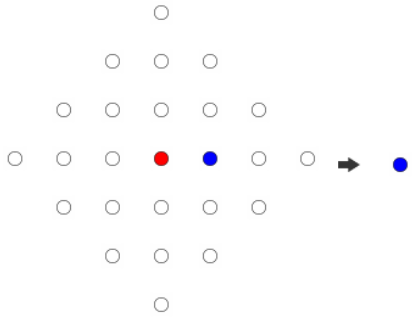
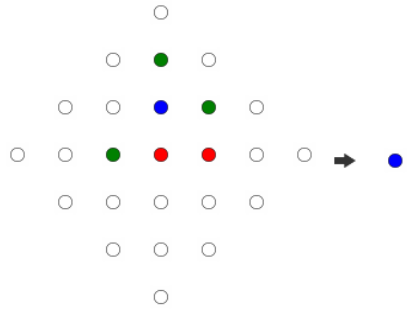
Theorem 6.3. *Decontamination using the road traffic approach with conserved flow is feasible in a 2D CA of size* $n * n$ *under the von Neumann neighbourhood by using exactly 2 decontaminating cells if the visibility Vh is equal to 3 and the immunity time It is* $2n-1$. *The decontamination process is performed using* $n * \left\lceil \frac{n}{2} \right\rceil$ *steps*

Proof:

First, we show that at least $2n-1$ units of immunity time are needed. Clearly, any cell in the first row needs at most n units of immunity time as it is automatically protected by the second row of cells. However, cells in the second row only receive protection when the third row gets decontaminated. The protection period depends on the flow of decontamination which has a direct impact on the time the equivalent cell below gets decontaminated. If the second row has a flow of decontamination from right to left (resp. from left to right), then the cell that needs the most duration of immunity is the cell located on the rightmost (resp. leftmost) of the second row. This cell gets decontaminated first and is exposed while its row processes the decontamination ($n-1$ units of time), and will need additional protection until the third row gets decontaminated (n units of time). Therefore, at least $2n-1$ immunity time is needed.

Second, with respect to the time completion of the process, it is obvious that a full row gets decontaminated with n steps. Since two rows get simultaneously decontaminated and the CA is composed of $\frac{n}{2}$ pair of rows, then if n is even, the CA is decontaminated in $n * \frac{n}{2}$ units of time. If n is odd, the process lasts $n * \left\lceil \frac{n}{2} \right\rceil$ units of time.

Third, to prove that it is feasible, we need to show that such a set of rules that will perform the operation exist. These rules are listed in the following table.

#	Configuration	Next State	Notes
R1			Any decontaminating cell will be decontaminated in the next step.
R2			Left to Right motion on the Horizontal line
R3			Right to Left motion on the Horizontal line
R4			Jump to the next decontaminating cell on the left vertical border

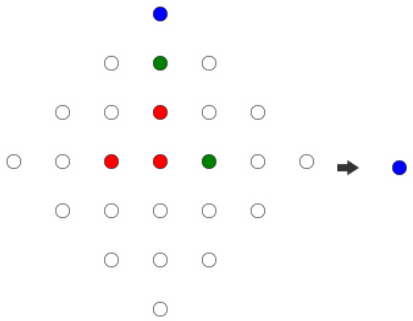
R5		Jump to the next decontaminating cell on the right vertical border

Table 6.1: Rules for Basic Decontamination in Finite CA using the Road Traffic approach (with flow conservation) under the von Neumann neighbourhood with *Vh*=3

6.2.3.2. The pattern retrieval with inverse decontamination flow

By following the pattern retrieval depicted in Figure 6.3b, we show that decontamination using the road traffic algorithm is *only* feasible:

- under a von Neumann neighbourhood of $Vh \geq 3$ or
- under a Moore neighbourhood of $Vh \geq 2$

Theorem 6.4. *Decontamination using the road traffic approach with inverse flow is not feasible in a 2D CA of size* $n * m\ (n \leq m)$ *under the von Neumann neighbourhood when using only 2 decontaminating cells if Vh= 2.*

Proof:

To prove that it is not feasible, we show a configuration of the CA during a transition that shows a non-deterministic behaviour. We use Figure 6.4 as a reference in the proofs.

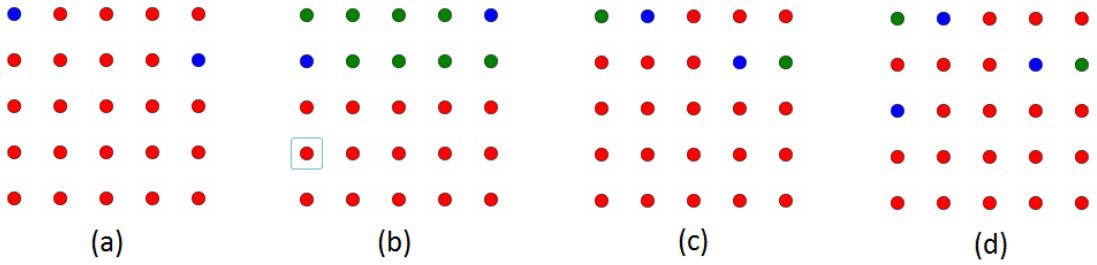
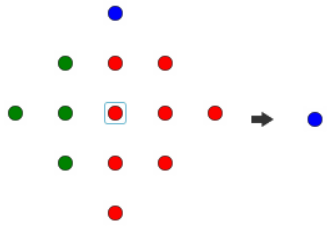


Figure 6.4: Counterexample of configuration during the Road Traffic approach when Vh=2

Without loss of generality, assume we have a CA with width=5 and height=5. At the initial stage of the road traffic algorithm, we have the configuration (*a*). At the end of the first iteration of the algorithm (*t*=4), the CA has the configuration (*b*). At *t*=5, the framed cell in (*b*), located in the first column and the 4th row, should transit to a decontaminating state.

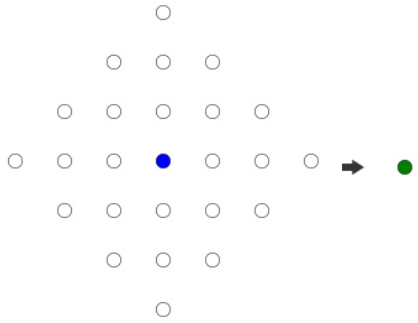
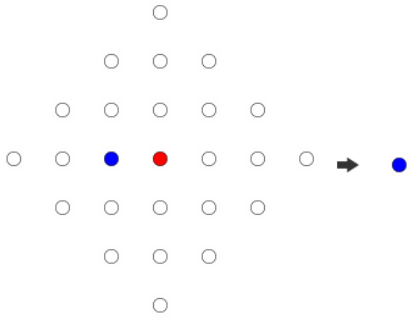
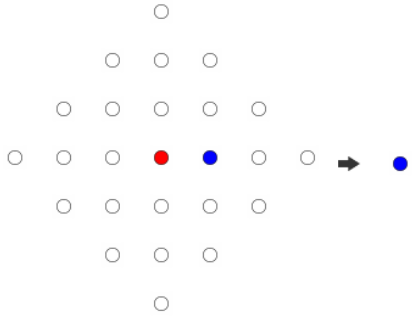
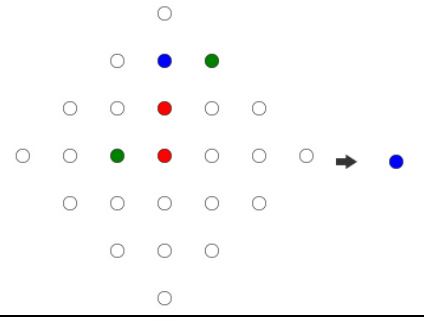
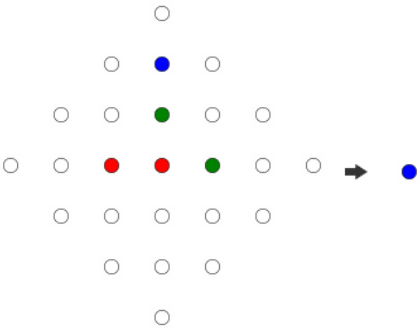


Therefore, the CA necessarily contain the following rule among its set of transition rules. However, the same rule will be applied to the cell located in the 3rd row and first column of configuration (*a*) which will give the configuration of (*d*) at *t*=1 instead of the desired configuration (*c*). This completes our proof. We show in the next theorem that by increasing the visibility from *Vh=2* to *Vh=3*, the configuration depicted in (*d*) can be avoided.

Theorem 6.5. *Decontamination using the road traffic approach with inverse flow is feasible in a 2D CA of size* $n * n$ *under the von Neumann neighbourhood when using only 2 decontaminating cells if* $Vh = 3$ *and the immunity time equal to* n .

Proof:

To prove that it is feasible, we need to show that such a set of rules that will perform the operation exists. Indeed, these rules are listed in the following table.

#	Configuration	Next State	Notes
R1			Any decontaminating cell will be decontaminated in the next step.
R2			Left to Right motion on the Horizontal line
R3			Right to Left motion on the Horizontal line
R4			Jump to the next decontaminating cell on the left vertical border.
R5			Jump to the next decontaminating cell on the right vertical border

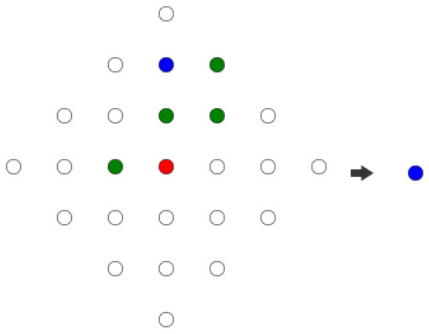
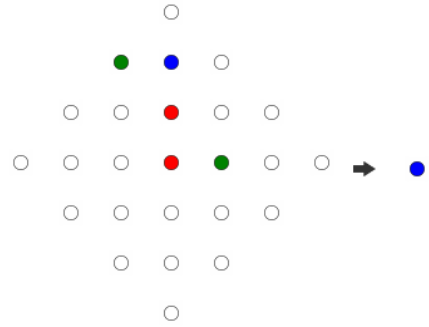
R6		The complementary of R4.
R7		The complementary of R5

Table 6.2: Rules for Basic Decontamination in Finite CA using the Road Traffic approach with inverse flow under the von Neumann neighbourhood with *Vh*=3

A few remarks emerge from this new algorithm:

- In order to overcome the unfeasibility of the algorithm when *Vh*=2 as stipulated in *Theorem 6.4*, a larger view of the neighbourhood is necessary. For the configuration example enunciated within the proof for Theorem 6.4, the presence of the decontaminated cell, located from a column offset of *1* and a row offset of *-2* from the center cell within the rule R4 (green cell on the top right of the rule), allows the distinction between the two previously mentioned cells which engender the non-deterministic behaviour stipulated in the proof.
- The first algorithm listed in Table 6.1 contains two fewer rules compared to the new rules listed in Table 6.2 even if both strategies uses the same visibility *Vh*=3. The explanation resides in the nature of the propagation flow of the second algorithm depicted by Figure 6.3b which requires a change of flow. This behaviour requires the addition of two more rules, R6 and R7. The benefit is that the new algorithm (Table 6.2) can have the first initiator decontaminating cell located in the left foremost or the right foremost position of the first row (and the second decontaminating cell in the second row

will be located on the opposite side). This is not the case for the algorithm in Table 6.1, which requires the initiator to be located on the left foremost in the first row and the right foremost in the second row. Changing the two initiators for the algorithm of Table 6.1 requires a new set of rules.

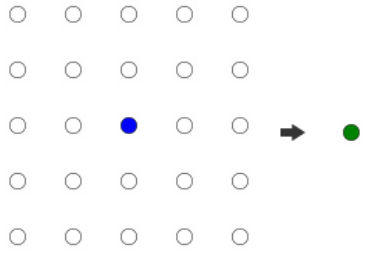
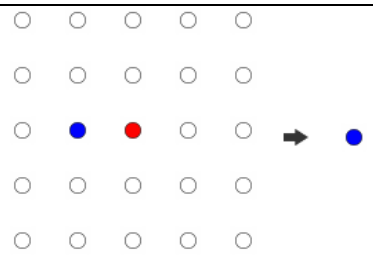
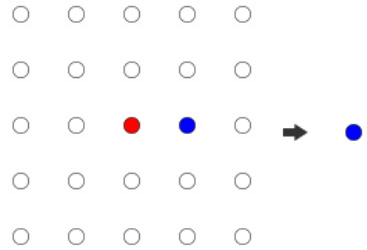
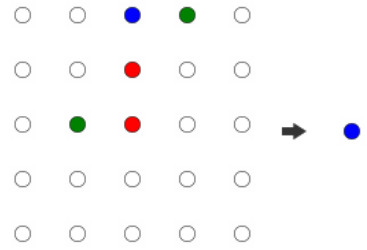
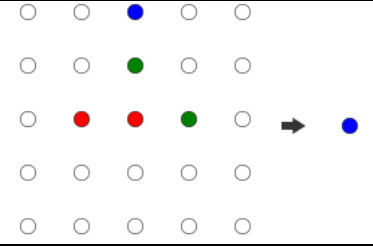
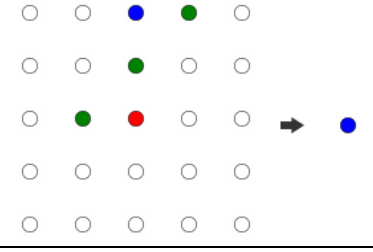
Theorem 6.6. *Decontamination using the road traffic approach with inverse flow is feasible and time-optimal in a 2D CA of size* $n * n$ *under the Moore neighbourhood when using only 2 decontaminating cells if Vh is equal to 2 and the immunity time equal to* n.

Proof:

To prove that it is feasible, we need to show that such a set of rules that will perform the operation exists.

Table 6.2 shows the rules of decontamination under the von Neumann neighbourhood when the visibility *Vh*=3. Our claim is that each rule can be transcribed using a Moore neighbourhood with a visibility *Vh*=2 and retain the same re-contamination properties. We prove that each rule can be replicated under the Moore neighbourhood. The first rule R1 is neighbour agnostic and can be defined in any CA. The rules R2 and R3 only involve the horizontal neighbourhood with a visibility *Vh*=1 (left or right neighbourhood) which are also part of the Moore neighbourhood. Regarding the last four rules (R4, R5, R6 and R7), one sees that every physical state (that is, each non generic cell in each configuration of a neighbourhood) are all located within a radius of Moore of a visibility *Vh*=2. The following Table 6.3 shows the rules of decontamination under the Moore neighbourhood when the visibility *Vh*=2.

Since the number of decontaminating cells is fixed at each stage of the algorithm and the strategy is monotone, *Corollary 4.1* induces that the raod-traffic strategy is time-optimal.

#	Configuration	Next State	Notes
R1			Any decontaminating cell will be decontaminated in the next step.
R2			Left to Right motion on the Horizontal line
R3			Right to Left motion on the Horizontal line
R4			Jump to the next decontaminating cell on the left vertical border.
R5			Jump to the next decontaminating cell on the right vertical border
R6			The complementary of R4.

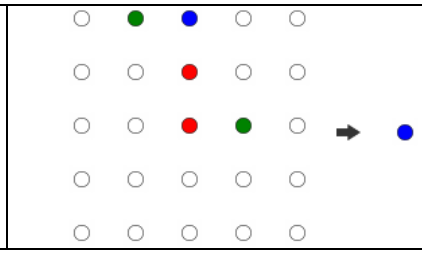
R7		The complementary of R5

Table 6.3: Rules for Basic Decontamination in Finite CA using the road Traffic approach (with inverse flow) under the Moore neighbourhood with *Vh*=2

6.2.4. Similar strategies on sub networks

Looking at the strategies in the previous subsection, we note that they already carry out a subdivision of the CA in groups of two rows, and the same movements are reapplied on each group by finding rules to jump to the next pair of rows. Since the movements are horizontal, we investigate another subdivision in which the CA are split by vertical cuts. The network could be seen as a family of disjoint sub networks and each could be decontaminated using one of the above algorithms. The idea is to subdivide the network and split it into k truncated sub-networks as in Figure 6.5. Each truncated sub-network is then modelled by a CA. By doing so, transition rules are applied to each sub CA according to the strategy mentioned in the previous section.

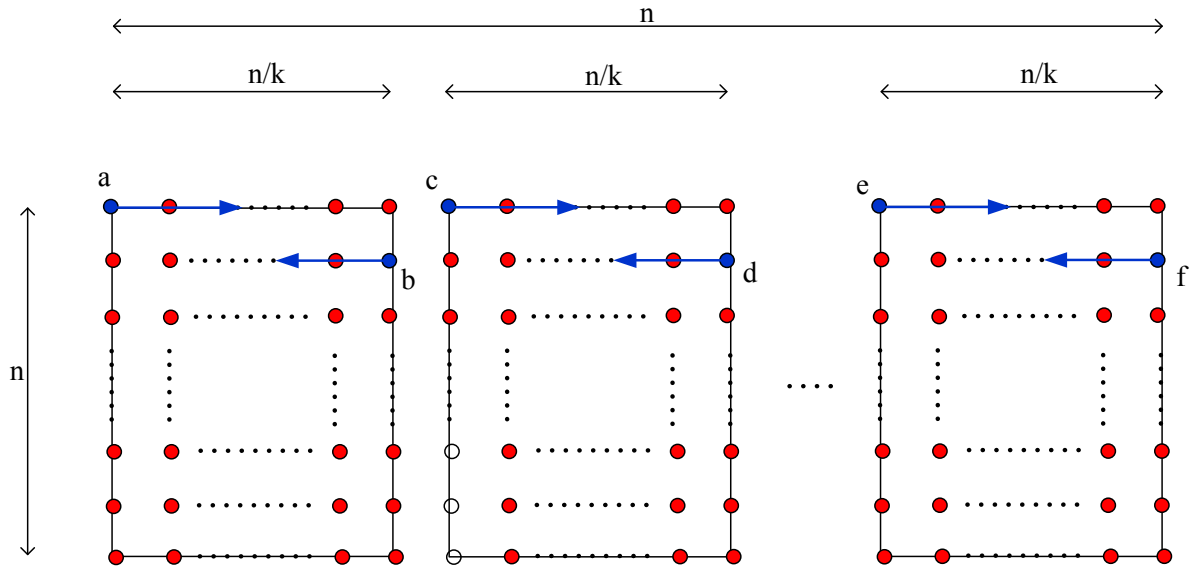


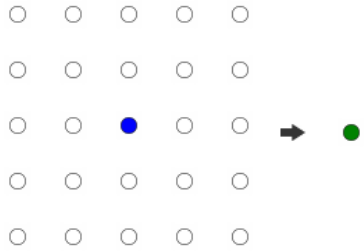
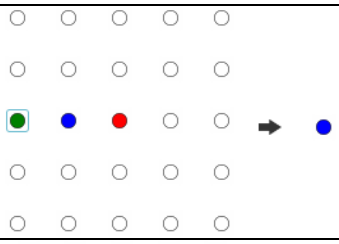
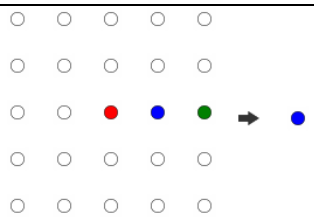
Figure 6.5: The cut strategy of the road traffic approach

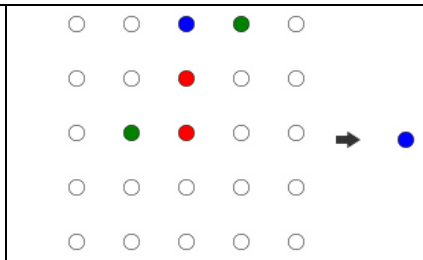
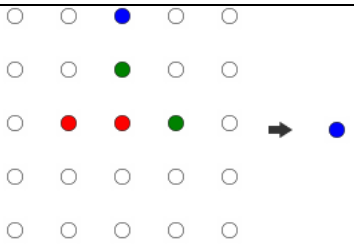
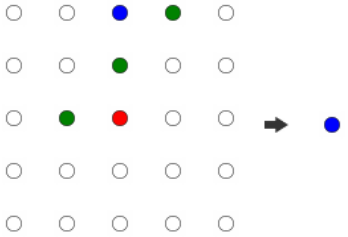
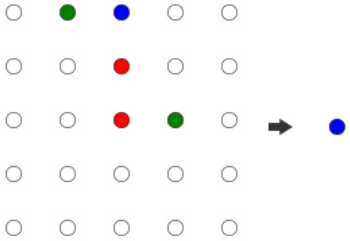
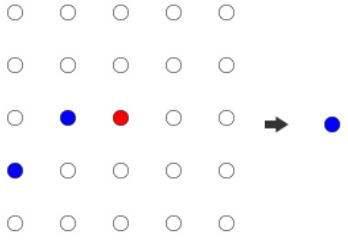
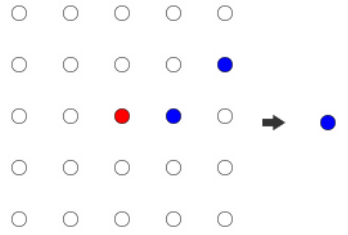
Theorem 6.7. *Decontamination using the road traffic approach can be achieved in a 2D CA of size* $n*n$ *by using 2*k decontaminating cells under the Moore neighbourhood of visibility Vh=2. The decontamination process is performed using* $\left\lceil \frac{n}{k} \right\rceil * \left\lceil \frac{n}{2} \right\rceil$ *steps and the immunity time that is needed is* $It = 2\left(\frac{n}{k} - 1\right)$

Proof:

To prove that it is feasible, we need to show that such a set of rules that will perform the operation exists.

Table 6.4 shows the rules of decontamination under the Moore neighbourhood. Note each rule below can be replicated using a von Neumann neighbourhood of *Vh*=3 since all non-generic cells involved within each rule is included within the von Neumann neighbourhood.

#	Configuration	Next State	Notes
R1			Any decontaminating cell will be decontaminated in the next step.
R2			Left to Right motion on the Horizontal line (except for the internal initiator) e.g. initiator located on the left border
R3			Right to Left motion on the Horizontal line (except for the internal initiator) e.g. initiator located on the right border

R4		Jump to the next decontaminating cell on the left vertical border.
R5		Jump to the next decontaminating cell on the right vertical border
R6		The complementary of R4.
R7		The complementary of R5
R8		Left to Right motion on the Horizontal line of the internal initiator e.g. internal initiator on the 1st row, 5th …
R9		Right to Left motion on the Horizontal line of the internal initiator e.g. internal initiator on the 2nd row, 6th …

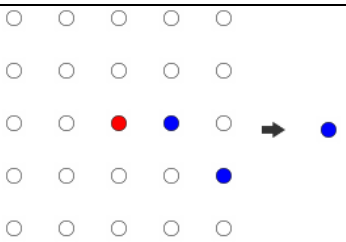
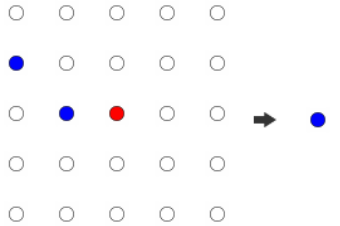
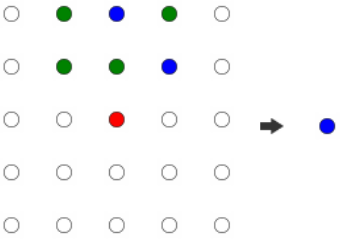
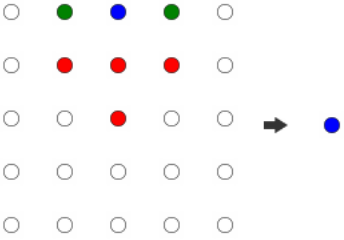
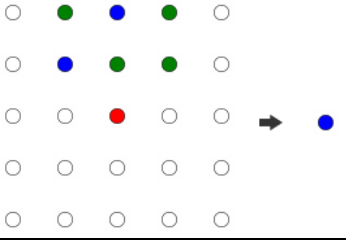
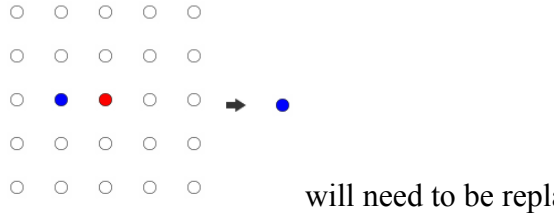
R10		Right to Left motion on the Horizontal line of the internal initiator (inverse flow) e.g. internal initiator on the 3nd row, 7th …
R11		Left to Right motion on the Horizontal line of the internal initiator (inverse flow) e.g. internal initiator on the 4th row, 8th …
R12		Jump to the next decontaminating cell of an internal cell from a left-to-right flow e.g. 1st row to 3rd row
R13		Jump to the next decontaminating cell of an internal cell from a right-to-left flow e.g. 2nd row to 4th row and its inverse left-to-right flow 4th row to 6th
R14		Jump to the next decontaminating cell of an internal cell from a right-to-left flow (Inverse flow of R12) e.g. 3rd row to 5th row

Table 6.4: Rules for Decontamination in Finite CA using the road traffic approach (with inverse flow) using 2*k decontaminating cells under Moore neighbourhood with *Vh*=2

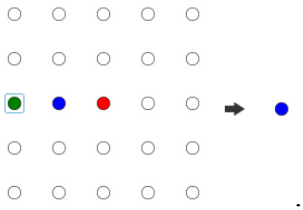
The difference between the base strategy (

Figure 6.1) and the one subdivided in *k* sub-networks (Figure 6.5) are the insertion of new internal cell initiators (cells *b* and *c* of Figure 6.5). Clearly, the system needs to have the equivalent of R2, R3…R7 for these new internal cells. We also need to make sure that the addition of these new rules is not interfering with the existing rules and vice versa.

1. Both rules R2 and R3 have to be more specific to target only the initiators located on the border to avoid interfering with the rules for internal initiators. (The original definition of R2 and R3 of Table 6.3 will set both the left and right neighbours of the internal initiators in a decontaminating state, which we want to avoid as we want the internal initiator to start the decontamination from one side only). Therefore, R2's definition

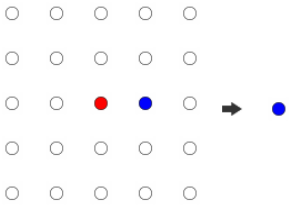


will need to be replaced by

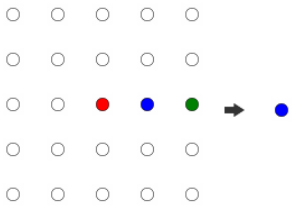


.

and R3's definition



will change to



.

2. We will need to add 4 new rules analogous to R2 and R3 dedicated to these internal cells. Two new rules similar to the flow encountered on the 1st row and 2nd row are needed (respectively R8 and R9), as are 2 other rules for the inverse flow, similarly encountered on the 3rd and 4th row (R10 and R11).

3. We will need to add the rules that will allow the jump of an internal cell when it reaches the extremity of the sub-network. Rule R12 will represent the jump of an internal cell from a left-to-right flow from the 1st row to the 3rd row (and continuously from the 5th to the 8th, etc.). Rule R4 accomplishes the same rule with its inverse flow. Additionally, rule R13 is able to embody both rules required for the jump of an internal cell of a normal flow (2nd row to 4th , 6th row to 8th row, etc.) and its inverse flow (4th to 6th, 8th to 10th, etc.).

4. With respect to the immunity time needed, we note that the cell which needs the most immunity time value is the one similar to the internal cell *b* of Figure 6.5. Since $\frac{n}{k}$ is the

sub-network width, $\frac{n}{k}-1$ units of time are needed for its contaminated right neighbour to reach a decontaminating state. Also, because of the Moore neighbourhood, the cell needs another $\frac{n}{k}-1$ units of time for its contaminated bottom-right neighbour to be in a decontaminating state. All of its remaining neighbours are already decontaminated. Therefore, the immunity time needed is $2\left(\frac{n}{k}-1\right)$ steps.

6.3. Diagonal snake Approach

6.3.1. Base Idea

The main goal is to be able to perform the decontamination using only a single decontaminating cell. The idea is to choose a single initiator located at the top left of our CA and propagate in a diagonal zig-zag flow towards the opposite diagonal cell (bottom right corner). The concept is depicted in Figure 6.6.

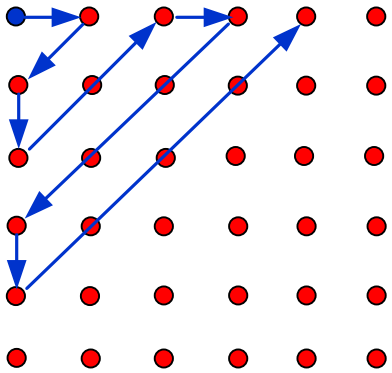


Figure 6.6: The diagonal snake approach within the Moore neighbourhood

Theorem 6.8. *Decontamination using the diagonal snake approach can only be achieved in a 2D CA of size* $n*n$ *under the Moore neighbourhood by using a single decontaminating cell if the immunity time is at least 2*(*n-1*).

Proof:

The cell that needs the most immunity time is the decontaminated cell which needs the longest protection time while all its direct contaminated neighbors are able to spread their viruses. These are cells laying on the border (horizontal or vertical) of the CA (see Figure 6.6). To ensure that the cell is protected, it needs to wait for the propagation of the decontaminating cell to navigate the entire diagonal, and to wait for the next diagonal to be fully decontaminated for a total of two complete steps of decontaminating two diagonals. As a comparison, an inner cell needs less as it is protected after approximately half of the containing diagonal and the next diagonal. .

In Figure 6.7, we differentiate the cases when n is even and when n is odd since the diagonal has the potential to be reached differently by the diagonal flow. In both cases, we note that the cells which need the most immunity time are a or e. After e is decontaminated, it is in danger of recontamination until d reaches the decontaminating state. In practice, this means that e needs the entire decontamination of the diagonal $\{e,a\}$ and $\{b,c\}$ and the cell d to be in a decontaminating state. Decontaminating the diagonal $\{e,a\}$ needs n-1 steps and the diagonal $\{b,c\}$ needs n steps for a total of (n-1)-1+n units of time ((n-1)- because a's immunity time begins only after a gets decontaminated). With the same logic applied to the cell a, the cell is open to recontamination until f reaches the decontaminating state. This means that a needs the entire decontamination of the diagonals $\{d,f\}$ and $\{b,c\}$. Decontaminating the diagonal $\{d,f\}$ needs n-1 steps and $\{b,c\}$ needs n steps, for a total of (n-1)-1+n units of time.

Since the algorithm requires n steps to navigate the full diagonal and n-2 steps to navigate the previous (or the next) diagonal, at least $2n$-2=2*(n-1) units of time are needed to protect the cell.

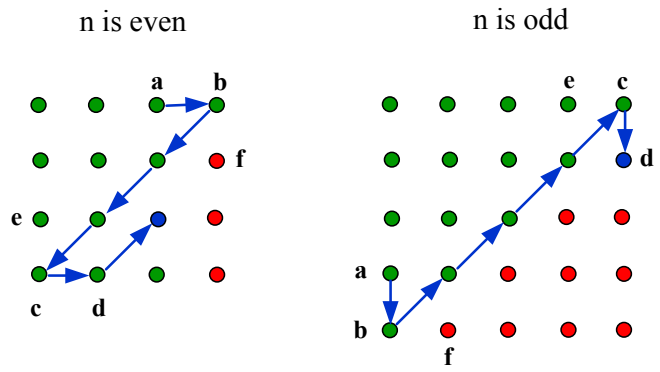


Figure 6.7: Execution difference around the diagonal depending on the value of n

6.3.2. Sample Execution

At the initial stage t=0, we choose one initiator located at the top left (at coordinate (1,1)) to start the algorithm (see Figure 6.8). At time t=1, the initiator will cause its right neighbor, located at coordinate (1,2), to become in a decontaminating state because it sees a flow of decontamination coming from the *left*. At time t=2, the cell at coordinate (2,1) goes into a decontaminating state because it sees a flow of decontamination coming from the *top-right*. At time t=3, a flow coming from the *top* makes the cell located at (3,1) to also be in a decontaminating state. And at time t=4, the internal cell (1,1) goes into decontaminating because of a *bottom-right* flow. In the remainder of the algorithm, cells process their state similar to these previous stages. After examination of the flow presented Figure 6.6 and the scrutiny of the sample execution, these various moves can be seen as the results of different propagation flows listed in Table 6.5.

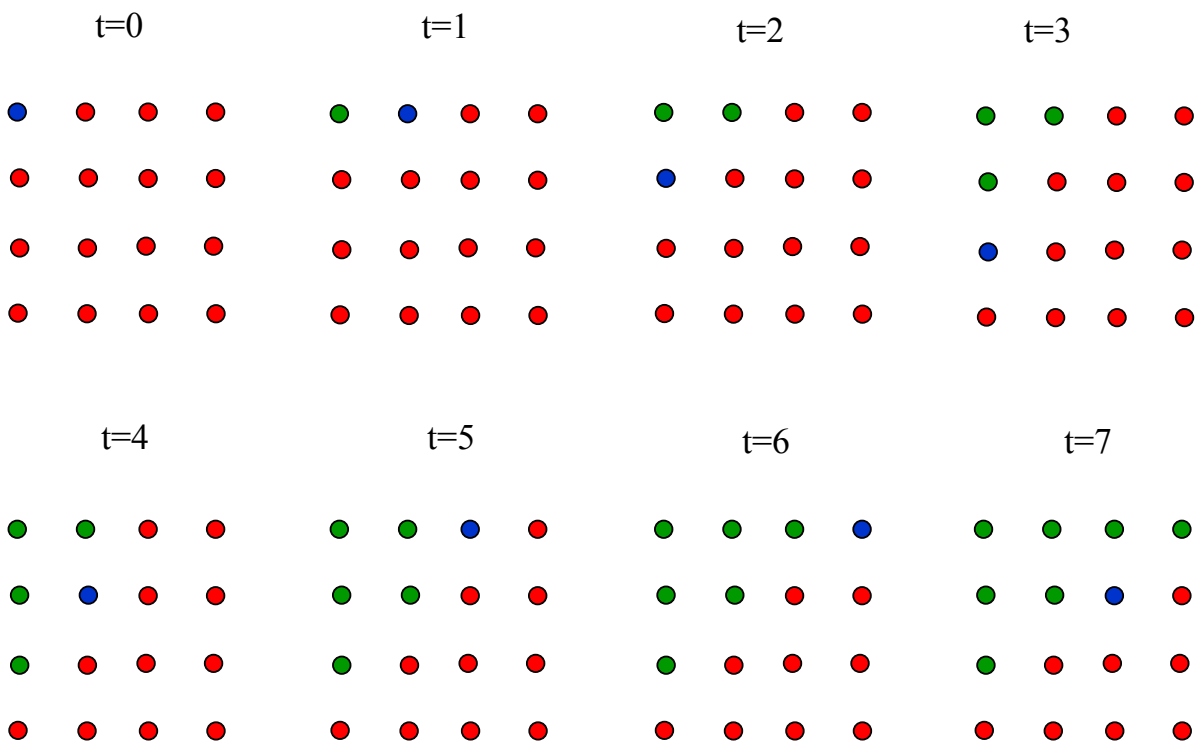


Figure 6.8: Propagation of the diagonal snake approach within the Moore neighbourhood

Table 6.5 presents four distinct propagation flows coming from the *left*, the *top*, the *bottom-left* and the *top-right*. A cell changes its state from contaminated to decontaminating by analyzing the propagation flow and with some additional parameters. For instance, at time t=3, one should expect that the 3rd cell of the top border (1,3) will transition into a decontaminating state, similar to its left neighbour (1,2) at time t=2. Our claim is that these additional parameters can be extrapolated into a Boolean function that analyzes the distant neighbourhood of the current cell. The 3rd cell of the top border (1,3) did not transition into a decontaminating state at time t=3 because it did not satisfy the function f_1 like its left neighbour (1,2) does at time t=2. We will show in the upcoming sections that these functions are in fact a verification of the state of the neighbourhood of *Vh=2*.

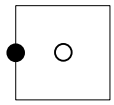
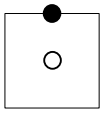
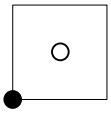
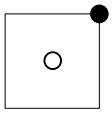
Direction flow	Partial neighbourhood configuration	Additional input function	Next State	Notes
Left-to-Right		f_1	●	Horizontal flow coming from the left with additional restriction f_1
Top-to-Bottom		f_2	●	Vertical Flow coming from the top with additional restriction f_2
Bottom Left to Top-Right		f_3	●	Diagonal Flow coming from the bottom left with additional restriction f_3
Top Right to Bottom Left		f_4	●	Diagonal Flow coming from the top right with additional restriction f_4

Table 6.5: Direction flow of the decontaminating transition state

We now show that consulting the direct neighbourhood is not sufficient for making a decision with regards to the transition state definition and that additional input functions f_1, f_2, f_3 and f_4 are required.

Theorem 6.9. *Decontamination using the Diagonal snake approach cannot be achieved in a 2D CA of size* $n * n$ *under the Moore neighbourhood of visibility Vh=1.*

Proof:

To prove the theorem, we will show that it is not possible to find decontamination rules if Vh=1.

To this end, we show that there are at least two cells within the CA that need to behave differently at time t+1 (they are in different states) even if both cells have exactly the same direct neighbourhood configuration (that is Vh=1) at time t. Indeed, having such rules makes

the automata non deterministic. The cells *a* and *c* in Figure 6.9 are these cells. Both cells have the same properties as they both lay on the top border of the CA. The neighbourhood configuration (with *Vh*=1) of *a* at time *t*=0 is exactly the same as the neighbourhood configuration of *c* at time *t*=1. At time *t*=0, *a* has its left neighbour in decontaminating mode, all remaining existing neighbours are in a contaminated state, and *a* does not have top neighbours. The cell *c* has exactly the same configuration at time *t*=1 since its left neighbour, which is *a*, will also be in decontaminating mode, all remaining existing neighbours are in a contaminated state, and *a* does not have top neighbours. The cell *a* must change its state to decontaminating in the next step (at time *t*=1), however, *c* must remain contaminated at the next step (at time *t*=2). Therefore, no rules that take account of a direct neighbourhood are feasible and thus ends our proof.

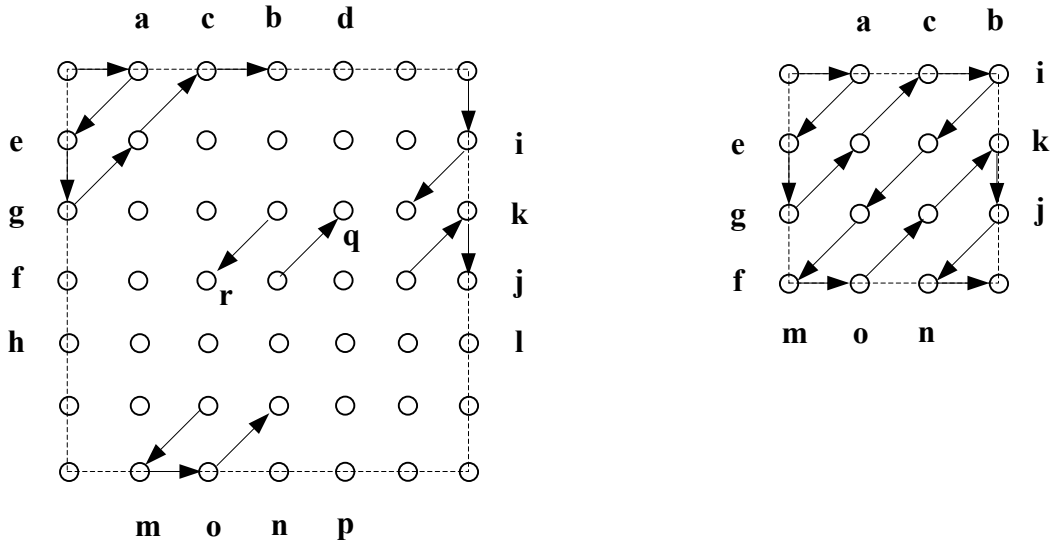


Figure 6.9: The different type of cells within the CA during the diagonal snake strategy

Let us investigate the nature of the functions f_1, f_2, f_3 and f_4.

We take the case of the cells *a* and *c* as an example to define the nature of f_1. The logic of the definition of the other functions f_2, f_3 and f_4 is the same. Let us consider the configurations of the CA shown in Figure 6.10, a snapshot of Figure 6.9 at time *t*=0 and *t*=1. Note that *a* is at coordinate (1,2). As observed, the *Vh*=1 neighbourhood configuration of the cell *a* at time *t*=0 is exactly the same as the neighbourhood configuration of the cell *c* at

time t=1, that is $N^0(1,2) = N^1(1,3)$. Our goal is to have the cell a in a decontaminating state at time t=1 but to allow c to keep its original state at time t=2. Therefore, a needs to recognize a left-to-right flow at time t=0 and c needs to know that is not a bottom-left flow. To do so, a needs to consult the value of the cell u, a cell located at distance Vh=2, and more precisely, located at an offset of 1 row and 2 columns on its left, that is (2, 0). Since the cell u is in a decontaminated state, a knows it is a flow from the left. At time t=1, the cell c consults the cell at the same offset, which in this case is the cell v located at (2,1). Since the cell v is not decontaminated yet, c knows that it needs to wait for the flow coming from the bottom-left before changing its state. The function f_1 is composed by a Boolean function that takes as its parameter a cell located at coordinate (i,j) and verifies if the cell located at coordinate (i+1, j-2) is in a decontaminated state.

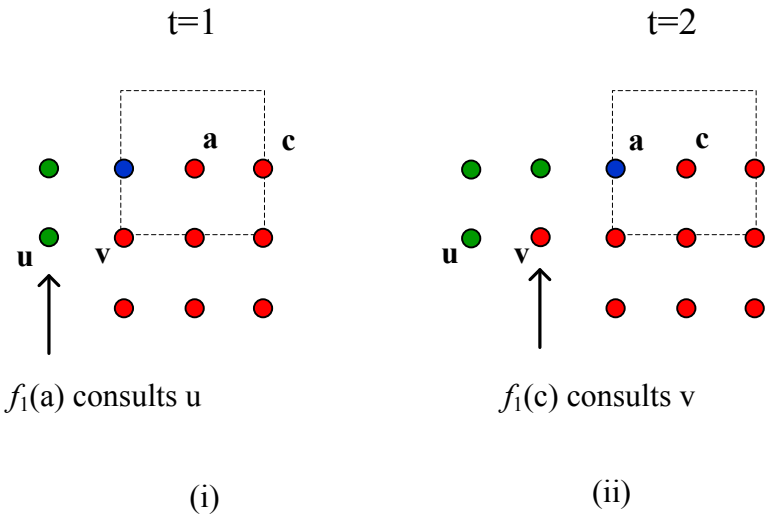


Figure 6.10: An attempt to define f_1 within the diagonal snake strategy

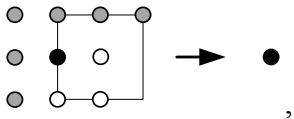
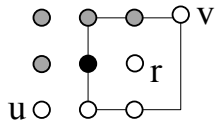
Theorem 6.10. *Decontamination using the Diagonal snake approach is achieved in a 2D CA of size* $n*n$ *under the Moore neighbourhood with a single decontaminating cell if the visibility Vh=2 and the immunity time It=2*(n*-1*)

Proof:

Note that we have already given some proofs that 2n-1 units of immunity time are needed.

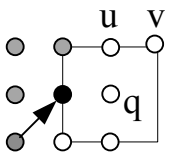
We now show that rules which fulfill the decontamination exist. To prove that these rules are valid and that there is no collision between the rules, we analyse the flow to distinguish the different types of cells in the CA with respect to the propagation of the flow. Figure 6.9 shows the different types of cells caused by the flow The cells *a, g, i, o, q* and *r* can represent any cells in the CA. That is, any cell of the automata during the algorithm execution has the same neighbourhood configuration as one and exactly one of these cells. Therefore, each cell in the decontamination rules table, listed in Table 6.6, contains as many rules as the number of cells previously listed.

In order to prove the validity of the rules listed in Table 6.6, a complete proof should list each rule R2, R3, ...,R7 and validate each against any possible configuration of *a, g, i, o, q* and *r* . An exhaustive proof should validate 6*6=36 tests. We follow with two examples of these tests.:

Example 1: Validation of rule R2 against the configuration of *r*. The rule R2, defined in gray scale mode as  , is a rule that defines a left-to-right flow applied to cells laying on the top border of the CA. We want to verify that the same rule is not causing a left-to-right flow against *r*. Thus, r should keep its state unchanged even if its left neighbour is decontaminating. At a certain time *t*, the decontamination reaches the left neighbour of *r* and the configuration of *r*'s neighbourhood is depicted as 

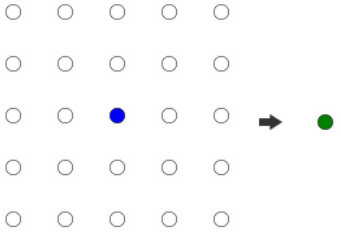
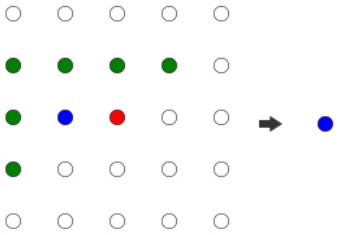
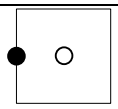
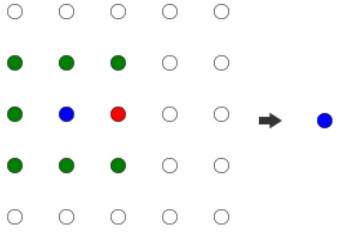
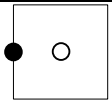
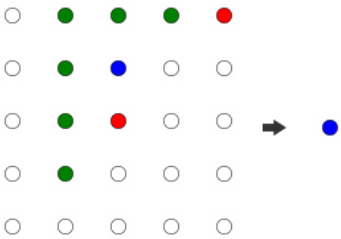
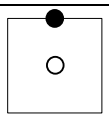
. We clearly see that the cells *u* and *v* show different states, therefore the rule R2 is valid for the configuration of *r*.

Example 2: Validation of rule R2 against the configuration of *q*. We want to verify that the same rule does not cause a left-to-right flow against *q*. Thus, *q* should keep its state unchanged even if its left neighbour is decontaminating. At a certain time *t*, the decontamination reaches the left neighbour of *q* and the configuration of *q*'s neighbourhood

is depicted as 

. Again, we see that the cells *u* and *v* show different states, therefore the rule R2 is valid for the configuration of *q*

Since the number of decontaminating cells is fixed at each stage of the algorithm and the strategy is monotone, *Corollary 4.1* induces that the diagonal-snake strategy is time-optimal.

#	Configuration	Next State	Notes
R1			Any decontaminating cell will be decontaminated in the next step.
R2			 Left-to-right flow against cells laying on the top border cell similar to cell to *a* & *b* of Figure 6.9
R3			 Left-to-right flow against cells laying on the bottom border (including Bottom-Right corner cell similar to cell to *o* & *p* of Figure 6.9
R4			 Top-to-Bottom flow against cells laying on the left border (including Bottom-left corner) cell similar to cell to *g* & *h* of Figure 6.9

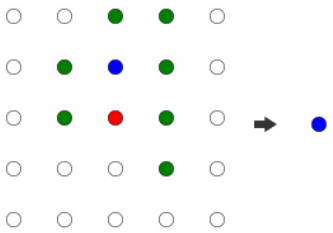
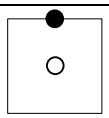
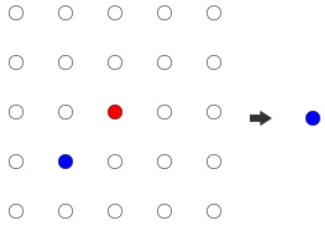
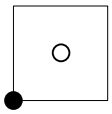
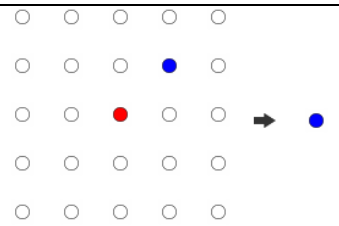
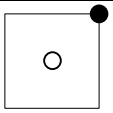
R5		 Top-to-Bottom flow against cells laying on the right border cell similar to cell to *i* & *j* of Figure 6.9
R6		 Diagonal flow from the bottom left cell similar to cell to *q, k* & *c* of Figure 6.9
R7		 Diagonal flow from the top right cell similar to cell to *r*, *e* & m of Figure 6.9

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Table 6.6: Rules for Decontamination in Finite CA using the diagonal snake approach move under the Moore neighbourhood when *Vh*=2 and for an immunity time *It=2n*-1

6.3.3. Division and Re-Application

The advantage of the diagonal snake method is the ability to decontaminate the network with only one single cell decontaminating. In addition, we note that the spread is done with a particular movement that can be easily replicated on different corners of the CA. This is possible because of the symmetric structure of the four corners of our CA.

6.3.3.1. Case with 2 corner initiators.

The execution can be started by two corner initiators: the top-left and the bottom right cell as shown by Figure 6.11.

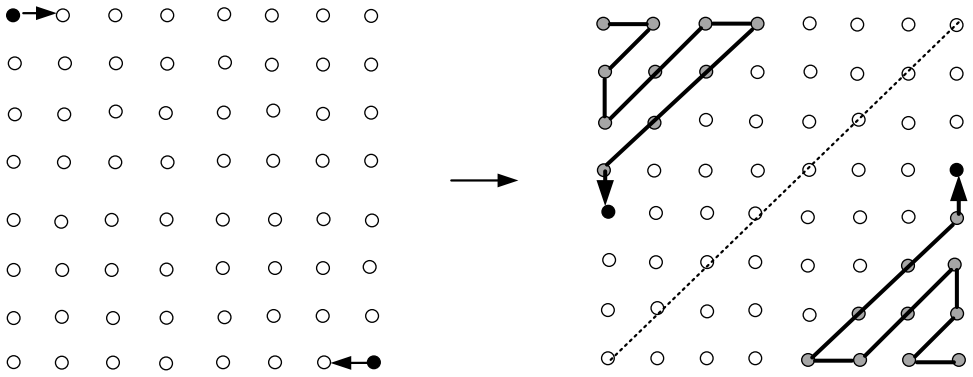


Figure 6.11: The subdividing strategy using 2 initiators.

The idea is to replicate the execution of the top left initiator with the initiator in the bottom-right corner. One can see that the execution of the algorithm from the bottom-right initiator is symmetric to the execution by the top-left corner initiator. Therefore, the rule building of this new strategy is to just use the same rule that controls the navigation of the original flow and rotate each rule to 180 degrees. The execution of the algorithm is completed when the two decontaminating cells meet along the diagonal of the CA.

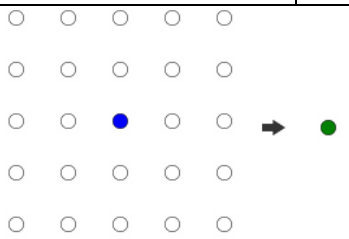
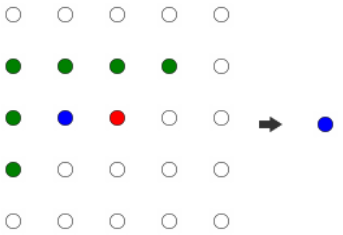
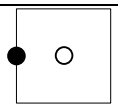
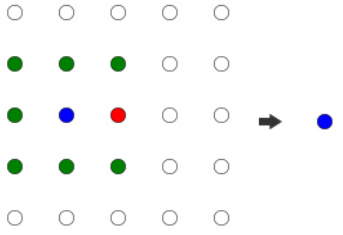
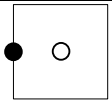
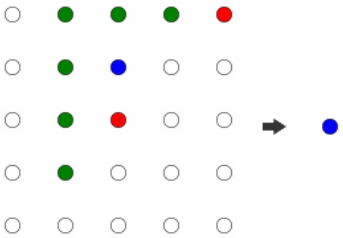
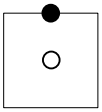
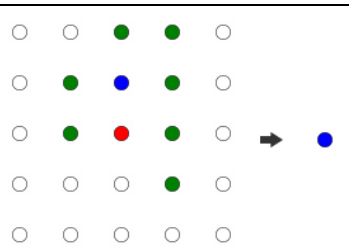
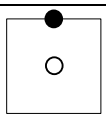
Theorem 6.11. *Decontamination using the Diagonal snake approach is achieved in a 2D CA of size n*n under the Moore neighbourhood with 2 simultaneously decontaminating cells if the visibility Vh=2 and the immunity time It=2n-3.*

Proof:

Similar to the proof of *Theorem 6.8* presented in the previous section, one can see that this time, the cell which needs the most immunity time is the one laying on the vertical border and located 3 rows below (or above) the corner cell containing the diagonal (the cells labeled *h* and *k* from Figure 6.9). The protection is required during the full decontamination of the diagonal containing the cell (*n*-4), the full decontamination of the next diagonal (*n*-1), and the first 2 cells of the full diagonal. The total of immunity time which is required is 2*n*-3 units of time..

The feasibility of the algorithm is presented in Table 6.7. The first seven rules are identical to the rules of the single initiator. The next four rules (R8, R9, R10, and R11) are added to

support the execution of the algorithm from the bottom-right initiator. Rule R8 is defined as symmetrical to rule R2. Similarly, rules R9, R10 and R11 are symmetrical to R3, R4 and R5 respectively. Note that both rules R6 and R7 do not have their symmetric rule defined as the diagonal flow of decontamination initiated by the bottom-right initiator is similar to the flow from the top-left initiator.

#	Configuration	Next State	Notes
R1			Any decontaminating cell will be decontaminated in the next step.
R2			 Left-to-right flow against cells laying on the top border cell similar to cell to *a* & *b* of Figure 6.9
R3			 Left-to-right flow against cells laying on the bottom border (including Bottom-Right corner cell similar to cell to *o* & *p* of Figure 6.9
R4			 Top-to-Bottom flow against cells laying on the left border (including Bottom-left corner) cell similar to cell to *g* & *h* of Figure 6.9
R5			 Top-to-Bottom flow against cells laying on the right border cell similar to cell to *i* & *j* of Figure 6.9

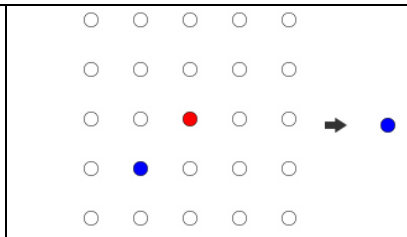
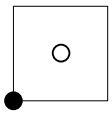
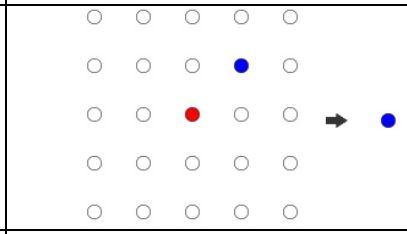
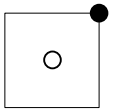
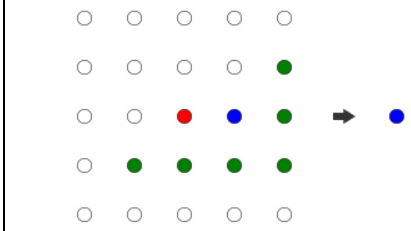
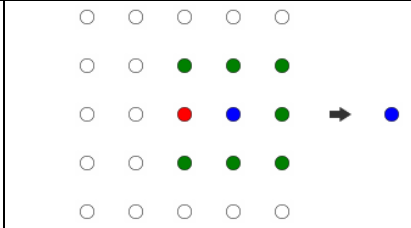
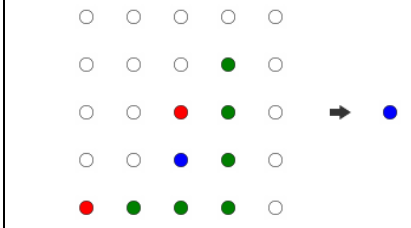
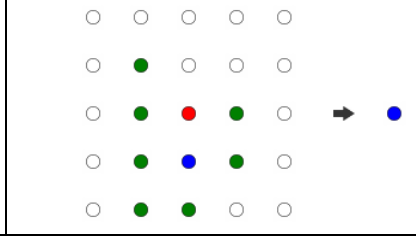
R6		 Diagonal flow from the bottom left cell similar to cell to *q*, *k* & *c* of Figure 6.9
R7		 Diagonal flow from the top right cell similar to cell to *r*, *e* & m of Figure 6.9
R8		The symmetric rule of R2
R9		The symmetric rule of R3
R10		The symmetric rule of R4
R11		The symmetric rule of R5

Table 6.7: Rules for Decontamination in Finite CA using the diagonal snake approach move with 2 corner initiators under the Moore neighbourhood of *Vh*=2.

6.3.3.2. Case with 4 corner initiators.

Figure 6.12 shows the way to cut the CA in order to produce sub-structure that it can be processed by 4 initiators. The goal is to reuse the same strategy on these substructures. In Figure 6.12(i), we easily retrieve the identical nomenclature of the parent because the size of the automata is even. What is needed is only a vertical and horizontal cut which separates our CA into 4 equal parts. To start the algorithm, the first step is to consider the four cell corners as initiators and execute the same strategy as in the base case (Figure 6.12a). The algorithm stops when the 4 central cells of our CA are decontaminated.

In Figure 6.12(ii), due to the size of the automata being odd, the CA could not be split into four equal parts. Obviously, there is always a possibility of splitting it into unequal blocks as suggested by Figure 6.12d. In this situation, the grid shall be divided into four parts of equal size plus one isolated single cell. The subdivision always holds when n is odd. Since n=2k+1, we can easily deduct that $n^2 = (2k+1)^2 = 4(k(k+1))+1$. Therefore, the size of each block is $k(k+1)$.

Proposition 6.1. *Decontamination using the Diagonal snake approach can be achieved in a CA under the Moore neighbourhood with 4 decontaminating cells if the visibility Vh=2 and the immunity time* $It = 2 * \left\lceil \frac{n}{2} \right\rceil - 1$

By looking at the behaviour of the decontamination flows between a CA of even size (see Figure 6.12(i)) and of an odd size (see Figure 6.12(ii)), we can see that the decontamination flow is similar in the early stage of the decontamination until the subdivided blocks meet on the border. For an even sized CA, the decontamination flow is resumed with a vertical or horizontal flow (Figure 6.12b). Conversely, the flow is resumed in a diagonal way for an odd sized CA (Figure 6.12d). The difference of execution automatically implies that the set of transition rules is different. The complexity of building the contamination rules for both cases is perceptible because one can see new configurations of neighbourhood arising. Therefore for both strategies, we have shown experimentally that decontamination is feasible and we have validated its feasibility by generating the rules using the research tool we have designed and that we present in the next chapter.

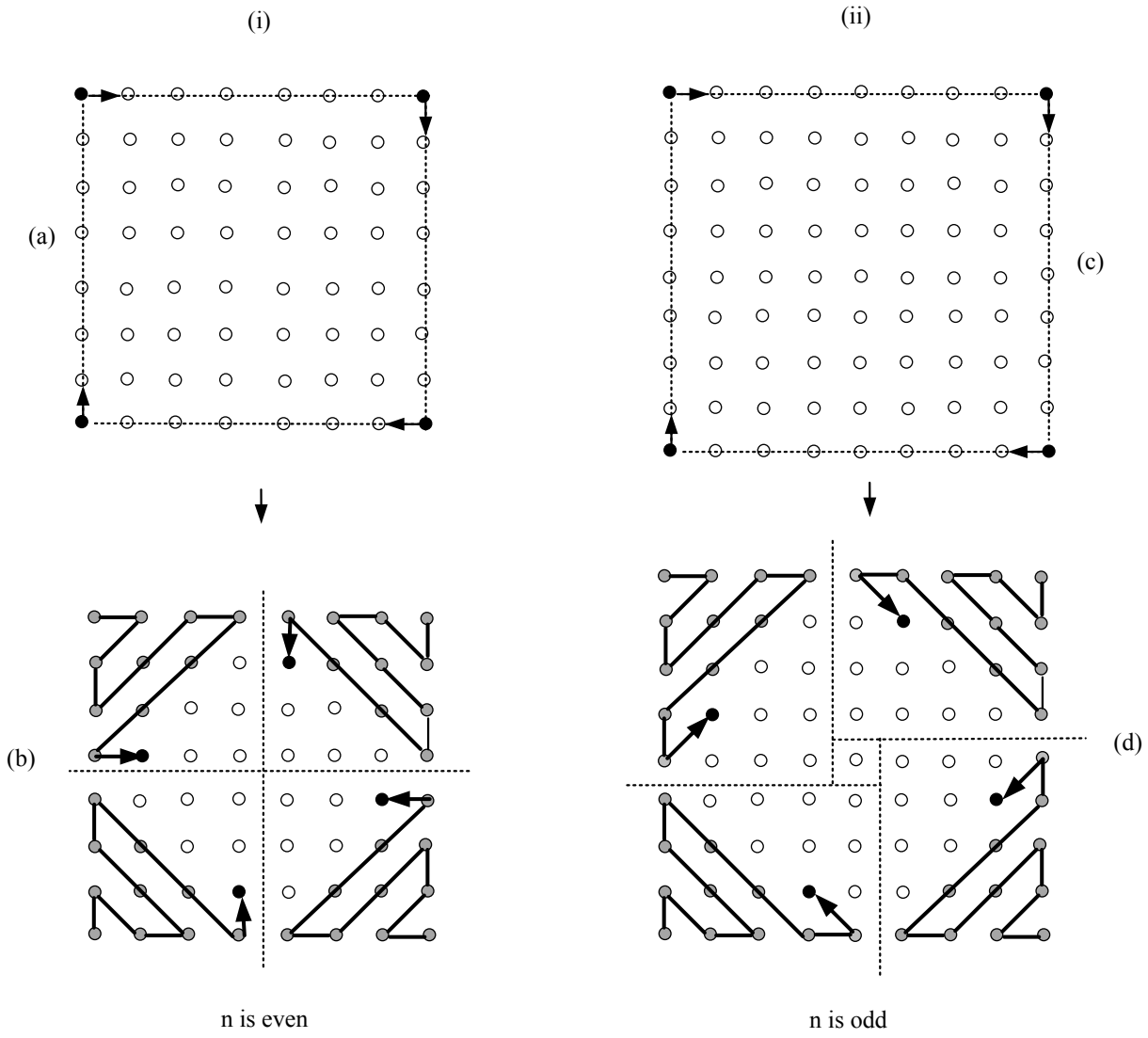


Figure 6.12: The subdividing strategy using the snake approach with 4 initiators

6.4. The subdividing strategy of the Diagonal Move Approach

In order to put the focus on the concept of subdivision, we consider the simplest diagonal approach which is the case of *Vh*=1 and *Cd*=1 as presented in Chapter 5. Indeed, the strategy of implementing the subdivision will be similar even for arbitrary values of *Vh* and *Cd*. We also recall that the topology that we consider is the *n***n* grid under the von Neumann neighbourhood. Besides, the value of the time of immunity is null since the base Diagonal Move performs without any Immunity.

Aside from the motivations dedicated to the diagonal move already mentioned in Chapter 5, another attractive property of the method is that its simple move pattern allows the launch of the diagonal movement from different areas of our CA.

6.4.1. Case with 2 corner initiators

Given that the motion pattern is from diagonal to diagonal, the most natural cut is to subdivide the CA into two triangles and begin decontamination from the two opposite corners of the triangles as suggested in Figure 6.13 (that is, from two corners of the CA diagonally opposite). For this, the algorithm just needs two initiators and starts decontamination diagonally as presented in Chapter 5. Taking the cell at the top-left corner as a decontaminating initiator will cause a flow to the right and downwards, while a decontaminating cell at the bottom-right corner will cause a flow to the left and upward. Eventually the two diagonals meet to stop decontamination. This process bring us to the next theorem.

Theorem 6.12. *Decontamination using the Diagonal approach is achieved in a 2D CA of size* $n*n$ *under the von Neumann neighbourhood with 2 initiators decontaminating cells during* n *units of time. Immunity time is not required*

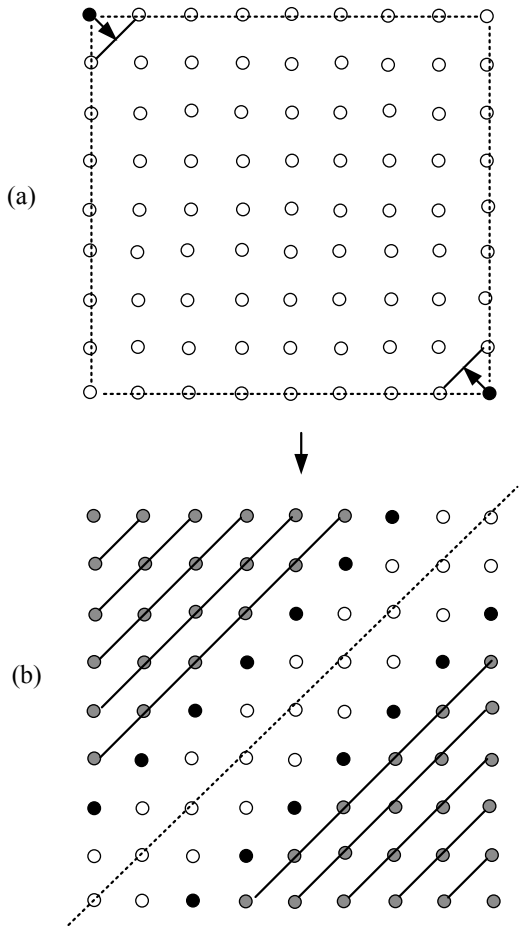


Figure 6.13: The divide and conquer diagonal strategy with 2 initiators

Proof:

Table 5.1 of Chapter 5 displays the rules for decontamination in Finite CA using basic diagonal move with the von Neumann neighbourhood when *Vh*=1 and *Cd*=1 with a single decontaminating cell initiator located on the top left of the CA. The rules were built according the type of cell for being either a cell laying on the border (R2 and R3) or an internal cell (R4). It is easy to see that the flow of decontamination started by a second initiator on the bottom right is diametrically symmetric to the flow of decontamination by the first initiator from the top left cell. Therefore, the new flow can be realized by adding new rules that are diametrically symmetric to R2, R3 and R4 which are R3, R4 and R5 respectively as seen in Table 6.8.

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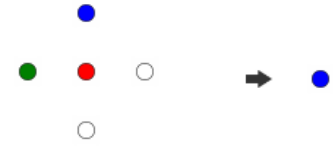
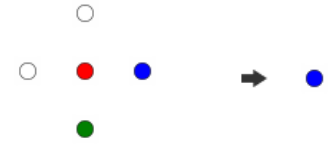
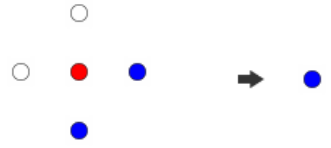
#	Configuration	Next State	Notes
R1			Any decontaminating cell will be decontaminated in the next step.
R2			Cell located on the top horizontal border of the CA
R3			Cell located on the left vertical border of the CA
R4			Internal Cell
R5			Diametrically symmetric to R2 Cell located on the bottom horizontal border of the CA
R6			Diametrically symmetric to R3 Cell located on the left vertical border of the CA
R7			Diametrically symmetric to R4 Internal Cell

Table 6.8: Rules for Basic Decontamination in Finite CA using basic diagonal move and two corner initiators under the von Neumann neighbourhood when Vh=1 and Cd=1

6.4.2. Case with 4 corner initiators

We saw that it was possible to reuse the diagonal approach with 2 decontaminating cells with the CA in two triangles. What is proposed in Figure 6.14 is the use of 4 decontaminating cells. We start the decontamination from the four corners of our CA. The decontaminating cell located at the top-left corner will propagate a flow to the right and

downward. Similarly, the decontaminating cell at the bottom-right corner will cause a flow to the left and upward, the cell to the top-right corner will propagate a flow to the left and downward, and finally the decontaminating cell at the bottom-left corner will propagate a flow to the right and upward. Implicitly, this strategy cuts the CA into four equal parts if *n* is even (Figure 6.14f) and in unequal parts if *n* is odd (Figure 6.14c). In the first case, decontamination ends when the 4 centre cells of the CA get decontaminated. In the second case, the decontamination of the cell at the centre of our CA marks the end of the algorithm execution. This strategy is supported by the theorem below

Theorem 6.13. *Decontamination using the Diagonal approach can be achieved in a 2D CA of size* $n*n$ *under the von Neumann neighbourhood with 4 decontaminating cells. The algorithm execution requires* $2*\left\lceil \frac{n}{2} \right\rceil - 1$ *units of time The maximum number of decontaminating cells encountered during the execution is* $4*\left\lfloor \frac{n}{2} \right\rfloor$.

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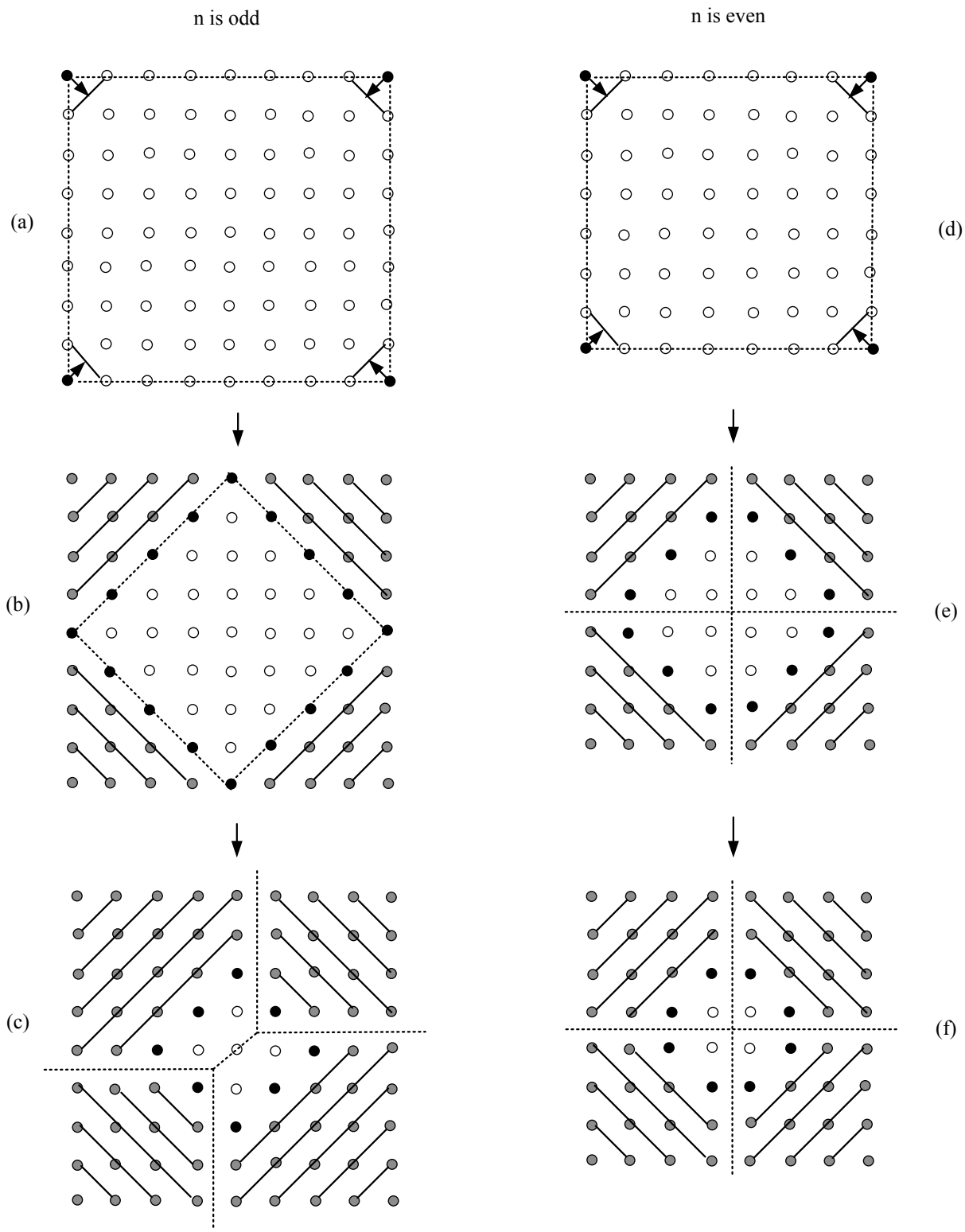


Figure 6.14: The subdividing strategy using diagonal move with 4 initiators

Proof:

By using the same techniques presented in the proof of Theorem 6.9, the rules for four corner initiators can be built in two different ways. The first option is to start with the three rules R2, R3 and R4 and symmetrically transpose these rules diametrically (R5, R6 and R7), vertically (R8, R9 and R10) and horizontally (R11, R12 and R13). Obviously, the three latter rules are vertically symmetric to R5, R6 and R7. These results are listed in Table 6.9. To prove that $2*\left\lceil \frac{n}{2} \right\rceil - 1$ units of time is needed to achieve the decontamination, we proceed by analogy with the decontamination of a CA of *Cd*=1 and *Vh*=1 with a single initiator which requires $2n-1$ units of time. The decontamination duration of a $n*n$ CA with four initiators is similar to the execution of the $\left\lceil \frac{n}{2} \right\rceil * \left\lceil \frac{n}{2} \right\rceil$ CA with a single initiator as the CA is split into four parts. This can be easily noticed when looking at Figure 6.14c when *n* is odd or Figure 6.14f when *n* is even. Therefore, by replacing *n* with $\left\lceil \frac{n}{2} \right\rceil$ in $2n-1$, we can deduce that the decontamination time is $2*\left\lceil \frac{n}{2} \right\rceil - 1$.

#	Configuration	Next State	Notes
R1			Any decontaminating cell will be decontaminated in the next step.
R2			Cell located on the top horizontal border of the CA
R3			Cell located on the left vertical border of the CA
R4			Internal Cell
R5			Diametrically symmetric to R2 Cell located on the bottom horizontal border of the CA
R6			Diametrically symmetric to R3 Cell located on the left vertical border of the CA
R7			Diametrically symmetric to R4 Internal Cell
R8			Vertically symmetric to R2 Cell located on the bottom horizontal border of the CA
R9			Vertically symmetric to R3 Cell located on the left vertical border of the CA

R10		Vertically symmetric to R4 Internal Cell
R11		Horizontally symmetric to R2 Vertically symmetric to R5 Cell located on the bottom horizontal border of the CA
R12		Horizontally symmetric to R3 Vertically symmetric to R6 Cell located on the left vertical border of the CA
R13		Horizontally symmetric to R4 Vertically symmetric to R7 Internal Cell

Table 6.9: Rules for Basic Decontamination in Finite CA using basic diagonal move and four corner initiators with the von Neumann neighbourhood when Vh=1 and Cd=1

6.4.3. Case with 3 corner initiators

It is important to note that the algorithm covers the scenario of three corner initiators, regardless of which three cells among the four corner initiators are selected. Since the transition rules covers all flows (top-left to bottom-right, top-right to bottom-left, bottom-right to top-left, bottom-left to top-right), the algorithm supports any execution started from any number of corner initiators (that is one, two, three or four initiators) and any combination of two or three corner initiators from any corner location. For instance, Figure 6.15 shows an execution of the divide and conquer diagonal move algorithm defined in Table 6.9 with a single corner initiator on the top-right (Figure 6.15a), two initiators located on the top-left and the bottom-left (Figure 6.15b), and three initiators sited on the top-right, bottom-right and bottom-left (Figure 6.15c).

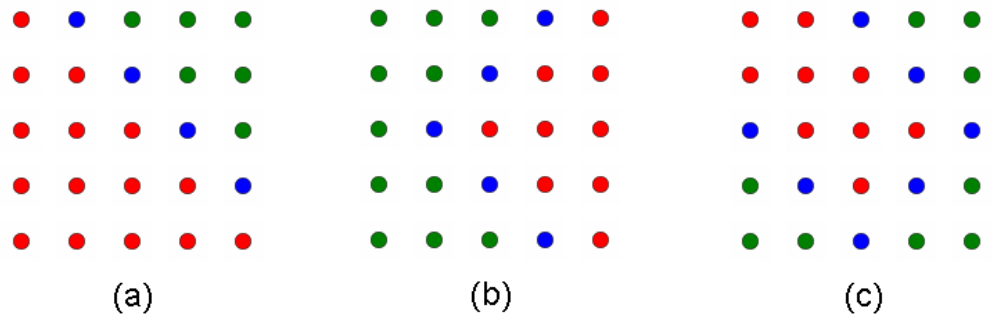


Figure 6.15: A sample of execution of the subdividing strategy using diagonal move algorithm using a dynamic number of initiators.

Theorem 6.14. *Decontamination using the Diagonal approach can be achieved in a 2D CA of size* $n*n$ *under the von Neumann neighbourhood with 3 decontaminating cells. The algorithm execution requires* n *units of time The maximum number of decontaminating cells encountered during the execution is* $3*\left\lfloor \frac{n}{2} \right\rfloor$.

Proof:

Any algorithm with four initiators will perform when three initiators are chosen, so Table 6.9 can then be used as the set of rules. Regarding the duration of the decontamination, *n* units of time are needed. One can see that the last cell to be decontaminated is the corner that was not selected as an initiator. The last corner cell can only be decontaminated after it is reached by the decontamination flow coming from its adjacent and horizontal (or vertical) corner, similar to the execution by two initiators. Therefore, *n* steps are needed. Following the same logic shown in the proof for Theorem 6.13, the maximum number of $3*\left\lfloor \frac{n}{2} \right\rfloor$ decontaminating cells is reached at time $t = \left\lfloor \frac{n}{2} \right\rfloor - 1$.

6.4.4. Rules minimization

In the previous section, the construction of the rules has been based on basic rules that act on a single initiator (top-left) and the transposition of these basic rules to create new rules based on the symmetry of execution. The basic rules are composed of three transition rules

based on the location of the cell within the CA, laying on a border (vertical or horizontal), or defined as an internal cell. Then, each rule is transposed. With this methodology, we manage to create the algorithm listed in Table 6.9. The three basic rules are transposed vertically, horizontally, and diagonally which gives a total of 12 rules. A good question is to ask if the same strategy can be performed with fewer rules. With respect to the diagonal move strategy, there are two different approaches that can be taken to minimize the number of rules.

6.4.4.1. Approach by "flow analysis".

#	Configuration	Next State	Notes
R1			Any decontaminating cell will be decontaminated in the next step.
R2			Rule triggering an horizontal flow
R3			Rule triggering a vertical flow

Table 6.10: Alternative rules for Basic Decontamination in Finite CA under the von Neumann neighbourhood using basic diagonal move and initiated by the top left initiator when Vh=1 and Cd=1

The first approach is to revisit the set of basic rules and try to minimize them. To do so, instead of producing rules that are based on the type of cell, one can concentrate on the type of flow that is propagated within the CA. A diagonal flow can be seen as both an horizontal and vertical propagation of the decontamination. Thus, the algorithm depicted by Figure 5.2 and defined in Table 5.1 with three rules can be improved by the simple rules defined in Table 6.10 above.

We can use the same transposition strategy in Table 6.10 to create the set of rules which can handle the execution with multiple initiators. A natural inclination is to think that one will need 6 additional rules to perform the execution in a case with 4 initiators. The reason for this assumption is both rules R2 and R3 have to be symmetrically transposed for each remaining corner (vertically for the top-right corner, diagonally for the bottom-right corner, and horizontally for the bottom-left corner). However, Table 6.11 shows that only 2 additional rules are needed to perform the entire decontamination. The vertical transposition of R2 and R3 to satisfy the flow initiated by the top right corner is embedded in R4 and R3 respectively. Similarly, the horizontal transposition of R2 and R3 to satisfy the flow initiated by the bottom left corner is contained in R2 and R5 respectively. Finally, the diagonal transposition of R2 and R3 is R4 and R5 respectively. Thus, the decontamination using a diagonal flow started by up to 4 corner initiators can be fulfilled with exactly 4 decontamination rules.

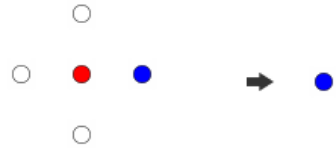
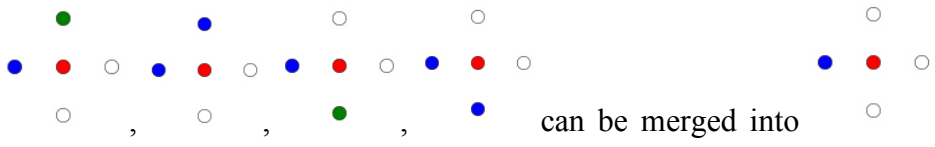
#	Configuration	Next State	Notes
R1			Any decontaminating cell will be decontaminated in the next step.
R2			A left-to-right flow that target cells located on: - the top horizontal border of the CA - the bottom horizontal border of the CA - internal cell
R3			A top-to-bottom flow that target cells located on: - the left vertical border of the CA - the right vertical border of the CA - internal cell
R4			A right-to-left flow that target cells located on: - the top horizontal border of the CA - the bottom horizontal border of the CA - internal cell
R5			A left-to-right flow that target cells located on: - the top horizontal border of the CA - the bottom horizontal border of the CA - internal cell

Table 6.11: Alternative rules for Basic Decontamination in Finite CA with the von Neumann neighbourhood using basic diagonal move and initiated by any corner initiators when Vh=1 and Cd=1

6.4.4.2. Approach by “transition rules merge”.

The second approach is to analyze the set of transition rules and to attempt to merge them into a new and more generic set of rules. This strategy presents some risks of falsifying the decontamination algorithm if additional rules are actually generated by the attempt.

By doing so, one can actually retrieve the transition rules defined in Table 6.11 by executing the merge process against the collection of rules defined in Table 6.9. For instance, the configuration found in R2, R4, R11 and R13 in Table 6.11, that is respectively



depicted as , , , can be merged into . Since the result state of these rules is identical (decontaminating), the rules R2, R4, R11 and R13 of Table 6.9 can be merged into a more generic rule, which is the rule R2 in Table 6.11. Since all possible combinations of states are being represented, it is important to note that no additional rules is being implicitly added by the creation of R2.

By applying the same merge strategy, the rules R3, R4, R9 and R10 of Table 6.9 are merged into rule R3 of Table 6.11. Also, the rules R5, R7, R8 and R10 of Table 6.9 are merged into rule R4 of Table 6.11. Finally, the rules R6, R7, R12 and R13 of Table 6.9 are merged into rule R4 of Table 6.11. By an exhaustive count, all rules of Table 6.9 are represented by at least one rule defined in the Table 6.11.

6.5. Summary

In this chapter, we started by introducing two new algorithms named *Road traffic* and *Diagonal Snake*. We used these algorithms as a foundation to implement new strategies by applying the base idea within different cuts of the CA. This allowed us to use different number of initiators as needed. We completed the chapter by studying the technique that accomplishes the same recursive idea using the base diagonal flow algorithm introduced in Chapter 5. A summary of results established in this chapter is listed in the following table.

Strategy	**N* Type**	***Vh***	***Cd***	***It***	**Number of Initiators**	**Max D*ing cells**	**Time**	**Ref.**
Road Traffic CF	VN	≥ 3	1	$2n-1$	2	2	$\left\lceil \frac{n}{2} \right\rceil * n$	Th. 6.3
Road Traffic IF	VN	≥ 3	1	n	2	2	$\left\lceil \frac{n}{2} \right\rceil * n$	Th. 6.5
Road Traffic IF	Moore	2	1	n	2	2	$\left\lceil \frac{n}{2} \right\rceil * n$	Th. 6.6
Road Traffic IF	Moore	2	1	$2\left(\frac{n}{k}-1\right)$	$2k$	$2k$	$\left\lceil \frac{n}{k} \right\rceil * \left\lceil \frac{n}{2} \right\rceil$	Th. 6.7
Diagonal snake	Moore	≥ 2	1	$2n-1$	1	1	n^2	Th. 6.8
Diagonal snake	Moore	≥ 2	1	$2n-3$	2	2	$\frac{n^2}{2}$	
Diagonal snake	Moore	≥ 2	1	$2*\left\lceil \frac{n}{2} \right\rceil -1$	4	4	$\frac{n^2}{4}$	Prop 6.1
Diagonal Move	VN	1	1	0	2	n	n	Th. 6.12
Diagonal Move	VN	1	1	0	3	$3*\left\lfloor \frac{n}{2} \right\rfloor$	n	Th. 6.14
Diagonal Move	VN	1	1	0	4	$4*\left\lfloor \frac{n}{2} \right\rfloor$	$2*\left\lceil \frac{n}{2} \right\rceil -1$	Th. 6.13

Table 6.12: Summary of decontamination results of a n*n CA using the Road Traffic, Diagonal Snake and Diagonal Move strategy.

Chapter 7

CAEDISI, a CA editor and simulator for Network Decontamination

In this chapter, we present a software [RZ13] that we have implemented with the aim to support the theoretical study of Network Decontamination using CA. The initial goal was to have simple software which could rapidly display the execution of a decontamination algorithm instead of scribbles on paper which is tedious and arguably unreliable. The final product is a research tool that not only acts as a simulator but also as an editor, a validation tool, and even as a rule generator for CA.

7.1. Motivation

7.1.1. Needs and existing software limitations

In previous chapters, we presented ideas whose ultimate goal was to provide decontamination algorithms. Obviously, the first question asked after the creation of an algorithm is about its feasibility even before judging its performance. Initially, the algorithm's execution was written and drawn on a sheet of paper. In the simplest cases, it was found that the verification of these algorithms is a tedious task, even just with respect to its correctness. It was then clear that simulation software was essential to our research.

The first step was to find existing software that could fulfill our needs. Not surprisingly, we found the existence of a considerable amount of software that simulates the execution of CA. Most of the software processing CA often deals with its natural form, that is, with two states and with a direct distance in the neighborhood. The limitation of having only two states (typically the "on" and "off" states) as stipulated in the original definition of a CA is important because in the field of Network Decontamination, the set of transition

states necessarily contains at least three states: contaminated, decontaminated, and decontaminating. In our research, we added a new state called *absent* (see Chapter 3) in order to study the decontamination algorithms of sub-truncated mesh. Some software supports the addition of new transition states or has its own way of expressing access to a wider area of the neighbourhood within the transition rule definition, but the use of the system turns out to be difficult and challenging. In our study, the requirement of writing transition rules using an extended visibility of the neighbourhood is essential.

There are other limitations which are technical rather than conceptual. Most existing software that interacts with CA are mainly simulation programs characterized by static features with respect to the characteristics of the CA model, including its grid (the size, visual appearance, etc.) and the definition of the neighbourhood. In some cases, the rules governing changes of the states of each cell are predefined and static in the code. This forces the researcher to dive into the source code of the program to update an existing algorithm or to implement a new algorithm. Thus, a researcher must necessarily have a fairly advanced knowledge of computer programming in order to have a visual overview of the heuristic that he wants to implement.

The major limitation of existing software is the inability to handle some of the additional parameters required by our study on Network Decontamination. This restriction is manifested by the system inflexibility of integrating of such properties. One example is that in our study, we needed a system that could support the integration of the *Time Immunity* parameter within the logic of updating the state of a CA's cell. Unfortunately, we could not find any system that offered the functionality or software that used similar functionality to accomplish this integration.

The need for software that can implement at least these three parameters (extended neighbourhood visibility, Contamination Distance, and Time Immunity) are among the main motivations to create our own CA software.

7.1.2. Overall characteristics

Usable. The software is using modern technologies which makes the software easy to use and does not require any special training. A user does not need any knowledge of programming in order verify its algorithm. For instance, visual controls have been used to

input transition rules instead of the traditional notation (string character) which gives a better visual representation of the rules.

Interactive. The software makes an effort to display informational, warning, or error messages. For instance, the system warns the user with pop-up messages when rules are not valid and allows the user to choose between corrections to the rules assuming a non-deterministic behaviour. Another example is that each cell state can be explored during simulation for more information around its attributes, such as the rule responsible for the current state result or its immunity time value at each stage. The software also provides the user with the ability to run the entire simulation in a continuous fashion (start to end with a stop condition) or in a step-by-step mode.

Generic. The system can process any CA in a non-static approach. All properties of CA are dynamic including the specification of the neighbourhood, the width, the height, the value of the Visibility Hop, and the Contamination Distance. The software is capable of creating and editing CA of any size. The user can choose to define any transition state, not only the usual three states for decontamination. The system supports any type of neighbourhood of any radius. The system will include the von Neumann and Moore neighbourhoods by default but the user can also define and save a new type of neighbourhood. When this case arises, the system can recursively compute the new extended neighbourhood when the Visibility Hop increases. A user can choose to test the same algorithm with a different topology such as tori (circular), with a different width and height, different visibility, different immunity, and different Contamination Distance. Furthermore, there is no limit (except machine memory) to the number of transition rules that can be edited (created, updated, or removed) at the user's request.

Configurable. All possible fields that can be configured in the system are configurable. For instance, the user can choose to consider the cell outside the CA as either "absent" or "decontaminated," or even another new defined state. The user can choose to end the simulation when a specific state of the CA is reached (e.g., all decontaminated or all contaminated) or after a number of steps, or can choose to run the simulation indefinitely. The visual aspects of the system are also configurable. For instance, the user can choose the color assigned to each state.

Complete. The system has been tailored to include some Network Decontamination parameters but can still be used to simulate the native form of a CA. During the simulation mode, contamination rules are generated on demand and not by default in order for the set of collection rules to be network contamination agnostic. For example, a user can simulate the execution of the "game of life" CA. The program will offer a rigorous method of validation of the rules, meaning the software will make sure that the configured CA is a deterministic automata. The software also provides some statistical data on the execution of the algorithm.

Collaborative. Additional effort has been made to make the system a collaborative tool for researchers. For instance, the system allows a user to register before its use. All collected data are stored in a database that can be questioned as required. A user can create new neighbourhood type and the latter can be reused by other users. Another example is that a user can have view access to algorithms created by others.

Portable. The software can be deployed as a standalone application on a desktop and can also be deployed on the web and accessed through a browser.

Advanced. The software is built using the latest technologies which makes it extensible for the future. It has technologies such as rich internet applications (RIA), object relational mapping (ORM with Entity Framework), web services (WCF RIA web services) and support for the installation of the database in the cloud.

7.2. Caedisi versus current CA Software

In this subsection, our purpose is to point out the particularity and strength of CAEDISI against current CA software. The effort has been made to bring comparisons against the most used CA simulator currently available in order to show its contributions. Mainly, we put the focus on its structure (including the data structure) and the approach difference with respect to the simulation functionality. We also highlight new features that is only found in Caedisi.

7.2.1. CA Structure

The Table 7.1 is a summary of difference between the overall data structure of Caedisi and its pairs. Most existing software saves the CA into an Array because it is the natural representation of a grid. However, with respect to its data structure, Caedisi saves the CA using a new structure named “Entity” in which relational data are already structured in a

graph similarity. In our case, it provides more flexibility especially when the neighbourhood is un-regular. Indeed, instead of computing the neighbours using an offset system, neighbours are already traced through implicit edge connections.

CA Properties	**Wolfram's MATHEMATICA**	**JCASIM**	**MCELL**	**GOLLY**	**CAEDISI**
CA data structure	Array	Array	Array	Array	graph of relational data
Supported CA Dimensions	1D, 2D, 3D	1D, 2D, 3D	1D, 2D	1D, 2D	2D, Open for 3D
Dynamic neighbourhood structure					✓
Transition rule data structure	Tree	Tree	Tree	Table & Tree	Relational data (graph)
Support multiple states	limited	limited	limited < 256	limited < 256	✓
Support larger radius					✓
Support circular CA		1D only			✓
Support Unbounded	✓	✓	✓	✓	✓ (with custom state for unbounded cells)

Table 7.1: CAEDISI vs current CA Software (Overall structure)

One of key difference between Caedisi and its converse is the ability to define any new neighbouring structure of radius r=1 and the software will be able to recursively compute any new neighbouring structure of larger radius. Even if the new neighbouring structure is

asymmetric (for instance, Moore and von Neumann neighbourhood are symmetric), the software is able to generate the correct transition rule structure (see for instance Figure 7.3 with von Neumann Vh=2 and Figure 7.10 for Moore Vh=1)

Obviously, Caedisi support larger radius (*Vh* and *Cd*) and 2D circular CA which are not found in current software. Another new functionality is to be able to specify an arbitrary state for "imaginary" cells outside the boundary of the 2D grid. Instead of controlling the grid offsets like the other software (for instance, a negative row index of a top neighbour means the current cell is on the 1st row) , Caedisi is flexible and assume that cells outside the boundary can be of any state: "Absent", 'Clean" , "decontaminated" or even a newly defined state. This idea is more realistic for Network decontamination because these unbound cells might be mapped to machines that are outside the infected network, or even just machines with an unknown state.

Another particular strength of Caedisi is the ability to dynamically generate the transition rule GUI configuration based on an arbitrary neighbourhood type and the value of Vh. (for instance see Figure 7.3 with von Neumann Vh=2 and Figure 7.10 with Moore Vh=1). The generation of the transition rule is derived from the recursive version of the well-known graph BFS algorithm (breadth-first-search) with the pseudo-code below:

```
Procedure GenerateGenericTransitionRule(
   NeighbourhoodType  NT,
   int Vh)
begin
   Let TR be a TransitionRule: output
   int minOffset ← Vh * (-1);
   int maxOffset ← Vh * (1);
   int xIndexCenterCell ← maxOffset;
   int yIndexCenterCell ← maxOffset;
   int zIndexCenterCell ← 0;
   int currentRadiusIndex ← 0;
   call Procedure GenerateNeighboursData  (TR, xIndexCenterCell,
yIndexCenterCell, zIndexCenterCell, NT, currentRadiusIndex, Vh)
End
```

As for most recursive function, the previous function is the initial set up which role is to only call the following procedure being called recursively within its body. Below, we display the partial content of the procedure but the user can easily deduce the content of the absent lines of code.

```
Procedure GenerateNeighboursData(
   TransitionRule TR,
   int xIndexCenterCell,
   int yIndexCenterCell,
   int zIndexCenterCell,
      NeighbourhoodType  NT,
   int currentRadiusIndex,
   int Vh)
begin
   Let xIndex, yIndex, zIndex be int variables
   Let Q be a queue (we use it to store    neighbours already being
generated)
   CurrentRadiusIndex←currentRadiusIndex+1
   if (CurrentRadiusIndex > Vh)
       Return
   if NT.IsTopLeftOn is  true
      xIndex ←xIndexCenterCell-1
      yIndex ← yIndexCenterCell-1
      zIndex ← 0
      Generate the cell in the UI at coordinate (xIndex, yIndex, zIndex)
      Q.enqueue (Tuple(xIndex, yIndex, zIndex))
   if NT.IsTopOn is  true
      xIndex ←xIndexCenterCell-1
      yIndex ← yIndexCenterCell
      zIndex ← 0
      Generate the cell in the UI at coordinate (xIndex, yIndex, zIndex)
      Q.enqueue (Tuple(xIndex, yIndex, zIndex))

    if NT.IsTopRightOn is  true
      ...
    if NT.IsRightOn is  true
      ...
    if NT.IsBottomRightOn is  true
      ...
    if NT.IsBottomOn is  true
      ...
    if NT.IsBottomLeftOn is  true
      ...
    if NT.IsLeftOn is  true
      xIndex ←xIndexCenterCell
      yIndex ← yIndexCenterCell-1
      zIndex ← 0
      Generate the cell in the UI at coordinate (xIndex, yIndex, zIndex)
      Q.enqueue (Tuple(xIndex, yIndex, zIndex))

    While Q is not empty
      Tuple (x,y,z)←dequeuer (Q)
      GenerateNeighboursData(TR, x,y,z, NT, currentRadiusIndex, Vh)
end
```

The operation is accomplished with $O(n)$ operations with n being the cardinality of the neighbours surrounding the current cell. Details about the implementation of the algorithm can be found in [R13] under the procedure name *GenerateGenericTransitionRule.*

7.2.2. Simulation properties

Simulation Properties	**Wolfram's MATHEMATICA**	**JCASIM**	**MCELL**	**GOLLY**	**CAEDISI**
Colouring states	✓	✓	✓	✓	✓ **(with tags)**
rules insertion	Scripts	Code, CDL UI Input	Code (external dlls)	Scripts	**UI input**
Support CA Editing during execution					✓
Conditional Execution Stop					✓
Support continuous execution	✓	✓	✓	✓	✓ (**with stop condition**)
Support sequential execution (play, pause, steps, etc)	✓	✓		✓	✓ (with jump to end according to stop condition)
Simulation Execution recorder					✓
Simulation Metadata					✓ **(stats**

					available at each step)
Support Stochastic CA	Unique probability (Domany-Kinzel only)				✓ (Different probability for each rule)
Support non-deterministic CA					✓ (states based-rules or user input)

Table 7.2: CAEDISI vs current CA Software (Simulation properties)

Some of the drawback of existing software (except JCASim) are the incapacity of inserting new rules without, either implementing program code intervention or writing scripts. These latter require a prior knowledge of the programming language, the script language and the insertion protocol. Instead, Caedisi can add new rules by simple interaction with the software. (Process is explained in further sections).

CA Editor.

Another primordial feature that is only available in Caedisi is the ability to edit the CA during execution. The user can pause the execution and arbitrarily change any state of any cell of the CA. The user can also consult any metadata property currently available, for instance the circumstances that lead into a specific state of an arbitrary cell. For instance, this functionality is needed for Network decontamination if there is a desire to investigate random faults during decontamination in which some already decontaminated hosts gets re-contaminated again.

Recording Execution.

Another new feature is the ability to record any execution and save it to the database for further consultations. It is important to note that current software only save the rules so that they can re execute the simulation in a later date. However since Caedisi allows the user to

edit the CA during the execution and possibly alter any states, it was necessary to have a "read-only" version of the execution without executing again the transition rules.

Stochastic CA.

The software also supports stochastic models that can be factored by probability on the Transition rules. The idea is to implement probabilistic model that is firstly relevant for Network Decontamination. One of the future variation of our study is to study realistic probabilistic model. For example, a very realistic situation is that every machine do not always gets decontaminated but instead the cleaning process is associated with a probability of success. For network decontamination, several situation arises, for instance:

1. Decontamination is (not) successful because of the quality of antiviral program. In this case, any transition rule from a decontaminating state into a decontaminated state is factored by a probability *p*. Therefore, the same value of *p* is applied to every candidate cell transiting into the previously mentioned transition state.
2. Decontamination is (not) successful in certain machines because of the machine characteristics (for instance, different hardware, different operating systems, etc). In this case, each cell has its own probability *q* that affects any transition rule applied to it.
3. The probability of the antiviral program of being successful increase when executed multiple times on the same machine. In this case, faults become dependent.
4. Also, we can see that both *p* and *q* can be both applies concurrently which gives different stochastic models.

Currently, Caedisi implements the case 1 above.

Non-determinist CA.

Furthermore, Caedisi can execute non-deterministic CA. The resulting state to be taken in account is

- either an interactive choice given to the user or
- an optimistic or pessimistic model configured within the software. In an optimistic model, the order of resulting state to be chosen is

decontaminated>decontaminating>contaminated in this order. Conversely, in a pessimistic model, the contaminated state gets the priority to be selected first.

7.2.3. Inverter and Reversability

INVERTER & REVERSABILITY	Wolfram's MATHEMATICA	JCASIM	MCELL	GOLLY	CAEDISI
Transition Rules Generator					✓
Determinism/Non-determinism Test					✓
Heuristic for Reversability Test					✓

Table 7.3: CAEDISI vs current CA Software (Inverter and Reversability)

The principal functionality that dissociate Caedisi from current simulation software is the ability to act as a rule generator. The general idea is to grab some given arbitrary execution (inputted by the user) and the software tries to reconstruct the rules that lead to that execution. It is easy to see that the same approach can be used as a heuristic to test the reversibility of a given CA who is known to be NP-Hard [Kar90]. Furthermore, the test of reversibility can be executed for a larger radius (For instance, the CA might not be reversible for r=1 but be successful for r=3) . Note that this functionality is scrutinized in upcoming sections of this chapter.

7.2.4. Database, Libraries and Software properties

The Table 7.4 below lists the various differences between Caedisi and various software with respect to structure used to save the CA. One can see that Caedisi uses a standard format to save the CA and the execution path as well. We note that current software saved its CA into proprietary format that is usually employs text based encoding. Even if the latter format is highly portable, issues rises when we want to complement the CA with metadata because the new data structure was not intended to be upgraded. (For instance, saving an

execution using RLE appears to show some complexity). Apart the fact that a SQL format can support any relational structure, the advantage of using it gives the researcher an ability to use advanced data mining tools (SQL is a standard format) and have a better alternative to study its dynamical properties (e.g. in opposition of custom format in which a plugging needs to be coded in order to translate the format).

Artifacts	**Wolfram's MATHEMATICA**	**JCASIM**	**MCELL**	**GOLLY**	**CAEDISI**
DATABASE & LIBRARIES					
File Savings	**Proprietary** CDF	**Custom**	**Custom** RLE	Image format (bmp, tiff…)	**Standard Inside a SQL database**
File Openings	From Disk CDF	From Disk CDL	From Disk RLE, Mcel, Life, dbLife	From Disk RLE, Mcel, Life	**From database**
CA Libraries format	**Proprietary format**	CDL	File logs	File logs	SQL tables
Execution records					✓ **(SQL tables)**
SOFTWARE PROPERTIES					
Programming Language	C/C++, Java, Fortran, C#	Java	Java Applet Desktop		UI: XAML Code: C# Database: SQL
Deployment	Desktop	Desktop	Java Applet Desktop	Desktop	Desktop/**Web application**
Licensing	Commercial	Open Source	Open Source	Open Source	Open Source

Table 7.4: CAEDISI vs other CA Software (Database and Libraries)

7.3. Software engineering approach

CAEDISI is a rich internet application (RIA) and a client-server web application that has the characteristics of a desktop application. In fact, the system can be deployed as a web application or a desktop application.

7.3.1. Architecture and Technology

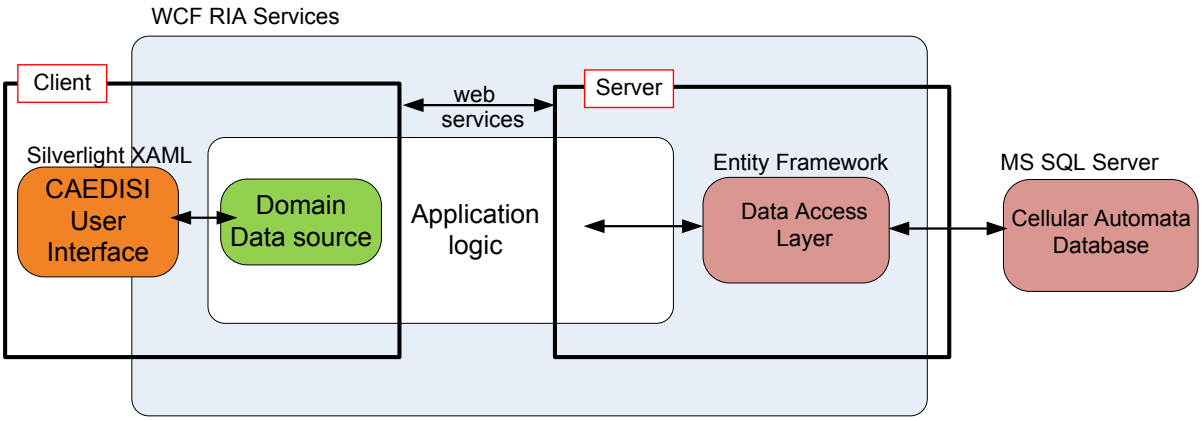


Figure 7.1: The CAEDISI software architecture

Client. The screens have been implemented using *Xaml* pages of *Microsoft Silverlight 5.0* [Sil10], Xaml pages are xml based files that have the particularity of producing a rich user interface. It also has a tight integration with a particular set of web services that provides its data source.

Server. CA data are stored in a *MS SQL* database [SQL05]. There are many advantages of saving the data into a SQL database including standardization, the ability to establish relational models, and flexibility around data management using crud operations (create, read, update, delete). Data is exposed by *WCF RIA services* [WCF04], a special type of web service, using a data access layer called *Entity framework* [EF08]. The latter is a powerful technology that allows developers to work at a higher level of abstraction when dealing with data, and can create and maintain data-oriented applications with less code than in traditional applications.

7.3.2. Functionality modules

CAEDISI functionalities are split in four modules.

1. A *simulation* module that can take any decontamination rules inputted by the user and simulate the decontamination algorithm on the screen, step-by-step or on a play mode. Additionally, it offers metadata information about the simulation and gives the command to the user to control the execution.
2. An *inverter* module that can interpret an idea of execution established by the user and generate the equivalent transition rules. The idea can be seen as an inversion of the simulation process. At each stage, the user chooses the candidate cells to be decontaminating and the system successively tries to recreate the transition rules that lead to the current state of the CA.
3. A *library* module that is responsible for storing common properties used by any CA in a database. These properties can be searched, referenced and re-used at a later stage. For instance, the user can define a new type of neighbourhood or a new transition state apart from contaminated, decontaminated, and decontaminating.
4. A *statistic* module that is used vertically by the other modules. It offers numbers and metrics to gauge the decontamination algorithm including the number of decontaminating cells at each stage or the total number of required steps.

Each module is implemented using an Oriented Object programming following the *Model-View-Controller* (MVC) pattern. The MVC design separates the modeling of the domain, the presentation, and the actions based on user input into three separate classes: the model (the data representation), the views (the UI screens), and the controller (the algorithm classes). In the architecture picture, the graphic user interface is the view, the domain data source is the model, and the application logic is represented by the controllers.

7.4. The main views

In this following section, we present a non-exhaustive list of wireframes that serve as user interfaces accessing these modules.

7.4.1. The Simulator wireframes and its functionalities

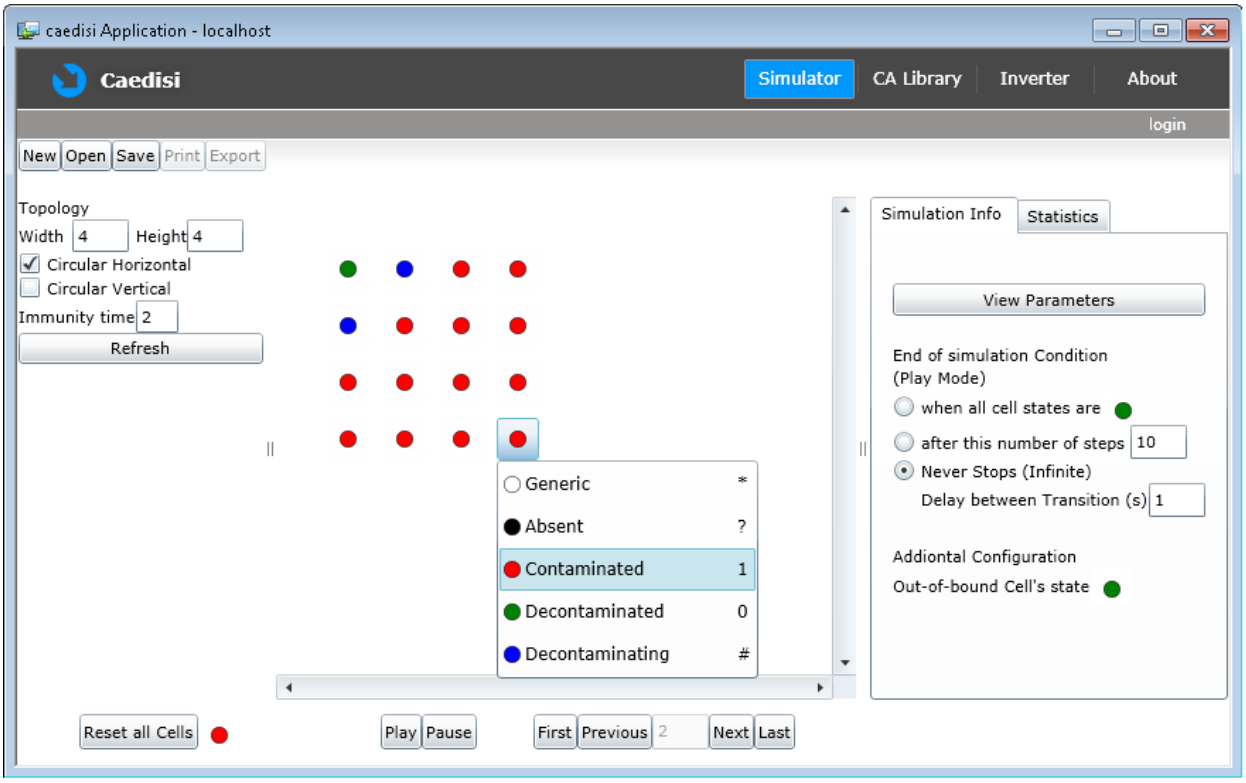


Figure 7.2: The simulator home screen

The S*imulator* screen is the home screen of the software as it exposes the most used functionality of the system. It is the main entry of the simulator module of functionality. The *Simulator* screen shows 6 different groupings of the user interface.

1. A standard file menu handler to create, open, print, save and export a new or an existing CA.
2. A statistic and information tab to show various properties of the current CA and some statistics of the execution of the current algorithm.
3. A simulation information tab that gives the user the ability to configure the execution of the simulation such as the stop condition when executing the simulation on a play mode. It also has an entry point to visualize the *CA Parameters* screen (defined in the next section).
4. A simulator and execution toolbar that serves as a dashboard for the current algorithm execution. After every CA property is set, the user is redirected back to this screen with

the CA being drawn in the drawing area. The user can execute the simulation by clicking the "play" button. If needed, the user can use the step-by-step process by choosing the appropriate buttons. The toolbar also offers utility tools such as the ability to reset the CA with any desired state.

5. A topology screen that gives the user the opportunity to refresh the execution by altering the topology, such as the size of the grid or the immunity time.
6. The drawing area itself located in the center of the software.

7.4.2. The CA Parameters wireframes and its functionalities

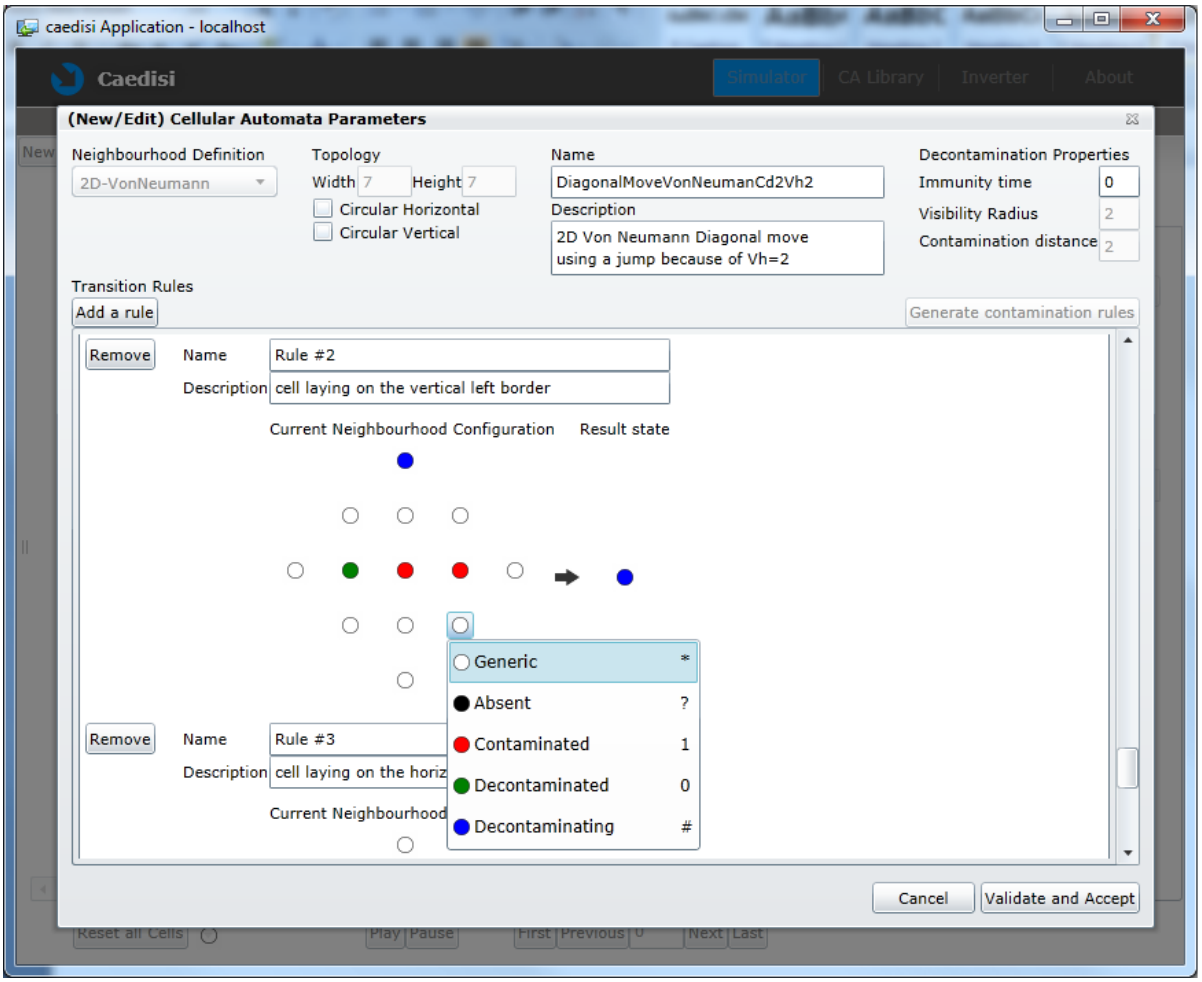


Figure 7.3: The CA parameters screen of the simulator module

The creation of a new CA and the editing of an existing CA will result in the opening of the *CA Parameters* screen. In this user interface, the user will set (or update) all required properties defining the CA (its name and description), its attributes (its width, its height, and flags to check whether the algorithm to be defined acts on circular CA). The user also selects the targeted neighbourhood from among the existing list of neighbourhood types saved in the library. The user also specifies the decontamination characteristics such as the value of the immunity time or the Contamination Distance, and of course, the *Visibility Hop* of the CA.

One important function offered by this screen is the creation/update/removal of the collection of transition rules associated with the CA. We take the decision to differentiate the contamination rules (that is, the transition rules that lead a cell from a decontaminated state into a contaminated one) among the other types of rules. The rationale is that contamination rules can be dynamically generated by the system based on the type of neighbourhood, the current Visibility Hop and the Contamination Distance (Algorithms for generating contamination rules can be consulted in *Appendix E*). However, we still let the user initiate the generation of contamination rules instead of relying on the system to automatically initiate the rules. The reason for this is to give the user the control especially if the previously mentioned parameters are updated.

Typically, after the contamination rules are generated, the user proceeds to successively add the transition rules into the system. The configuration of the neighbourhood will be constructed appropriately and the user just needs to select the correct cell state for the current state, the result state, and the list of coherent states among the neighbourhood. By default, all neighbour states are set to a "generic" value which can be altered with a specific value. When the user finishes entering the input, the system will perform the validation of the transition rules and show the *Rules Validation Results* screen.

7.4.3. The Inverter wireframes and its functionalities

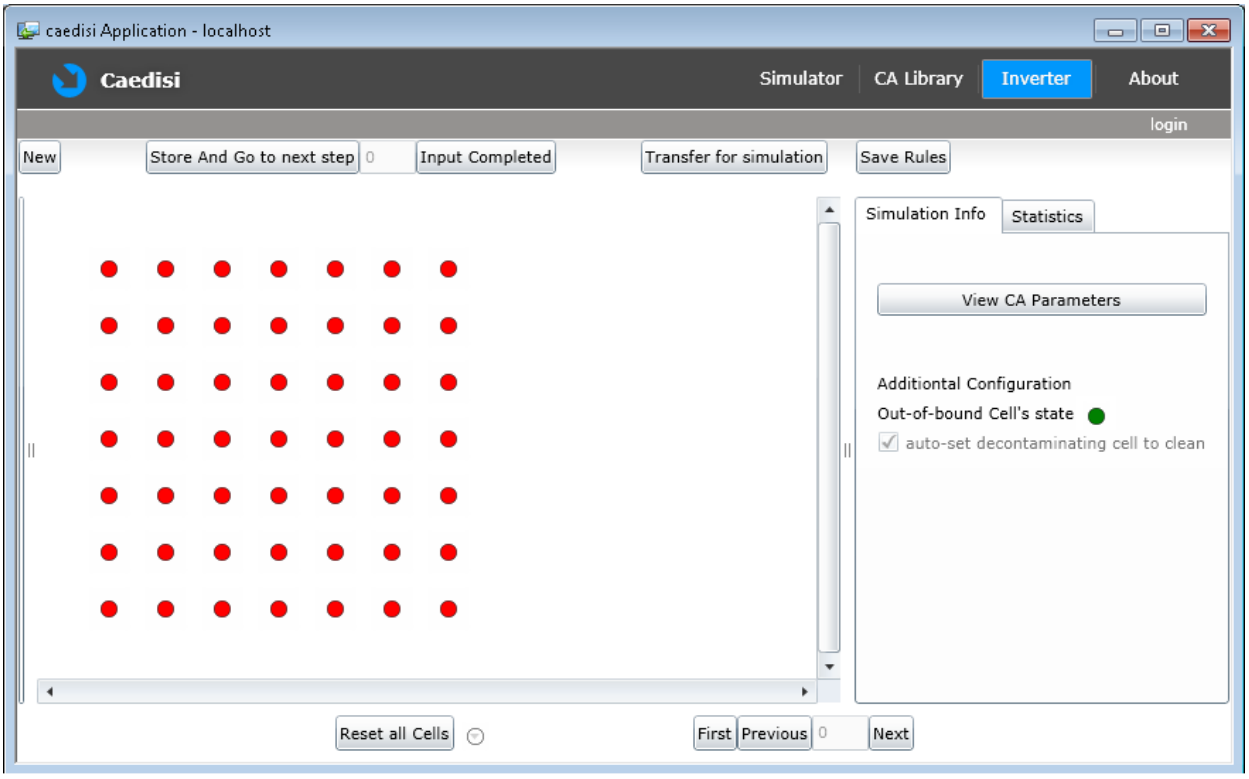


Figure 7.4: The inverter home screen

The *Inverter* screen is the entry point of the Inverter module. The user interface has a slight resemblance to the *Simulator* screen but has different purposes. The *Inverter* screen shows six different groupings of the user interface.

1. A toolbar that serves as a dashboard for the Inverter process. It allows the user to create a new inverter execution via the classic "new" button which will then open the *Inverter Parameter* screen. After all parameters have been set, the user is directed back to this screen with the CA generated on the drawing area. The user then selects the candidate cells that are in a decontaminating state for each specific step. Meanwhile, at each step, the system validates that the rules to be created do not invalidate the existing rules saved to date. If there are conflicts, the system will display the errors through the *Rules Validation Results* screen. At any time, the user can consult the list of rules already created up to the current point. At his discretion, the user can indicate the end of the entries' capture and proceed to the recording of the generated rules. One key point is that

the generated rules are stored in the same database that store the transition rules for the simulator module and therefore, the user can validate the algorithm by executing it through the Simulator module.

2. A statistic and information tab to show various properties of the current execution and some up to date statistics.
3. A simulation information tab that gives the user the ability to configure the execution of the simulation. For instance, the user can configure the desired state of the cells outside the boundary of the CA. The user can arrange to automatically set a decontaminating state into decontaminated in the next step, if desired. This tab also has an entry point to visualize the *Inverter Parameters* screen (defined in the next section).
4. A simulator and execution toolbar that serves as a dashboard for the current algorithm execution. After the software successfully validates the transition rules, the user executes the process by clicking the "play" button in the simulator and execution tool. If needed, the user can use the step-by-step process by choosing the appropriate buttons.
5. A topology screen that gives the user the opportunity to refresh the execution by altering the topology such as the size of the grid or the immunity time.
6. The drawing area itself located in the middle area of the software.

7.4.4. The Inverter-Parameter wireframes and its functionalities

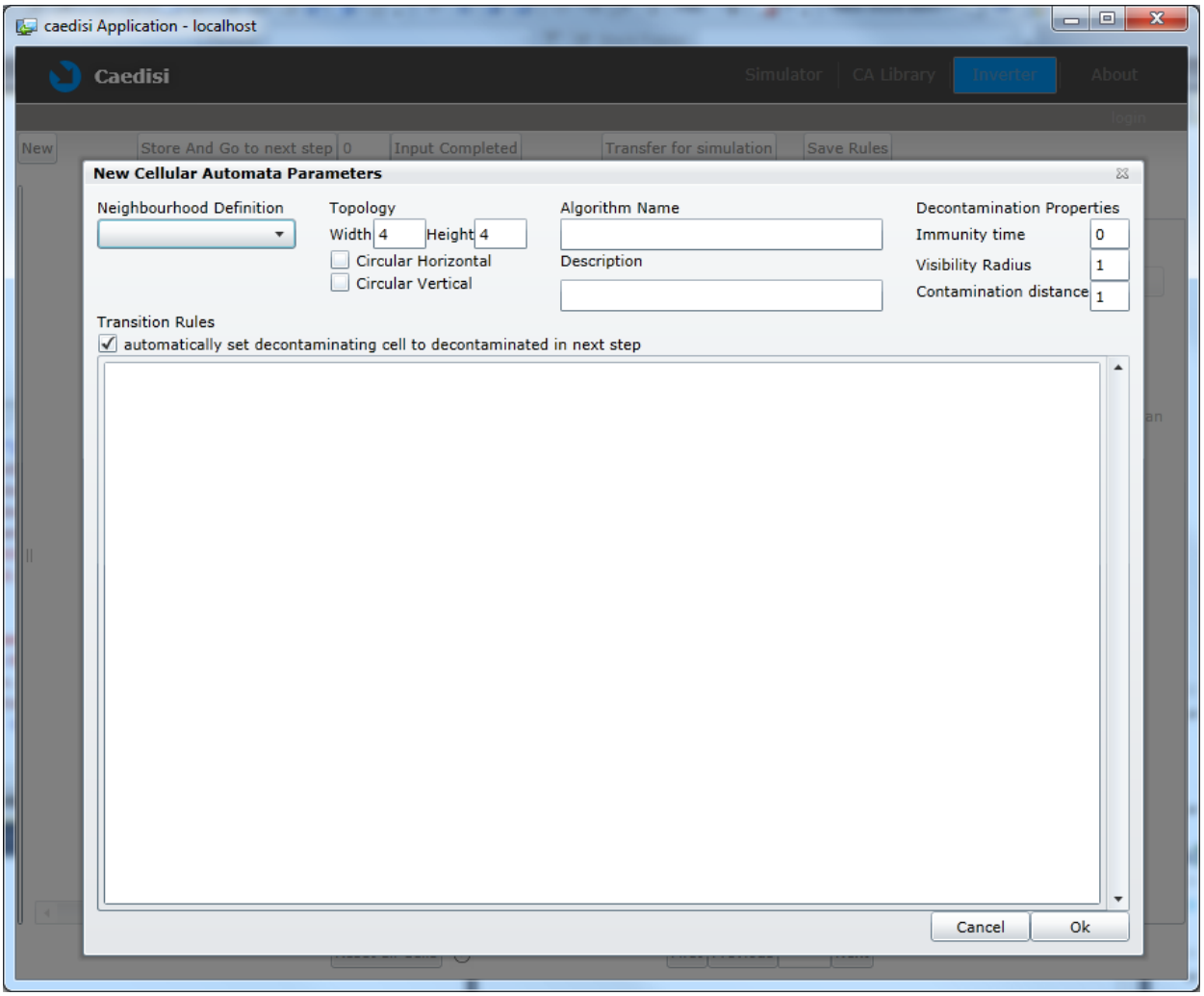


Figure 7.5: The CA parameter screen of the inverter module

The creation of a new Inverter process and the editing of the CA's current parameters of the execution will result in the opening of the *Inverter Parameter* screen. In this user interface, similar to the *CA Parameter* screen, the user will set all required properties defining the current CA. The key difference between these two parameter screens (and the backend functionality) is that in the CA Screen transition rules are added manually by the user, while in the Inverter process, transition rules are generated by the system (the Inverter algorithm) and these rules are only consulted on a read-only basis.

7.5. The Library Module

7.5.1. Pertinence and goals

The idea behind having a CA database is to be able to consult these data for many purposes. One obvious motivation is to reference these data to avoid data redundancy. In other words, data in the library can be reused across various CA without recreating it. For instance, the list of transition states only needs to be defined once and all future CA will only require a pointer to the list. The same motivation holds for the list of neighbourhood types. Another motivation is the ability to filter the required CA by questioning the database based on properties that have been saved. This will then provide faster access to a researcher who is interested in a specific set of CA. In a larger vision, these data can be analyzed by their structure and properties for data mining exercises.

7.5.2. The Transition State Definition user interface

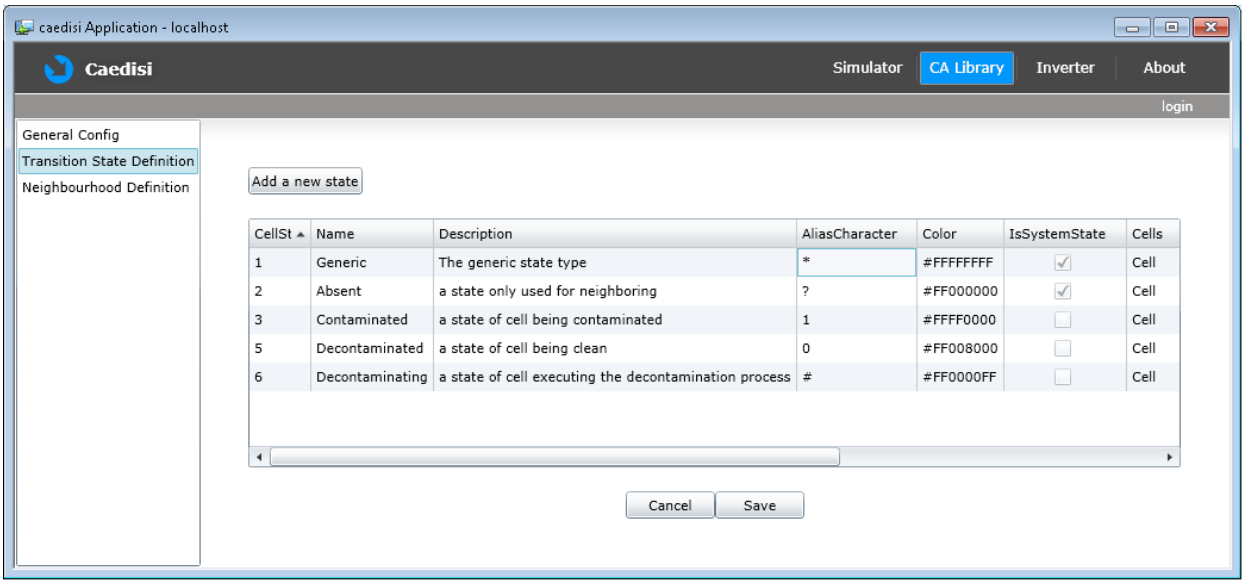


Figure 7.6: The Transition State Definition screen of the library module showing the current list of cell state types.

The Transition State Definition screen allows the user to create as many type of states as desired. By default, the system contains two predefined states that the user cannot alter: the *generic* state denoted by * and the *absent* state as defined in our model (see Chapter 3).

The user can create three states: contaminated, decontaminated and decontaminating if the software is used for a Network Decontamination investigation. The user can also associate a color and a character for each state. The color will serve to differentiate each cell during the decontamination process. However, the character can be used if the user wishes to define the rule using the traditional notation (see upcoming screen for the ruled definition)

7.5.3. The Neighbourhood Definition user interface

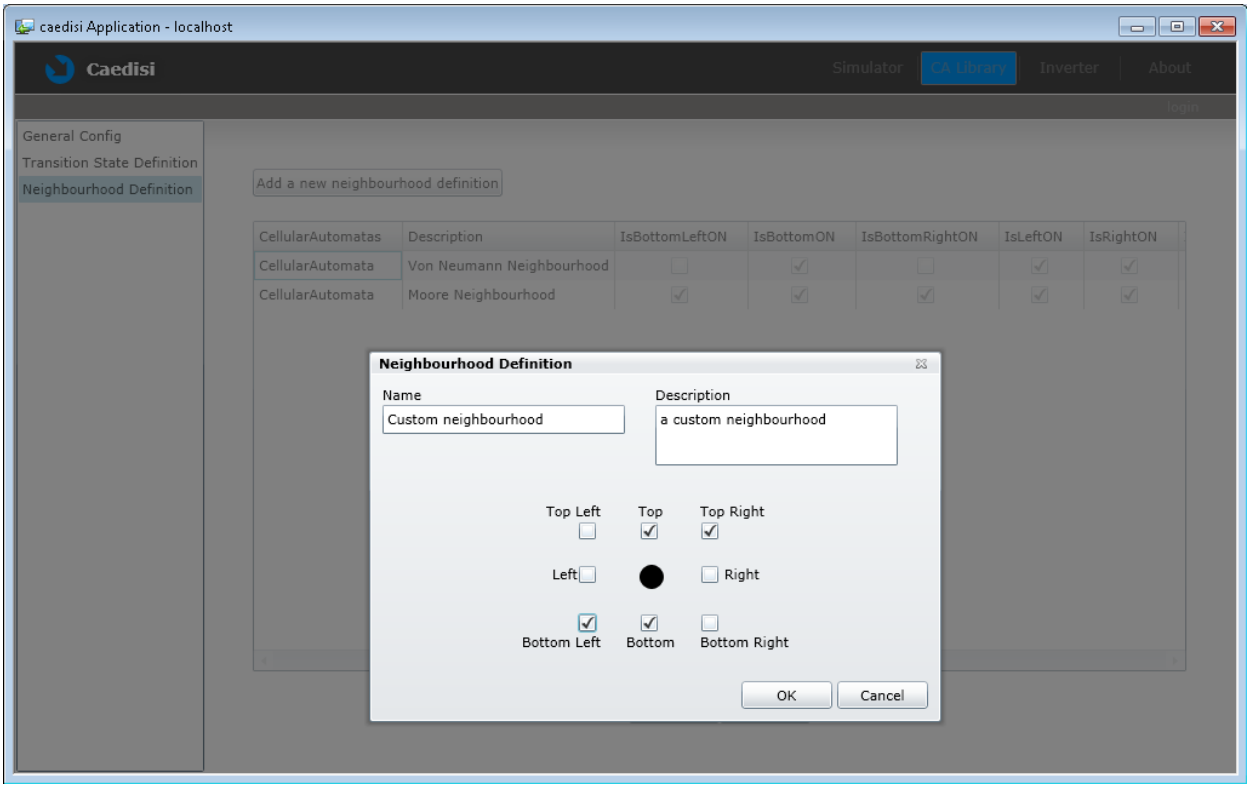


Figure 7.7: The Neighbourhood Definition edit screen of the library module showing how to create a new type of neighbouhood

The *neighbourhood definition* tool allows the user to define a new type of neighbourhood that he intends to use. By default, the system contains the von Neumann and Moore neighbourhood. The collection of pre-saved neighbourhood types can later be associated to the desired CA.

7.6. The Model

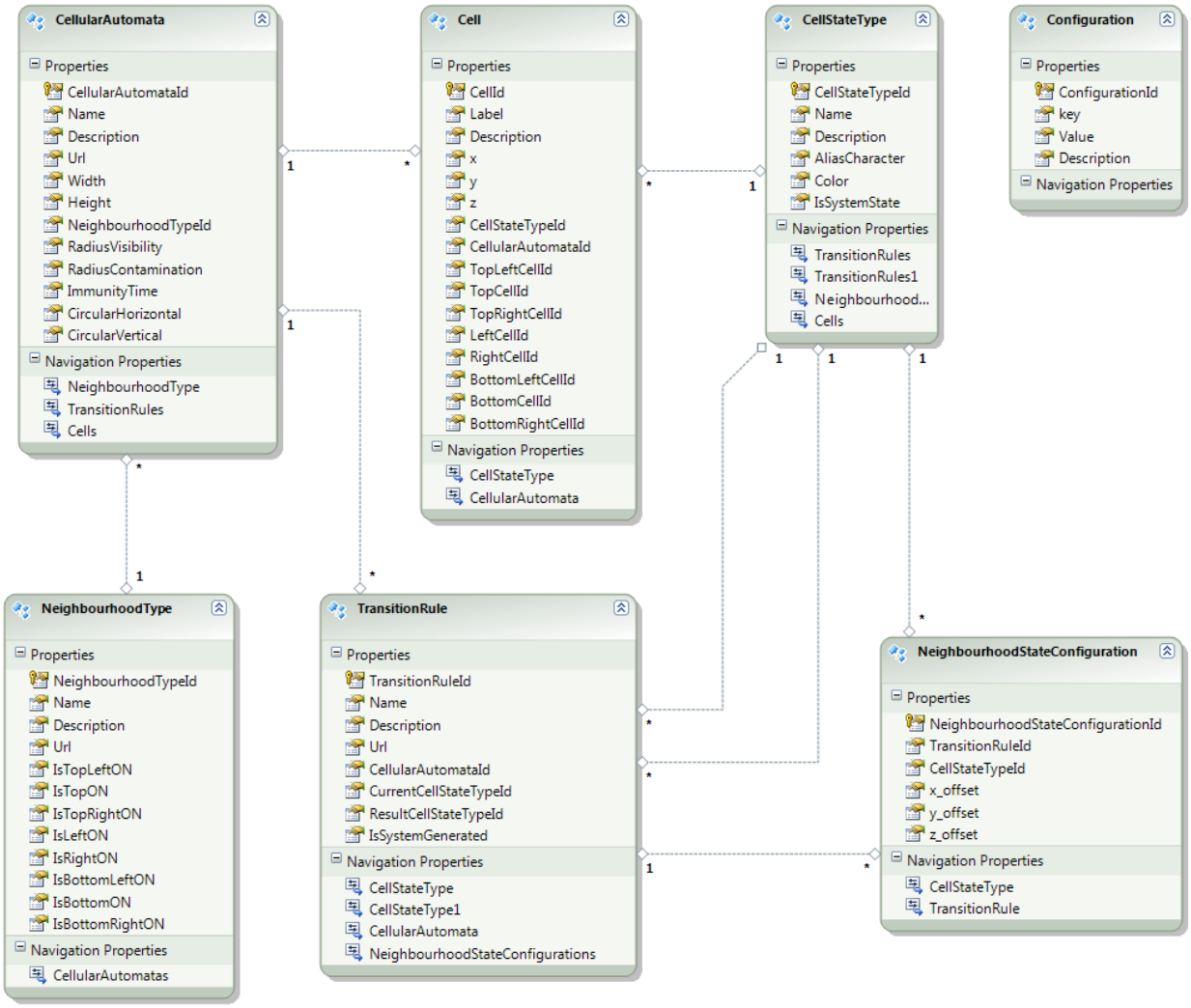


Figure 7.8: the data entity model of CAEDISI

The entity data model is a set of concepts that describe the structure of the data regardless of its stored form. The conceptual model of the system is represented in the above figure showing the data as entities and the relationships between these data.

The main entity of the system is the ***CellularAutomata*** object. Its name and description helps the user for identification on a future use. It is also defined with an Id that serves to key the object inside the database. Rather than just being considered a grid with a *width* and a *height*, the *CellularAutomata* object is the root object of the system responsible

for materializing a specific algorithm. Therefore, it contains some particulars of the topology such as Boolean values that identify for example if the CA is circular.

The *CellularAutomata* object is characterized by a single ***NeighbourhoodType*** attribute. A *NeighbourhoodType* object is defined by the presence/absence of the cells around it. For instance, the von Neumann neighbourhood has the flags IsTopOn, IsRightON, IsBottomOn and IsLeftOn set to true and the remaining flags set to false.

A *CellularAutomata* is composed of several ***Cell*** objects whose number *is* the product of the *CellularAutomata's Width* and its *Height*. Each *Cell* is equipped with coordinates which indicate its position within the grid. Note that the entity data model stipulates that the *Cell* is defined in 3D, but the current implementation only supports a 2D dimension. Additionally, each *Cell* is provided with a description and a label which by default is the concatenation of its coordinates itself (e.g., the label value of the cell at the top-left corner of the CA is [0,0,0]). The user can alter these values as needed. For convenience, each *Cell* also has a reference to its surrounding neighbours.

Each cell is characterized by a ***CellStateType***, which can be a specific transition state (contaminated, decontaminating, or decontaminated), an abstract state transition (e.g., generic and may represent any transition state), or just a qualification that expresses the existential state of a cell (e.g., absent and therefore the cell is not present within the grid). The generic type is only used in the expression of the definition of a transition rule while the absent type is used simultaneously in the transition rules and in the grid when representing sub-truncated CA. The idea of modeling an absent cell as a kind of transition state is motivated by two reasons. Firstly, it facilitates the interpretation of the transition rules by any algorithm, and secondly because an absent cell is seen by its neighbors as just a cell with a particular state. The operation of representing a missing cell in the grid is identical to changing the state of the cell.

A *CellularAutomata* object has a collection of ***TransitionRule*** objects assigned to it. A *TransitionRule* object is defined by three criteria: the current cell state, the future cell state, and the neighbourhood conditions of the current cell which specify the rules with respect to transit from the current state to the future state. These neighborhood conditions are modeled by a list of *NeighbourhoodStateConfiguration* objects.

A ***NeighbourhoodStateConfiguration*** object is a cell that only figures in the definition of a neighbourhood. Thus, it has also a state. More importantly, its role is to be able to locate itself relatively to the current cell to be transitioned. This is done through a coordinate structure based on an offset. The use of an offset is motivated by the fact that the neighbour cell can be present or missing within in the rule depending on the chosen neighborhood type and the Visibility Hop.

7.7. The Simulator module

7.7.1. Pertinence and goals

The goal of simulation software is to be a tool to test and validate the feasibility of any decontamination algorithm. Without simulation software, our algorithms would be tested on paper. Unlike a traditional procedural algorithm, for which it is generally easy to find a formal proof that the algorithm works optimally against certain criteria, it is often difficult to simply show that an algorithm executed against a CA works as predicted. A procedural algorithm is sequentially analyzed through its instructions; however, a CA algorithm runs in a parallel fashion on each cell. Each cell may be subject to every transition rule depending on its neighborhood at a given time t. Therefore on paper, each cell must be checked at each stage to determine if it satisfies the neighborhood configuration of all recorded transitions' rules. This may still be feasible in very simple conditions, for example in a small size CA of visibility Vh=1 and equipped with a small neighborhood (e.g. von Neumann). However, the same checking process would require considerable effort when the visibility increases (e.g. Vh=3) and the neighborhood is large (e.g. Moore). In a simple algorithm, such as the basic algorithm that decontaminates from left to right, cells can be classified into equivalence classes with respect to their localization within the grid. When the flow decontamination is not as regular, as in the Diagonal Snake, it becomes difficult or impossible to test the algorithm on paper as there are many combinations of neighbourhood configuration during the execution of the algorithm. Having software will not only save time in the testing of the algorithms, but it can quickly provide an output and can offer a counter example of neighbourhood configuration when the algorithm fails.

7.7.2. Application logic

The purpose of the simulation process is to sequentially produce the contents of a dictionary whose key is a pair composed by the cell Id and the current step of execution *t*. The value referenced by the key is an object containing the value of the cell state, the immunity value at step *t*, and additional metadata that we will discuss in the next subsection. To produce the contents of the dictionary, the algorithm relies on the CA data modeled on the structure described in the entity model. The dictionary contents are consumed by the UI with $O(1)$ operation for each cell at any time *t*. The implementation of the main algorithm can be consulted in *Appendix A*.

7.7.3. Simulation Metadata

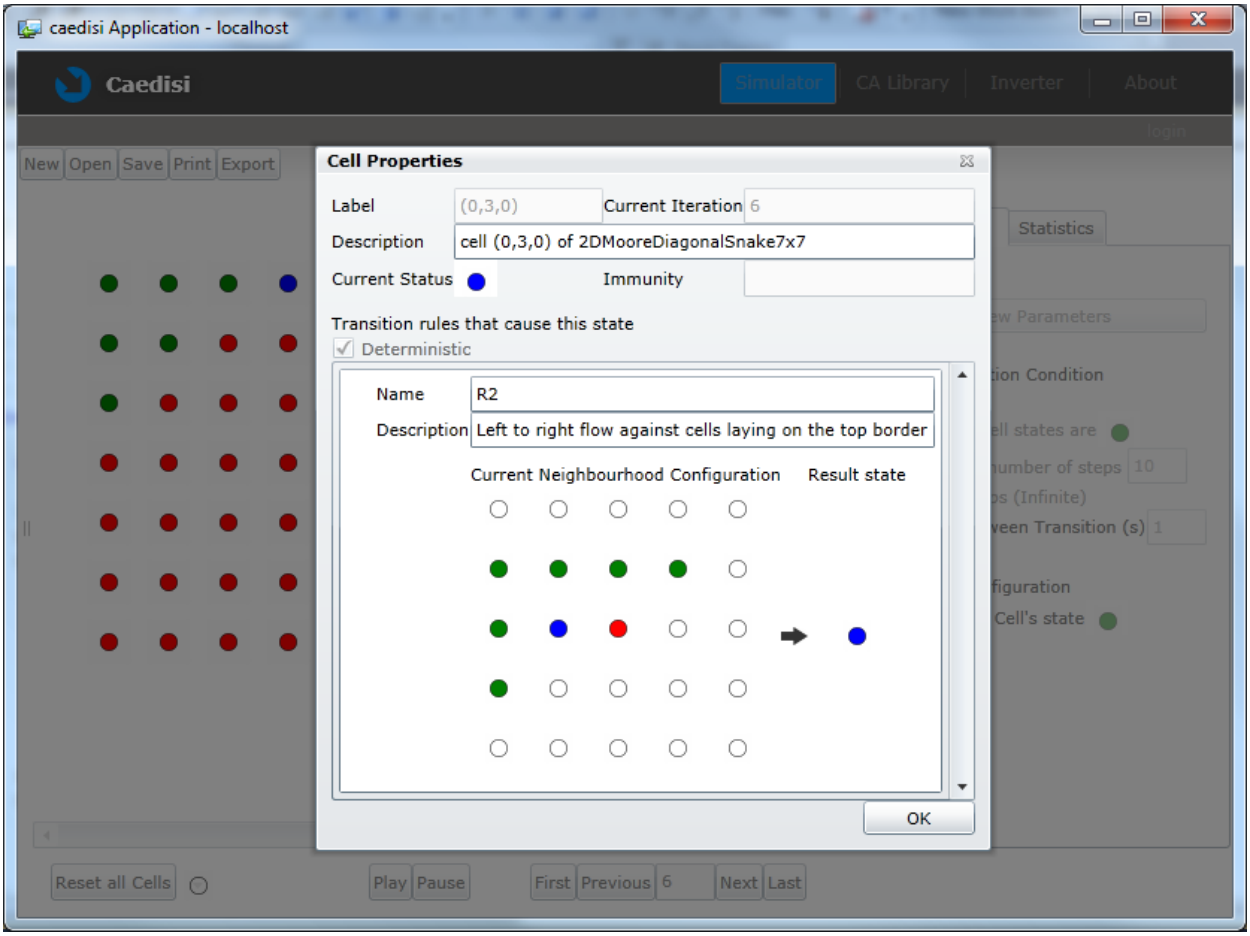


Figure 7.9: A sample view of the metadata screen of the simulation module

The advantage of having simulation software is the ability to add features that provide additional data generated by the execution. For example, within the data structure of the simulation, we added a feature that allows the user to identify the exact rule that permits the cell to pass into its new state. This additional information is shown in the figure above (Figure 7.9) which illustrates the potential to have information regarding a cell at any given time. In this example, during the *Diagonal Snake* algorithm, the user right-clicks on the cell located in the first row and fourth column, and concludes that the rule R2 is responsible for the transit of the cell (0, 3, 0) from contaminated to decontaminating. This feature gives a confirmation of the status change, and it also allows us to access additional information such as the value of the cell immunity (which is expected to decline at each step). A crucial benefit is also the knowledge of when multiple rules are applicable for same cell and thus could lead to a non-deterministic state of the cell in question.

7.8. Rules Validation & (Non) determinism

7.8.1. The transition rule collision validation

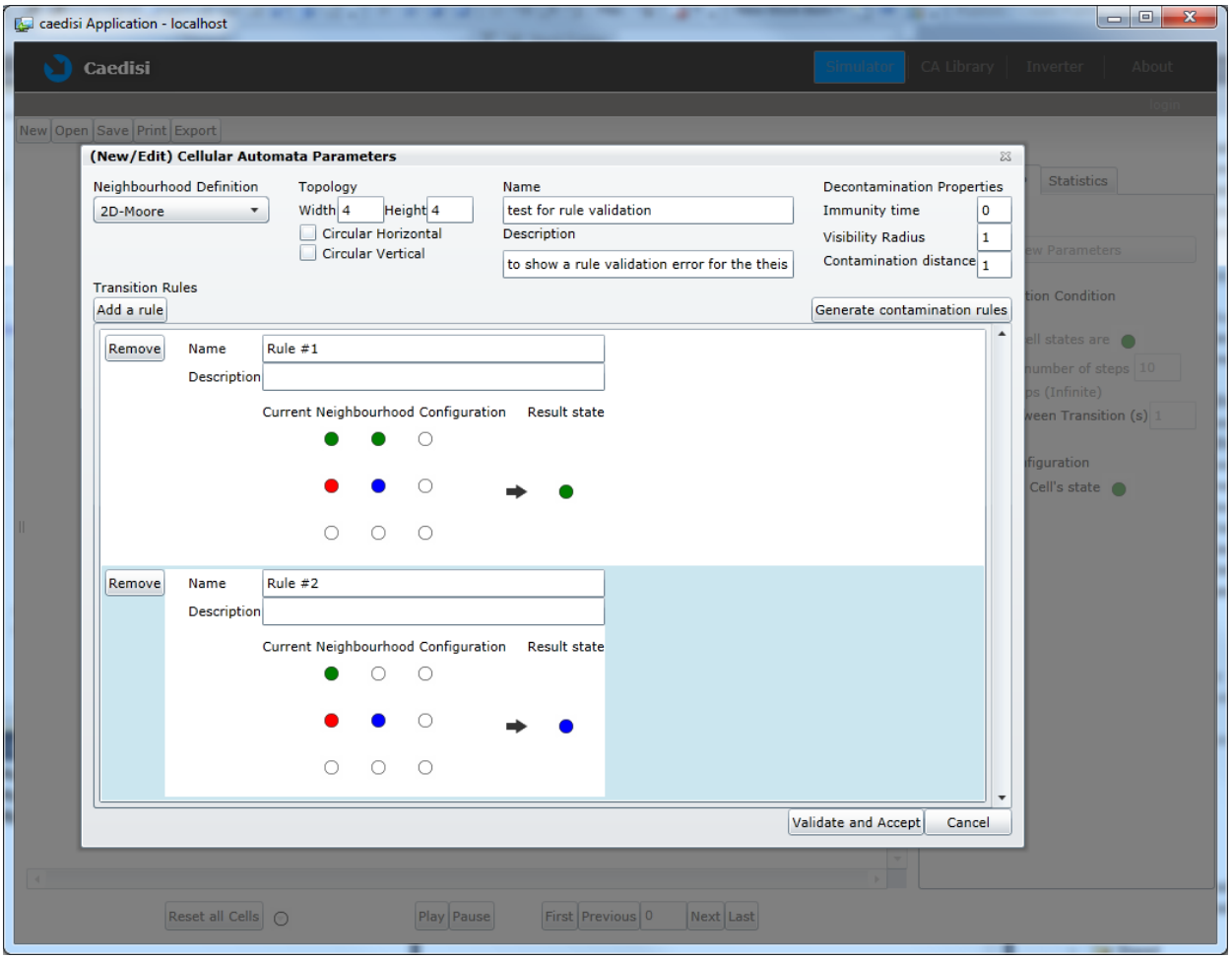


Figure 7.10: An example of two rules having collision errors

One condition that the software must validate is the presence of *collision rules.* Two or more transition rules collide when they can target the same cell but the result state of these elected rules are different (Figure 7.10). This means that the CA will face some non-deterministic behaviour if the neighbourhood configurations referred to by the elected transition rules are met during the execution.

When collisions are found during validation, the system displays a validation results screen with all rules that collide. Then, it prompts the user to correct the issue (desired behaviour) or to ignore the error messages and to assume the non-deterministic behaviour

(Figure 7.11). The implementation of the collision validation algorithm can be consulted in *Appendix D*.

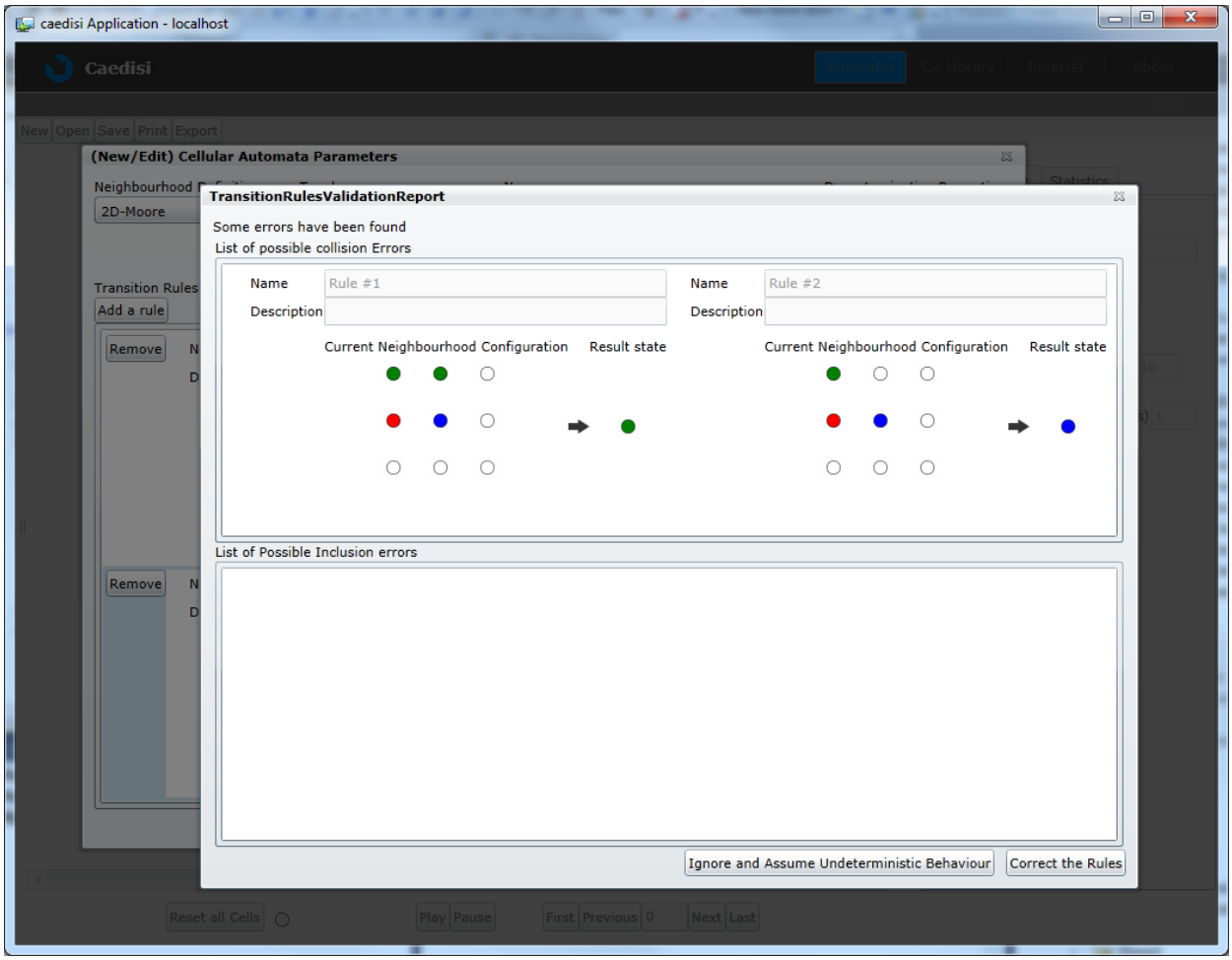


Figure 7.11: A view of the Rules Validation Results screen showing collision errors

7.8.2. The transition rule inclusion validation

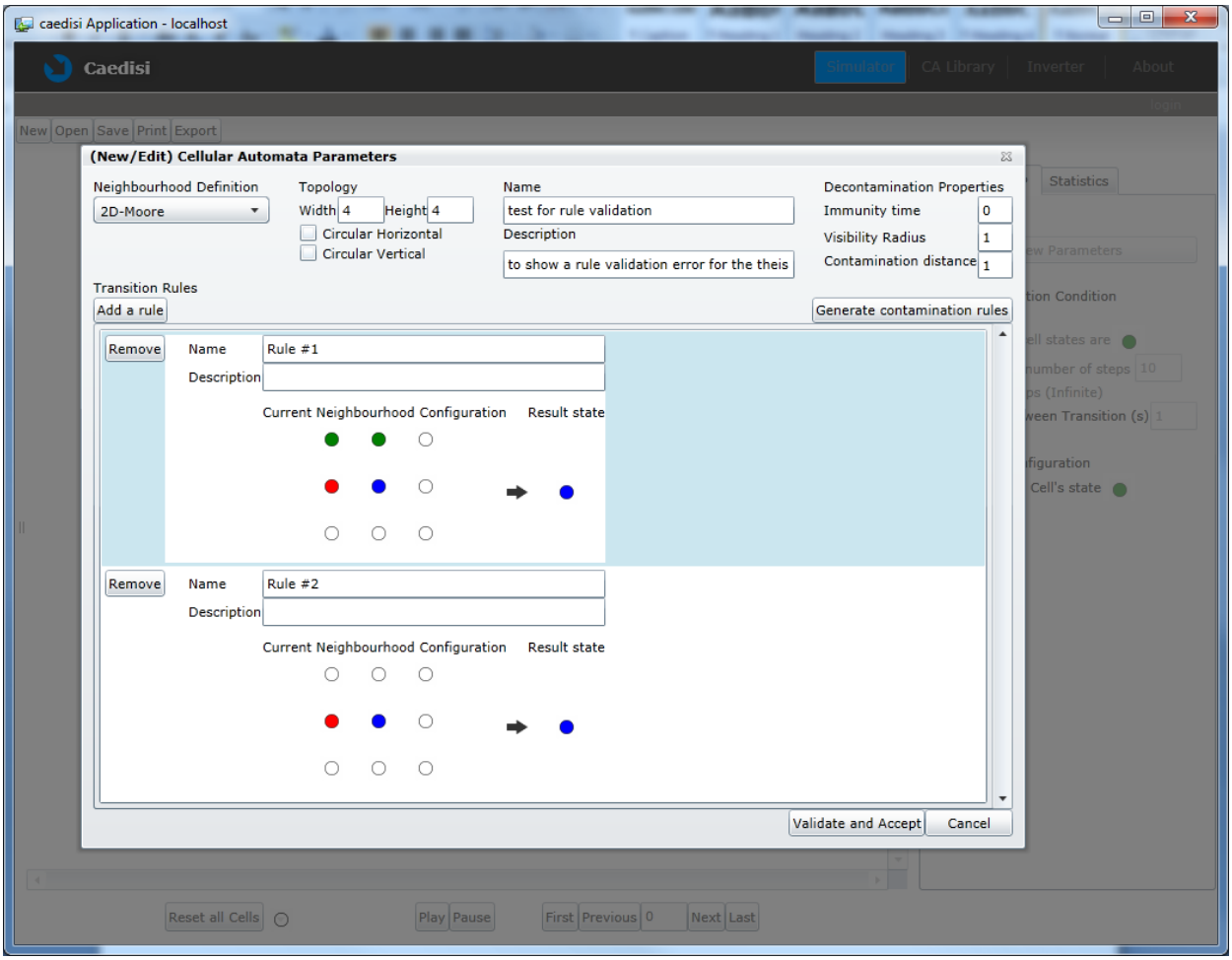


Figure 7.12: An example of two rules having inclusion errors

Another condition that the software must also validate is the presence of *inclusion rules.* Inclusion errors happen when there are multiple transition rules with identical result states targeting the same cell (Figure 7.12). Unlike collision rules in which the software must react with rejections, the system only needs to warn the user in the case of inclusion errors. In most cases, this situation happens because of the use of the "generic" state when expressing the state value of a cell during the transition rule definition. Unlike collision rules, inclusion rules do not harm the system with a possibility of non-deterministic behaviour. However, inclusion rules have an impact on the software performance because the system will perform additional and unnecessary operations when evaluating a rule which is already expressed by another existing rule.

When inclusion rules are found during validation, the system displays a validation results screen with all rules that collide. Then, it prompts the user to correct the issue (desired behaviour) or to ignore the error messages (Figure 7.13). The implementation of the inclusion validation algorithm can be consulted in *Appendix D*.

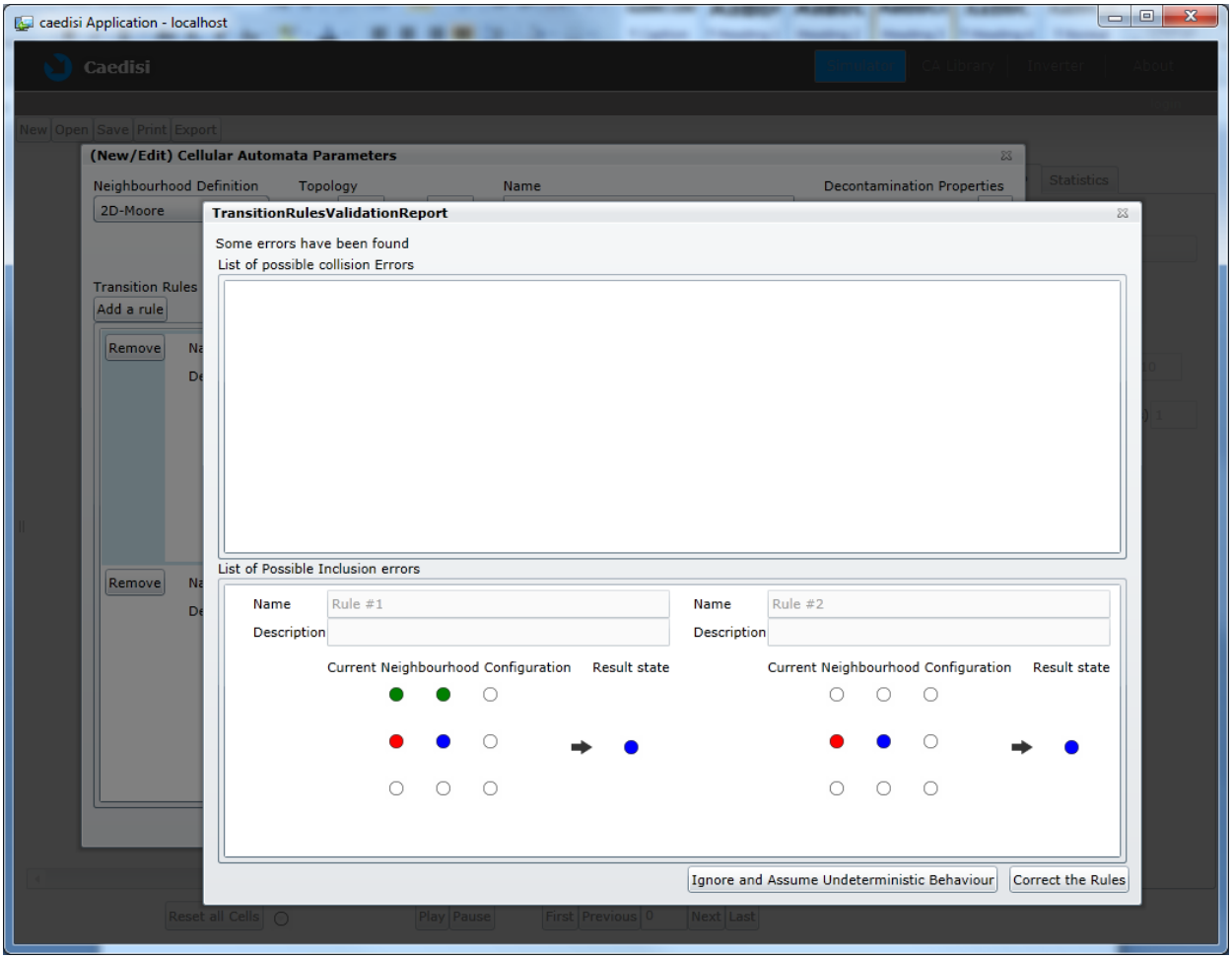


Figure 7.13: A view of the Rules Validation Results screen showing inclusion errors

7.8.3. Validation Rules algorithm

Clearly, both inclusion and collision validation algorithms has to compare each pair of saved rules. In the case of the collision rule validation, the first check is to verify if the result state is different. However, in the inclusion rule, the result state has to be identical. In

both cases, the second step is to verify if the current neighbourhood configuration are isomorphic with the pseudo-code below:

```
Procedure boolean IsInputIsomorphic(
      TransitionRule t1,
      TransitionRule t2)
begin
   For each NeighbourhoodStateConfiguration Nt1 in t1
     If state of Nt1≠*
     begin
         Nt2 ← the equivalent   NeighbourhoodStateConfiguration in t2
          If Nt2≠∅ and
             state of Nt2≠* and
            state of Nt1 ≠ state of Nt2
          begin
            Return false
          end
     end
   Return true
End
```

In the case of collision rule, the input configuration is isomorphic and the result state is different. In the case of inclustion rule, the input configuration is also isomorphic but the result state is identical. Since the *IsInputIsomorphic* is done with $O(1)$ operation (the cardinality of `NeighbourhoodStateConfiguration` is constant as to the number neighbours is fixed), both validation test executes in $O(n^2)$ in worst case as each pair of validation rules has to be tested with n being the number of transition rules saved within the system. Both implementation can be seen in [R13] with the procedure name *ValidateTransitionRulesInclusion* and *ValidateTransitionRuleCollision*.

7.9. The Inverter module

7.9.1. Pertinence and goals

The *Inverter* module is the second major feature of the software and can be seen as an inversion of the simulation process. At each stage, the user chooses the candidate cells for being decontaminating and the system successively tries to recreate the transition rules. The main motivation was to be able to quickly validate the feasibility of an idea for

decontamination through the stages of execution. If successful, the system would then be responsible for generating the rules of decontamination. One advantage is that after the generation of the rules, the user can revalidate the transition rules using the simulation module. In the case of unfeasibility, the system would show a counter-example by displaying a specific situation that contradicts the execution.

It is worth mentioning that unfeasibility is not fatal because it is possible that while the decontamination idea does not work within the parameters entered, it might still be possible with other parameters. As we have seen in Chapter 6, the diagonal snake algorithm is unfeasible with von Neumann of visibility Vh=2 but is feasible with von Neumann of visibility Vh=3 or in the vicinity of Moore visibility Vh=2. Fortunately, the software allows the user to use the Inverter module by varying different parameters such as visibility, neighborhood, and immunity. Under this approach, the software can be used as a research tool by helping the researcher to understand the dynamics of the decontamination strategy and the influence of the CA properties.

7.9.2. Application logic

The purpose of the inverter algorithm is to create the collection of transition rules generated by the Inverter. The Figure 7.14 below shows the execution of the Inverter and the content of the transition rules during a recreation of the diagonal move algorithm on a CA of Vh=1, Cd=1 and It=0. At the initial stage, only the contamination rules are contained in the TransitionRules object (Figure 7.14a). The user initiates the Inverter process by selecting the first decontaminating cell (at position [0,0]) at step t=0 (Figure 7.14b), Then, the user commands the system to store and validate this data, which automatically sets the cell [0,0] to decontaminated at step t=1. The user sets both cells at position [0,1] and [1,0] to a decontaminating state (Figure 7.14c). The user then commands the system again to move to the next step t=2. At this stage, the TransitionRules object will add the last 3 rules displayed in Figure 7.14d. The implementation of the main Inverter algorithm can be consulted in *Appendix B* (with Immunity) and *Appendix C*(without Immunity).

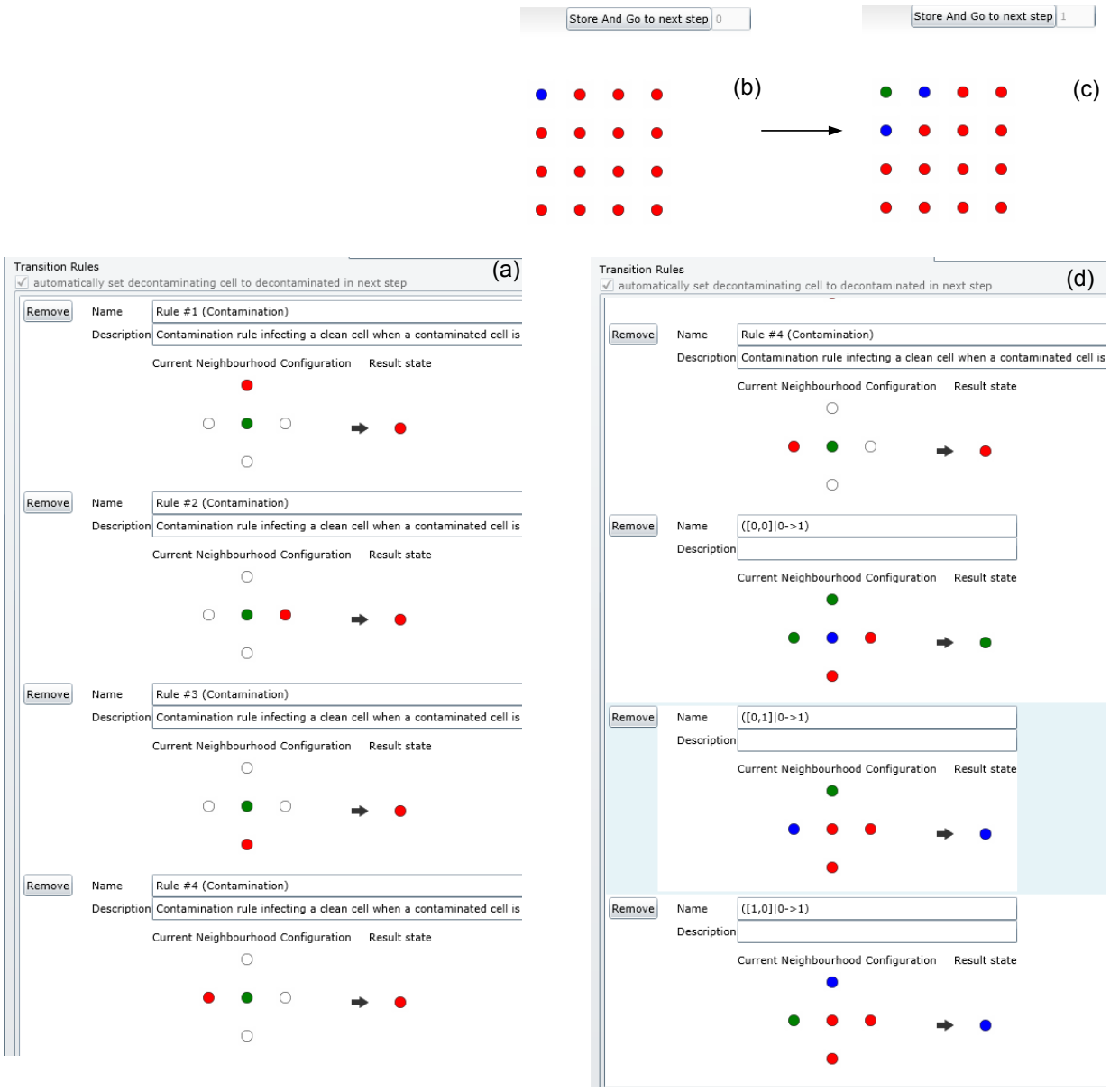


Figure 7.14: An example of the Inverter execution showing the creation of rules

Unlike the simulation module where a specific data structure is needed to hold each cell state at each step, the Inverter process does not necessarily rely on only one unique data structure. As data storage, we actually use the CA object as specified in the entity data model to store the inverter parameters. The collection rules are also stored in its *TransitionRule* child object. In order to support a preview of the pre-entered data (with the *forward* and *backward* buttons) for the user to re-verify his entry, we use the same type of dictionary used by the simulation module. Once the user has decided the value of each

parameter defining the CA, the size of the latter is static and fixed during each execution. Therefore, a regular array is used as a temporary data structure to store the state of each CA at each step. Transition rules are built based on the contents of the previous and the current step arrays.

7.9.3. Miscellaneous notes

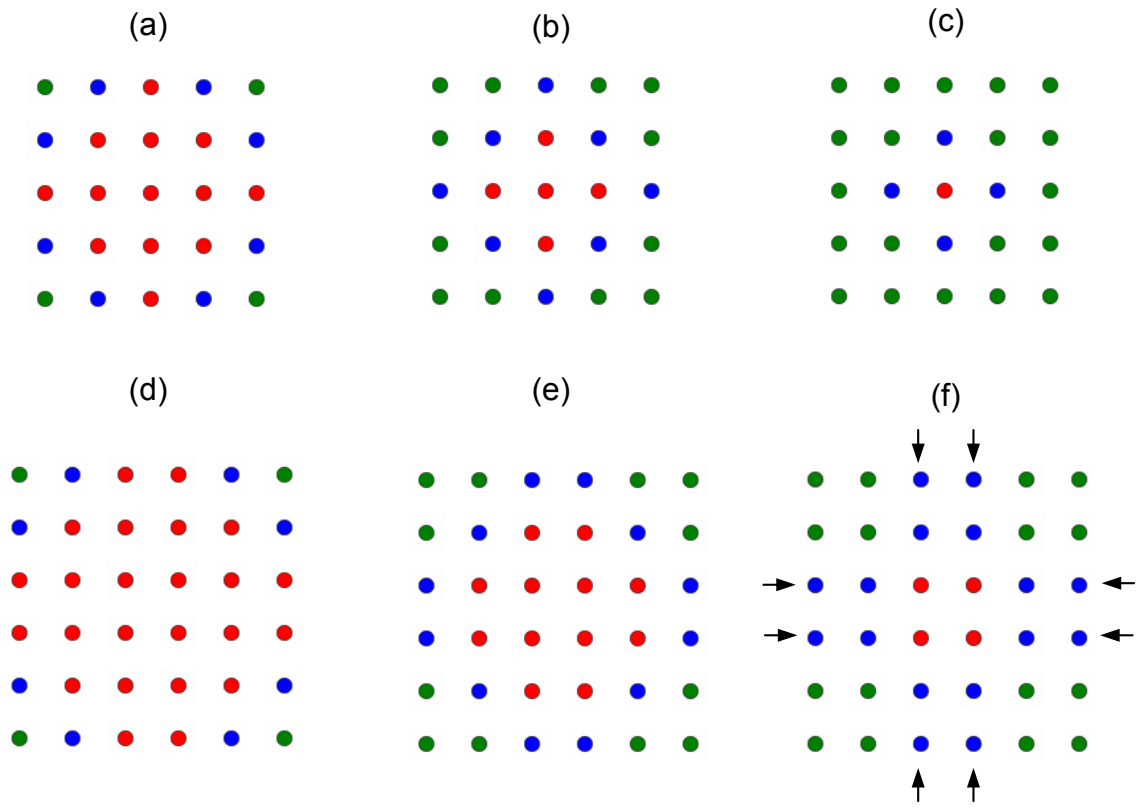


Figure 7.15: The impact of an even/odd sized CA on the Inverter

It is important to note that the performance of the inverter only takes into account the "exact" neighborhood during the construction of each transition rule. (Indeed, the software is not trying to create rules using generic state). As noted in the previous chapter, there are some cases in which created rules still require intervention in order to work for any size of CA. The diagonal snake algorithm, whose rules generated by the execution of the Inverter on a CA with an even size, could not be directly generalized to any size *n* and moreover, the generalization is not trivial.

The same situation is encountered when we look at the example of using the inverter to generate the rules of the diagonal move approach. In this scenario, we see that the generalization can be done easily. Take the example shown in the previous figure where the rules were generated by running the inverter algorithm on a CA of an odd size. When executing the inverter for $n = 5$, we note that decontamination performs as expected (Figures (a) , (b) and (c)). However, when executing the rules against a CA of an even size, we notice some runtime defects as shown in Figure (f) because the cells pointed to by the arrows should be in a decontaminated state in stage (f). The reason is that the configuration of the stage shown in Figure (e) has never been treated during the execution. We do not find the configuration of Figure (e) in (a), nor (b) and (c). To fix the issues, we can add the simple rule  . With this addition, we end up with a set of rules which work with both even and odd sized CA.

Chapter 8

Summary & Future work

In this chapter, we summarize the work that we have completed so far. We discuss possible directions for future work based on the solutions that we have proposed, and we also discuss some new ideas.

8.1. Summary

In this thesis, we have studied the decontamination in CA through two new additional concepts: *Visibility Hop* and *Contamination Distance*. Specifically, we have proposed different solutions and evaluated these solutions according to the established complexity measures. Our goal was to understand the impact of these two assumptions on existing solutions. Then, we proposed new algorithms occasioned by these concepts.

In Chapter 2, we provided a survey of the current state of research in external and internal Network Decontamination with a concentration on internal Network Decontamination. We also briefly discussed CA. This survey helped by providing an in depth understanding of the decontamination problem, and the different techniques useful in our study of Network Decontamination problems.

In Chapter 3, we formally described the model used in this thesis: Network Decontamination using CA under the new assumptions *Visibility Hop* and *Contamination Distance*. Our model is a regular grid of cells, having three states (contaminated, decontaminating, and decontaminated) and where the cells change their state synchronously according to local rules. In our study, we also considered the notion of *Time Immunity* in some cases.

In Chapters 4, 5 and 6, we have shown the pertinence of these two new parameters. In Chapter 4, we analyzed known basic decontamination algorithms with different values for Visibility Hop and Contamination Distance. We started by analyzing existing basic algorithms under these new assumptions and we provided some solutions on how these strategies can be updated to have better results.

In Chapter 5, we proposed new algorithms characterized by diagonal moves. We have also shown that the use of *Visibility Hop* leads to better results when applied to our diagonal algorithms, especially when considering the average number of decontaminating cells being utilized. We gave a list of rules that accomplish the decontamination for specific values of *Cd* and *Vh*. We also gave a general algorithm for any arbitrary values of these two parameters.

In Chapter 6, we proposed some new ideas that can only be fulfilled if *Visibility Hop* $Vh \geq 2$ holds. We proposed two new algorithms called *Road Traffic* and *Diagonal Snake,* and we indeed claim that they are only feasible if the CA allows *greater visibility* and *Immunity time*. Initial results have shown improvement with respect to the decontamination time and the maximum Immunity time when compared to existing algorithms. We have shown that we can transpose these ideas and complement them with some divide-and-conquer strategies by applying similar ideas against different locations within the CA. We also studied the possibility of subdividing the execution by using the diagonal moves introduced in Chapter 5.

In Chapter 7, we presented software that we implemented to support our study. Among all functionalities, there are two key pieces. One is the software's simulator module which allows the user to enter any pre-defined list of decontamination rules and witness the execution of the decontamination in a flexible manner. The other important functionality is the software's rules generator module which allows the software to generate some decontamination rules based on a idea of an execution. The building of the tool was essential because of the non existence of a tool that can take account of *Visibility Hop*, *Contamination Distance,* and *Time Immunity*. The resulting software is a complete research tool which can assist any researcher who focuses his work on CA, or Network Decontamination under that structure.

8.2. Current work extension and Future work

There are several ways in which we propose to continue the work begun here.

In this thesis, we concentrated our effort on studying the CA model in which the transition rules' results are defined in a precise way, and as soon as a neighbourhood configuration is met, the result state is final. We would like to investigate the case when the

result state is not necessarily fixed, but instead has a probabilistic factor of transiting to the new defined state. We have inserted the code to support this behaviour within the software but we would like to have a theoretical study of the possible stochastic models that are meaningful for Network Decontamination. This model responds to a very realistic situation in which some of the decontamination programs executed against the machine do not automatically succeed. For instance, during the diagonal move process, what happens when some of cells laying on the next diagonal do not necessarily transit to a decontaminating state? Can the defined algorithm still perform? How are we to classify existing algorithms which can positively react to this new input? Ultimately, we want to know how to build classes of algorithms that are immune to these probabilistic factors.

In this thesis, we have assumed monotone strategies to decontaminate the network. We would like to investigate the implementation of non-monotone strategies and the impact on Time Immunity and recontamination. The study of Network Decontamination using CA with non-monotone strategies is still very open and few results are known.

In this thesis, we assumed that the network is reliable, that is, the links and the nodes are not broken. What happens when, for example, a node cannot receive the state of its neighbour? What happens if the node sends the wrong state value to its neighbour? We gave a brief introduction of the possible issues in Chapter 3. Undeniably, the addition of fault tolerance in our algorithms is another attractive future work.

We also want to complement our software with new set of requirements. One evident functionality is to add the support of Mobile agents, which has the most interest among researchers in distributed computing. This will allow an experimental analysis of the impact of *Visibility Hop* on the new model introduced in [DFZ11] called Mobile CA MCA, a CA navigated by a *Mobile Agent*.

Finally, we intend to continue and finalize our research related to sub-truncated networks. We want to know the largest sub-truncated mesh that decreases the number of decontaminating cells. We expect that the understanding of the problem of decontamination in a sub network with fewer hosts, yet close enough to the full network, will allow us to find different perspectives on a new decontamination algorithm. We present a brief explanation of the problem.

Problem definition. Assume an optimal decontaminating strategy requires p simultaneously decontaminating cells to decontaminate a n*m 2D mesh. The goal is to identify the minimum number of cells x to be removed from the topology in order to decontaminate the newly sub-truncated network with a predefined k (with $k<p$) simultaneously decontaminating cells at any time t. The goal may also be to identify the maximum number of cells k which can be added to the topology without increasing the p simultaneously decontaminating cells. We believe that the research tool we have developed can offer us significant support during our exploration.

Bibliography

[ADF07] L. Acerbi, A. Dennunzio, E. Formenti. Shifting and lifting of CA. *In Proceedings of the 3rd conference on Computability in Europe: Computation and Logic in the Real World*, pages 1-10, Berlin, Heidelberg, 2007.

[ADF09] L. Acerbi, A. Dennunzio, E. Formenti. Conservation of some dynamical properties for operations on CA. *Theor. Comput. Sci*.,410:3685-3693, 2009.

[Als04] B. Alspach, Searching and sweeping graphs: a brief survey*, International Conference in Combinatorics*, Le Matematiche, Vol LIX - Fasc. I-II, pp. 5–37, 2004.

[Awa08] A. Awazu, Input-dependent wave propagations in asymmetric CA: possible behaviors of feed-forward loop in biological reaction network, *Mathematical Biosciences and Engineering*, Volume 5, Issue 3, 419 - 427, 2008.

[BFFS02] L. Barrière, P Flocchini, P. Fraigniaud, and N. Santoro. Capture of an Intruder by Mobile Agents. *In ACM Symposium on Parallelism in Algorithms and Architectures* (SPAA), pages 200-209, 2002.

[Bre67] R. Breisch., An intuitive approach to speleotopology, *Southwestern Cavers,* vol. VI, no. 5, pp. 72-78, 1967.

[CD98] B. Chopard and M. Droz. CA Modeling of Physical Systems, *Cambridge University Press*, 1998.

[Cel88] CelLab, http://www.fourmilab.ch/cellab/, online.

[Daa12] Y. Daadaa. Network Decontamination with Temporal Immunity, *phd Thesis*, University of Ottawa, Ottawa, Ontario, Canada, 2012.

[DFZ10] Y. Daada, P. Flocchini, N. Zaguia. Network Decontamination with temporal immunity by CA, *9th Int. Conference on CA for Research and Industry (ACRI),* 287-299, 2010

[DFZ11] Y. Daadaa, P. Flocchini, N. Zaguia, Decontamination with Temporal Immunity by Mobile CA, *In proceeding of: 3rd annual CA Workshop* (CSC), 2011.

[DLFM09] A. Dennunzio, P .Di Lena, E .Formenti, and L. Margara. On the Directional Dynamics of Additive CA. *Theoretical Computer Science*, 410:4823-4833, 2009.

[EF08] Entity Framework, http://www.asp.net/entity-framework, online.

[FHL06] P. Flocchini, M.J. Huang, F.L. Luccio., Decontamination of chordal rings and Tori, *Proc. 8th Workshop on Advances in Parallel and Distributed Computational,* 2006.

[FHL07] P. Flocchini, M.J. Huang , F.L. Luccio. Decontamination of chordal rings and tori using mobile agents. *International Journal of Foundation of Computer Science,* 18(3), 547-564, 2007

[FHL08] P. Flocchini, M.J. Huang, F.L. Luccio. Decontamination of hypercubes by mobile agents, *Networks,* 52(3): 167-178, 2008

[FIP+05] P. Fraigniaud, D. Ilcinkas, G. Peer, A. Pelc, and D. Peleg. Graph Exploration by a Finite Automata. *Theoretical Computer Science*, 345(2-3):331-344, 2005.

[Flo09] P. Flocchini. Contamination and decontamination in majority-based systems, *Journal of CA,* 4(3):183-200, 2009.

[Fia01] FiatLux, http://webloria.loria.fr/~fates/FiatLux/presentation-fr.html, online.

[FLPS13] P. Flocchini, F. Luccio, L. Pagli, N. Santoro, Optimal Network Decontamination with threshold immunity, *8th International Conference on Algorithms and Complexity* (CIAC), 2013.

[FMS08] P. Flocchini, B. Mans, and N. Santoro. Tree Decontamination with Temporary Immunity. *In 19th International Symposium on Algorithms and Computation* (ISAAC), pages 330-341, 2008.

[FNS05] P. Flocchini, A. Nayak, and A. Schulz. Cleaning an Arbitrary Regular Network with Mobile Agents. *In 2nd International Conference Distributed Computing and Internet Technology* (ICDCIT), pages 132-142, 2005.

[Gar70] M. Gardner. The Fantastic Combinations of John Conway's New Solitaire Game "Life". *Sci. Am*., 223:120-123, 1970.

[Gol00] Golly, http://golly.sourceforge.net/, online.

[JCA00] JCASim: CA simulation system, http://www.jcasim.de/, online.

[Kar05] J. Kari, Theory of CA: A survey, *Theoretical Computer Science*, Volume 334, Issues 1–3, Pages 3–33, April 2005.

[Kar90] J. Kari, Reversibility of 2D CA is undecidable, *Physica D: Nonlinear Phenomena*, Volume 45, Issues 1–3, Pages 379–385, 1990.

[KK07] E. Kranakis, D. Krizanc. An Algorithmic Theory of Mobile Agents, *In proceedings of TGC 2006*, *2nd Symposium on Trustworthy Global Computing*, Lucca, Italy, 2007.

[KP00] S. Kutten, D.Peleg. Tight Fault locality. *SIAM Journal on Computing*, 30:247-268, 2000.

[KVZ09] J. Kari, P. Vanier, and T. Zeume. Bounds on Non-Surjective CA. *In 34th International Symposium on Mathematical Foundations of Computer Science* (MFCS), 439-450, 2009.

[Lap93] A. S. LaPaugh. Recontamination Does Not Help to Search a Graph. *Journal of the ACM*, 40(2):224-245, 1993.

[LM08] P. di Lena and L. Margara. Computational Complexity of Dynamical Systems: The Case of CA. *Information and Computation*, 206(9-10):1104-1116, 2008.

[LM10] P. di Lena, L. Margara. On the Undecidability of the Limit Behavior of CA, *Theoretical Computer Science*, 411(7-9), 1075-1084, 2010.

[LP09] F. Luccio, Linda Pagli. A general approach to toroidal mesh decontamination with local immunity. In *Proceedings of the 2009 IEEE International Symposium on Parallel & Distributed Processing* (IPDPS '09). IEEE Computer Society, 1-8, 2009.

[LPS06] F. Luccio, L. Pagli, N. Santoro. Network Decontamination with local immunization. In *Proceedings of the 20th international conference on Parallel and distributed processing* (IPDPS'06), 2006

[LPS07] F. Luccio, L. Pagli, N. Santoro, Network Decontamination in presence of local immunity, *Int. Journal of Foundations of Computer Science,* 18 (3): 457-474, 2007

[Mce99] MCell, http://www.mirekw.com/ca/index.html, online.

[Mes08] M.-E. Messinger, Methods of Decontaminating Networks, *Phd Thesis*, Dalhousie University, Halifax, Nova Scotia, Canada, 2008.

[MHG+88] N. Megiddo, S. Hakimi, M. Garey, D. Johnson, and C. Papadimitriou. The complexity of searching a graph. *Journal of the ACM*, 35(1):18–44, 1988.

[MG68] E. F. Moore, G. G. Langdon. A generalized firing squad problem, *Information and Control* 12 (3), 212–220, 1968.

[Mit96] M. Mitchel, Computation in CA: A Selected Review, *Technical Report*, Santa Fe Institute, New Mexico, 1996.

[Neu51] J. v. Neumann, The general and logical theory of automata, *L.A. Jeffress, ed., Cerebral Mechanisms in Behavior – The Hixon Symposium, John Wiley & Sons, New York,* pp. 1-31, 1951.

[Neu96] J.v.Neumann, theory of self-reproducing automata, Univ. of Illinois, Urbana 1996.

[Pac86] N. H. Packard. Lattice Models for Solidification and Aggregation. *In First International Symosium for Science on Form,* 1986.

[Par76] T. D. Parsons, Pursuit-evasion in a graph. *Theory and Applications of Graphs*. Springer-Verlag. pp. 426–441, 1976.

[Par78] T. D. Parsons. The Search Number of a Connected Graph. *In 9th Southeastern Conference on Combinatorics*, Graph Theory and Computing, Utilitas Mathematica, pages 549-554, 1978.

[Pel02] D. Peleg. Local majority voting, small coalitions and controlling monopolies in graphs: A review. *Theoretical Computer Science* 282, 231–257, 2002.

[Qiu07] J. Qiu. Best Effort Decontamination of Networks. *Master's thesis*, University of Ottawa, 2007

[R13] L. Rakotomalala, Caedisi source code, https://caedisi.codeplex.com/, online.

[RZ15] L. Rakotomalala, N. Zaguia, CAEDISI: A Cellular Automata Editor and Simulator for Network Decontamination, *The society for Modeling and Simulation International, SummerSim'15 (SCSC2015)*, Chicago, IL, USA, 2015.

[Sab08] M. Sablik. Directional Dynamics for CA: a Sensitivity to Initial Condition Approach. *Theoretical Computer Science*, 400(1-3):1-18, 2008.

[Sch02] B. Schonfisch. Propagation of Fronts in CA. *Physica D*, 80:433-450, October 2002.

[Sil10] Silverlight, http://www.microsoft.com/silverlight/, online.

[SQL05] SQL Server, http://www.microsoft.com/sql, online.

[WCF04] WCF RIA Services, http://msdn.microsoft.com/en-us/library/ee707344(v=vs.91).aspx, online.

[WMS88] Wolfram Mathematica Software, http://wolfram.com/, online

[Wol84] S. Wolfram. Universality and complexity in CA, *Physica D: Nonlinear Phenomena,* Volume 10, Issues 1–2, 1–35, 1984.

[Wol88] S. Wolfram. High Speed Computing, *Scientific Application and Algorithm Design*, ed. Robert B. Wilhelmson. University of Illinois Press, 1988.

[Wol94] S. Wolfram. Theory and Applications of CA, *World Scientific* (1986), CA and Complexity, Addison-Wesley, Massachusetts, 1994.

[Wol02] Stephen Wolfram, A new kind of science, *Wolfram Media*, 2002.

Appendix A: Implementation of the Simulation algorithm

```
/// <summary>
/// Processes the transition rules algorithm. The goal is to produce new state for each cell of the cellular automata
/// based on which transition rules is eligible applied to that cell. The data structure that holds the state for each
/// step is the SystemStateDictionary.
/// </summary>
/// <param name="cellularAutomata">The cellular automata.</param>
/// <param name="newStep">The new step.</param>
private void ProcessTransitionRulesAlgorithm(Web.DataModel.CellularAutomata cellularAutomata, int newStep)
{
    int numberOfRows = cellularAutomata.Height;
    int numberOfColumns = cellularAutomata.Width;

    for (int i = 0; i < numberOfRows; i++)
    {
        for (int j = 0; j < numberOfColumns; j++)
        {
            int k = 0;  // only 2D for now
            Cell myCell = cellularAutomata.CellularAutomataAsArray[i, j, k];
            SimulationIterationItem previousIterationItem = GetSimulationIterationItem(myCell.CellId, newStep-1, false);
            SimulationIterationItem newIterationItem = GetSimulationIterationItem(myCell.CellId, newStep, true);
            newIterationItem.Reset();

            //grab which rules applies to myCell
            foreach (TransitionRule rule in cellularAutomata.TransitionRules)
            {
                bool doesCellCurrentStateSatisfyRule =
                    DoesCellConfigurationSatisfyTransitionRule(myCell, rule, cellularAutomata);
                if (doesCellCurrentStateSatisfyRule)
                    newIterationItem.TransitionRulesCause.Add(rule);
            }

            //by default, the result state is the old value
            int resultCellStateTypeId = myCell.CellStateTypeId;
            if (newIterationItem.TransitionRulesCause.Count > 0)
            {
                if (newIterationItem.IsDeterministic)
                {
                    int tentativeResultCellStateTypeId =
                        newIterationItem.TransitionRulesCause.First().ResultCellStateTypeId;
                    if (tentativeResultCellStateTypeId == ((int)EnumCellStateType.Decontaminated))
                    {
                        resultCellStateTypeId = ((int)EnumCellStateType.Decontaminated);
                        //each time the cell gets decontaminated (i.e the virus has been cleant),
                        //the immunity timer is reset
                        newIterationItem.ImmunityTimerValue = cellularAutomata.ImmunityTime;
                    }
                    else if (tentativeResultCellStateTypeId == ((int)EnumCellStateType.Contaminated))
                    {
                        //it will goes to contaminated if the cell is no more immune
                        if (previousIterationItem == null || previousIterationItem.ImmunityTimerValue == 0)
                        {
                            resultCellStateTypeId = ((int)EnumCellStateType.Contaminated);
                        }
                        else
                            resultCellStateTypeId = myCell.CellStateTypeId;

                        //decrease the timer
                        newIterationItem.ImmunityTimerValue =
                            (previousIterationItem.ImmunityTimerValue > 0 ?
                            previousIterationItem.ImmunityTimerValue - 1 : 0);
                    }
                    else
                        resultCellStateTypeId = tentativeResultCellStateTypeId;
                }
```

```
                else
                {   // Undeterministic (We found multiple transition rules that can be applied to the
                    // cells but their result state are different) The Code decision is to keep the previous
                    // transition result but we flag that the cell has an issue
                    resultCellStateTypeId = myCell.CellStateTypeId;
                    //even for underterministic case, we still decrease the immunity timer when the previous
                    //state has a timer value set
                    if (previousIterationItem.CellStateTypeId == ((int)EnumCellStateType.Decontaminated))
                        newIterationItem.ImmunityTimerValue =
                            (previousIterationItem.ImmunityTimerValue > 0 ?
                            previousIterationItem.ImmunityTimerValue - 1 : 0);
                }
            }
            else
            {
                if (resultCellStateTypeId == ((int)EnumCellStateType.Decontaminated))
                {
                    newIterationItem.ImmunityTimerValue =
                        (previousIterationItem.ImmunityTimerValue>0 ?
                        previousIterationItem.ImmunityTimerValue-1 : 0);
                }
            }
            //setting the final result state
            newIterationItem.CellStateTypeId = resultCellStateTypeId;

            Tuple<Guid, int> newIterationItemKey= new Tuple<Guid,int>(myCell.CellId, newStep);
            this.SystemStateDictionary[newIterationItemKey] = newIterationItem;
        }
    }
}
```

Appendix B: Implementation of the Inverter (without immunity) algorithm

```
private  void ValidateAndStoreStatesNoImmunity(InverterExecution currentInverterExecution,
    Collection<RuleValidationError> validationResultsCollisionRules)
{
    int currentStep = currentInverterExecution.CurrentStep;
    int previousStep = currentInverterExecution.CurrentStep - 1;

    int numberOfRows = currentInverterExecution.CellularAutomata.Height; ;
    int numberOfColumns = currentInverterExecution.CellularAutomata.Width;

    InvertedCellItem[, ,] previousCellularAutomataAsArrayInvertedCellItem =
        currentInverterExecution.TemporalCellularAutomata[previousStep];

    //foreach (Cell cell in this.CurrentCellularAutomata.Cells)
    for (int i = 0; i < numberOfRows; i++)
    {
        for (int j = 0; j < numberOfColumns; j++)
        {
            Cell myCell = currentInverterExecution.CellularAutomata.CellularAutomataAsArray[i, j, 0];
            int currentCellStateTypeId = myCell.CellStateTypeId;

            //get the previousCellStateTypeId
            int previousCellStateTypeId =
                    previousCellularAutomataAsArrayInvertedCellItem[i, j, 0].CellStateTypeId;

            //build the transition Rule
            TransitionRule newTransitionRule = EntityHelper.GenerateGenericTransitionRule(
                        "([" + i + "," + j + "]|" + previousStep + "->" + currentStep + ") ",
                        string.Empty,
                        currentInverterExecution.CellularAutomata.NeighbourhoodTypeId,
                        currentInverterExecution.CellularAutomata.RadiusVisibility);

            newTransitionRule.CurrentCellStateTypeId = previousCellStateTypeId;
            newTransitionRule.ResultCellStateTypeId = currentCellStateTypeId;
            //even though it is system generated, it is still simulating a user created.
            newTransitionRule.IsSystemGenerated = false;
            //now set the neighbourhood
            foreach (NeighbourhoodStateConfiguration ruleStateConfiguration
                    in newTransitionRule.NeighbourhoodStateConfigurations)
            {
                ruleStateConfiguration.CellStateTypeId = EntityHelper.GetNeighbourCellStateTypeId(
                    myCell,
                    previousCellularAutomataAsArrayInvertedCellItem,
                    ruleStateConfiguration,
                    currentInverterExecution.CellularAutomata.CircularVertical,
                    currentInverterExecution.CellularAutomata.CircularHorizontal,
                    currentInverterExecution.OutOfBoundCellStateTypeId);
            }
```

```
            //validate the new rule
            bool hasInclusion = false;
            bool hasCollision = false;
            foreach (TransitionRule existingRule in currentInverterExecution.CellularAutomata.TransitionRules)
            {
                if (newTransitionRule.CurrentCellStateTypeId == existingRule.CurrentCellStateTypeId)
                {
                    //inclusion
                    if (newTransitionRule.ResultCellStateTypeId == existingRule.ResultCellStateTypeId
                        && EntityHelper.IsInputIsomorphic(newTransitionRule, existingRule))
                    {
                        hasInclusion = true;
                    }
                    //collision
                    if (newTransitionRule.ResultCellStateTypeId != existingRule.ResultCellStateTypeId
                        && EntityHelper.IsInputIsomorphic(newTransitionRule, existingRule))
                    {
                        hasCollision = true;
                        newTransitionRule.CellularAutomata = currentInverterExecution.CellularAutomata;
                        validationResultsCollisionRules.Add(new RuleValidationError(newTransitionRule, existingRule));
                    }
                }
            }

            if (!hasCollision && !hasInclusion)
                currentInverterExecution.CellularAutomata.TransitionRules.Add(newTransitionRule);
        }

    }
}
```

Appendix C: Implementation of the Inverter (with immunity) algorithm

```
private  void ValidateAndStoreStatesWithImmunity(InverterExecution currentInverterExecution,
                            Collection<RuleValidationError> validationResultsCollisionRules)
{
    int currentStep = currentInverterExecution.CurrentStep;
    int previousStep = currentInverterExecution.CurrentStep - 1;

    int numberOfRows = currentInverterExecution.CellularAutomata.Height; ;
    int numberOfColumns = currentInverterExecution.CellularAutomata.Width;

    InvertedCellItem[, ,] previousCellularAutomataAsArrayInvertedCellItem =
        currentInverterExecution.TemporalCellularAutomata[previousStep];

    //foreach (Cell cell in this.CurrentCellularAutomata.Cells)
    for (int i = 0; i < numberOfRows; i++)
    {
        for (int j = 0; j < numberOfColumns; j++)
        {
            Cell myCell = currentInverterExecution.CellularAutomata.CellularAutomataAsArray[i, j, 0];
            int currentCellStateTypeId = myCell.CellStateTypeId;

            if (currentCellStateTypeId == ((int)EnumCellStateType.Contaminated))
            {
                ; //no need to perform as we explicity ignore immunity.
            }
            else
            {
                //get the previousCellStateTypeId
                int previousCellStateTypeId =
                            previousCellularAutomataAsArrayInvertedCellItem[i, j, 0].CellStateTypeId;
                //build the transition Rule
                TransitionRule newTransitionRule = EntityHelper.GenerateGenericTransitionRule(
                            "([" + i + "," + j + "]|" + previousStep + "->" + currentStep + ") ",
                            string.Empty,
                            currentInverterExecution.CellularAutomata.NeighbourhoodTypeId,
                            currentInverterExecution.CellularAutomata.RadiusVisibility);

                newTransitionRule.CurrentCellStateTypeId = previousCellStateTypeId;
                newTransitionRule.ResultCellStateTypeId = currentCellStateTypeId;
                //even though it is system generated, it is still simulating a user created.
                newTransitionRule.IsSystemGenerated = false;
                //now set the neighbourhood
                foreach (NeighbourhoodStateConfiguration ruleStateConfiguration
                     in newTransitionRule.NeighbourhoodStateConfigurations)
                {
                    ruleStateConfiguration.CellStateTypeId = EntityHelper.GetNeighbourCellStateTypeId(
                        myCell,
                        previousCellularAutomataAsArrayInvertedCellItem,
                        ruleStateConfiguration,
                        currentInverterExecution.CellularAutomata.CircularVertical,
                        currentInverterExecution.CellularAutomata.CircularHorizontal,
                        currentInverterExecution.OutOfBoundCellStateTypeId);
                }
```

```
                    //validate the new rule
                    bool hasInclusion = false;
                    bool hasCollision = false;
                    foreach (TransitionRule existingRule
                                in currentInverterExecution.CellularAutomata.TransitionRules)
                    {
                        if (newTransitionRule.CurrentCellStateTypeId == existingRule.CurrentCellStateTypeId)
                        {
                            //inclusion
                            if (newTransitionRule.ResultCellStateTypeId == existingRule.ResultCellStateTypeId
                                && EntityHelper.IsInputIsomorphic(newTransitionRule, existingRule))
                            {
                                hasInclusion = true;
                            }
                            //collision
                            if (newTransitionRule.ResultCellStateTypeId != existingRule.ResultCellStateTypeId
                                && EntityHelper.IsInputIsomorphic(newTransitionRule, existingRule))
                            {
                                if (existingRule.ResultCellStateTypeId == ((int)EnumCellStateType.Contaminated)
                                    && newTransitionRule.ResultCellStateTypeId == ((int)EnumCellStateType.Decontaminated))
                                {
                                    if (previousCellularAutomataAsArrayInvertedCellItem[i, j, 0].ImmunityTimerValue == 0)
                                    {
                                        hasCollision = true;
                                        newTransitionRule.CellularAutomata = currentInverterExecution.CellularAutomata;
                                        validationResultsCollisionRules.Add(new RuleValidationError(newTransitionRule, existingRule));
                                    }
                                    else
                                    {
                                        ; //no collision, protected by immunity
                                    }
                                }
                                else
                                {
                                    hasCollision = true;
                                    newTransitionRule.CellularAutomata = currentInverterExecution.CellularAutomata;
                                    validationResultsCollisionRules.Add(new RuleValidationError(newTransitionRule, existingRule));
                                }
                            }
                        }
                    }
                    if (!hasCollision && !hasInclusion)
                        currentInverterExecution.CellularAutomata.TransitionRules.Add(newTransitionRule);
                }
            }
        }
    }
```

Appendix D: Implementation of the rules collision/inclusion validation algorithm

```
public static Collection<RuleValidationError> ValidateTransitionRulesCollision(CellularAutomata cellularAutomata)
{
    Collection<RuleValidationError> result = new Collection<RuleValidationError>();
    int size = cellularAutomata.TransitionRules.Count;

    for (int i = 0; i < size; i++)
    {
        TransitionRule t1 = cellularAutomata.TransitionRules.ElementAt(i);
        for (int j = i + 1; j < size; j++)
        {
            TransitionRule t2 = cellularAutomata.TransitionRules.ElementAt(j);
            // A collision occurs between 2 rules when their current state is the same, their resulting state are different
            // however the input neighbourhood configuration are similar
            if (t1.CurrentCellStateTypeId == t2.CurrentCellStateTypeId && t1.ResultCellStateTypeId != t2.ResultCellStateTypeId)
            {
                //validate if the input are the same.
                bool isInputIsomorphic = IsInputIsomorphic(t1, t2);
                if (isInputIsomorphic)
                    result.Add(new RuleValidationError(t1, t2));
            }
        }
    }
    return result;
}

public static Collection<RuleValidationError> ValidateTransitionRulesInclusion(CellularAutomata cellularAutomata)
{
    Collection<RuleValidationError> result = new Collection<RuleValidationError>();
    int size = cellularAutomata.TransitionRules.Count;

    for (int i = 0; i < size; i++)
    {
        TransitionRule t1 = cellularAutomata.TransitionRules.ElementAt(i);
        for (int j = i + 1; j < size; j++)
        {
            TransitionRule t2 = cellularAutomata.TransitionRules.ElementAt(j);
            // An inclusion occurs between 2 rules if  their current state are the same , their resulting state is the same,
            // and the neighbourhood configuration neighbourhood configuration are similar or one is contained in another
            if (//!t1.IsSystemGenerated && !t2.IsSystemGenerated &&
                t1 != t2 &&
                t1.CurrentCellStateTypeId == t2.CurrentCellStateTypeId &&
                t1.ResultCellStateTypeId == t2.ResultCellStateTypeId)
            {
                //validate if the input are the same.
                bool isInputIsomorphic = IsInputIsomorphic(t1, t2);
                if (isInputIsomorphic)
                    result.Add(new RuleValidationError(t1, t2));
            }
        }
    }
    return result;
}

public static bool IsInputIsomorphic(TransitionRule t1, TransitionRule t2)
{
    bool isInputIsomorphic = true;

    foreach (NeighbourhoodStateConfiguration t1Neighbour in t1.NeighbourhoodStateConfigurations)
    {
        if (t1Neighbour.CellStateTypeId != (int)EnumCellStateType.Generic) //no need to check if one is generic
        {
            NeighbourhoodStateConfiguration t2EquivalentNeighbour =
                t2.NeighbourhoodStateConfigurations.Where(
                neighbour => neighbour.x_offset == t1Neighbour.x_offset
                          && neighbour.y_offset == t1Neighbour.y_offset
                          && neighbour.z_offset == t1Neighbour.z_offset).SingleOrDefault();
            if (t2EquivalentNeighbour != null
                && t2EquivalentNeighbour.CellStateTypeId != (int)EnumCellStateType.Generic
                && t1Neighbour.CellStateTypeId != t2EquivalentNeighbour.CellStateTypeId)
            {
                isInputIsomorphic = false;
                break;
            }
        }
    }
    return isInputIsomorphic;
}
```

Appendix E: Implementation of the contamination rules generation algorithm

```
public static void GenerateContaminationRule(CellularAutomata cellularAutomata,
    NeighbourhoodType selectedNeighbourhoodType,
    ref int numberOfRulesCreated)
{
    //using a temporary rule to loop through all existing neighbours
    TransitionRule tempRule = EntityHelper.GenerateGenericTransitionRule(
            string.Empty,
            string.Empty,
            selectedNeighbourhoodType,
            cellularAutomata.RadiusVisibility);

    //then create all contamination rule
    foreach (NeighbourhoodStateConfiguration configuration in tempRule.NeighbourhoodStateConfigurations)
    {
        //only generate when the contamination radius is smaller than the visibility radius
        if (configuration.DistanceFromCenter <= cellularAutomata.RadiusContamination)
        {
            numberOfRulesCreated++;

            TransitionRule newContaminationRule = EntityHelper.GenerateGenericTransitionRule(
                "Rule #" + numberOfRulesCreated + " (Contamination)",
                "Contamination rule infecting a clean cell when a contaminated cell is located at a contamination radius=" +
                cellularAutomata.RadiusContamination + " and a visibility radius=" +cellularAutomata.RadiusVisibility,
                selectedNeighbourhoodType as NeighbourhoodType,
                cellularAutomata.RadiusVisibility);

            newContaminationRule.CurrentCellStateTypeId = (int)EnumCellStateType.Decontaminated;
            newContaminationRule.ResultCellStateTypeId = (int)EnumCellStateType.Contaminated;
            newContaminationRule.IsSystemGenerated = true;
            NeighbourhoodStateConfiguration thisConfiguration =
       newContaminationRule.NeighbourhoodStateConfigurations.Where(stateConfiguration =>
                               stateConfiguration.x_offset == configuration.x_offset
                            && stateConfiguration.y_offset == configuration.y_offset
                            && stateConfiguration.z_offset == configuration.z_offset).First();
            //set this neighourhood to contaminated and leave the remaining neighbours as generic
            thisConfiguration.CellStateTypeId = (int)EnumCellStateType.Contaminated;
            cellularAutomata.TransitionRules.Add(newContaminationRule);
        }
    }
}
```

```
public static TransitionRule GenerateGenericTransitionRule(string name, string description,
    NeighbourhoodType neighbourhoodType, int radiusVisibility)
{
    TransitionRule transitionRule = new TransitionRule()
    {
        Name = name,
        Description = description
    };
    int minOffset = radiusVisibility * (-1);
    int maxOffset = radiusVisibility * (1);
    int xIndexCenterCell = maxOffset;
    int yIndexCenterCell = maxOffset;
    int zIndexCenterCell = 0;  //for now we only deal with 2D
    //Generate recursively the neighbouring cells data according to the neighbourhoodtype
    int currentRadiusIndex = 0;
    EntityHelper.GenerateListNeighboursData(transitionRule,
        xIndexCenterCell, yIndexCenterCell, zIndexCenterCell, neighbourhoodType, currentRadiusIndex, radiusVisibility);

    return transitionRule;
}
```

Appendix F: Implementation of the recursive generation of neighbourhood data algorithm

(called by the contamination rules generation algorithm (Appendix E))

```
/// <summary>
/// Generates the list neighbours data.
/// The code recursively generate the list of neighbours starting from the center cell based on the
/// neighbourhood type and the radius visibility. The approach uses a breadth-first-search (BFS)
/// </summary>
/// <param name="transitionRule">The transition rule.</param>
/// <param name="xIndexCenterCell">The x index center cell.</param>
/// <param name="yIndexCenterCell">The y index center cell.</param>
/// <param name="zIndexCenterCell">The z index center cell.</param>
/// <param name="neighbourhoodType">Type of the neighbourhood.</param>
/// <param name="currentRadiusIndex">Index of the current radius.</param>
/// <param name="radiusVisibility">The radius visibility.</param>
/// <returns>A collection of NeighbourhoodStateConfiguration</returns>
public static EntityCollection<NeighbourhoodStateConfiguration> GenerateListNeighboursData(
        TransitionRule transitionRule, int xIndexCenterCell, int yIndexCenterCell, int zIndexCenterCell,
NeighbourhoodType neighbourhoodType, int currentRadiusIndex, int radiusVisibility)
{
    currentRadiusIndex++;
    if (currentRadiusIndex > radiusVisibility)   //the recursion ends when the distance thresold  has ben met
        return null;
    //we use this storage to store the list of existing neighbourhood coordinate
    Collection<Tuple<int, int, int>> listOfExistingNeighboursCoordinate = new Collection<Tuple<int, int, int>>();

    if (neighbourhoodType.IsTopLeftON)
    {
        int xIndex = xIndexCenterCell - 1;
        int yIndex = yIndexCenterCell - 1;
        int zIndex = 0;
        GenerateDirectNeighbourData(transitionRule, xIndex, yIndex, zIndex, currentRadiusIndex, radiusVisibility);
        listOfExistingNeighboursCoordinate.Add(new Tuple<int, int, int>(xIndex, yIndex, zIndex));
    }
    if (neighbourhoodType.IsTopON)
    {
        int xIndex = xIndexCenterCell - 1;
        int yIndex = yIndexCenterCell;
        int zIndex = 0;
        GenerateDirectNeighbourData(transitionRule, xIndex, yIndex, zIndex, currentRadiusIndex, radiusVisibility);
        listOfExistingNeighboursCoordinate.Add(new Tuple<int, int, int>(xIndex, yIndex, zIndex));
    }
    if (neighbourhoodType.IsTopRightON)
    {
        int xIndex = xIndexCenterCell - 1;
        int yIndex = yIndexCenterCell + 1;
        int zIndex = 0;
        GenerateDirectNeighbourData(transitionRule, xIndex, yIndex, zIndex, currentRadiusIndex, radiusVisibility);
        listOfExistingNeighboursCoordinate.Add(new Tuple<int, int, int>(xIndex, yIndex, zIndex));
    }
    if (neighbourhoodType.IsRightON)
    {
        int xIndex = xIndexCenterCell;
        int yIndex = yIndexCenterCell + 1;
        int zIndex = 0;
        GenerateDirectNeighbourData(transitionRule, xIndex, yIndex, zIndex, currentRadiusIndex, radiusVisibility);
        listOfExistingNeighboursCoordinate.Add(new Tuple<int, int, int>(xIndex, yIndex, zIndex));
    }
    if (neighbourhoodType.IsBottomRightON)
    {
        int xIndex = xIndexCenterCell + 1;
        int yIndex = yIndexCenterCell + 1;
        int zIndex = 0;
        GenerateDirectNeighbourData(transitionRule, xIndex, yIndex, zIndex, currentRadiusIndex, radiusVisibility);
        listOfExistingNeighboursCoordinate.Add(new Tuple<int, int, int>(xIndex, yIndex, zIndex));
    }
```

```
    if (neighbourhoodType.IsBottomON)
    {
        int xIndex = xIndexCenterCell + 1;
        int yIndex = yIndexCenterCell;
        int zIndex = 0;
        GenerateDirectNeighbourData(transitionRule, xIndex, yIndex, zIndex, currentRadiusIndex, radiusVisibility);
        listOfExistingNeighboursCoordinate.Add(new Tuple<int, int, int>(xIndex, yIndex, zIndex));
    }
    if (neighbourhoodType.IsBottomLeftON)
    {
        int xIndex = xIndexCenterCell + 1;
        int yIndex = yIndexCenterCell - 1;
        int zIndex = 0;
        GenerateDirectNeighbourData(transitionRule, xIndex, yIndex, zIndex, currentRadiusIndex, radiusVisibility);
        listOfExistingNeighboursCoordinate.Add(new Tuple<int, int, int>(xIndex, yIndex, zIndex));
    }
    if (neighbourhoodType.IsLeftON)
    {
        int xIndex = xIndexCenterCell;
        int yIndex = yIndexCenterCell - 1;
        int zIndex = 0;
        GenerateDirectNeighbourData(transitionRule, xIndex, yIndex, zIndex, currentRadiusIndex, radiusVisibility);
        listOfExistingNeighboursCoordinate.Add(new Tuple<int, int, int>(xIndex, yIndex, zIndex));
    }
    //Now need to call recursively the generation for each existing neighbour
    foreach (Tuple<int, int, int> coordinate in listOfExistingNeighboursCoordinate)
        GenerateListNeighboursData(transitionRule,
            coordinate.Item1, coordinate.Item2, coordinate.Item3, neighbourhoodType, currentRadiusIndex,
radiusVisibility);

    return transitionRule.NeighbourhoodStateConfigurations;
}


/// <summary>
/// Generates the direct neighbour data.
/// </summary>
/// <param name="transitionRule">The transition rule.</param>
/// <param name="xIndex">Index of the x.</param>
/// <param name="yIndex">Index of the y.</param>
/// <param name="zIndex">Index of the z.</param>
public static void GenerateDirectNeighbourData(TransitionRule transitionRule,
    int xIndex, int yIndex, int zIndex, int currentRadiusIndex, int radiusVisibility)
{
    int x_offset = xIndex - radiusVisibility;
    int y_offset = yIndex - radiusVisibility;
    int z_offset = 0;

    if (x_offset == 0 && y_offset == 0 && z_offset == 0) // no need to create the center data
        return;


    bool neighbourNotCreatedYet = transitionRule.NeighbourhoodStateConfigurations.Where(
        neighbourhoodStateConfiguration => neighbourhoodStateConfiguration.x_offset == x_offset
                                    && neighbourhoodStateConfiguration.y_offset == y_offset
                                    && neighbourhoodStateConfiguration.z_offset == z_offset).Count() == 0;
    if (neighbourNotCreatedYet)
    {
        NeighbourhoodStateConfiguration newNeighbourState = new NeighbourhoodStateConfiguration()
        {
            x_offset = x_offset,
            y_offset = y_offset,
            z_offset = z_offset,
            CellStateTypeId = (int)EnumCellStateType.Generic,
            DistanceFromCenter = currentRadiusIndex
        };
        transitionRule.NeighbourhoodStateConfigurations.Add(newNeighbourState);
    }
}
```