Report on the workshop
Probabilistic Cellular Automata: Theory, Applications and Future Perspectives
(EURANDOM, TU Eindhoven, The Netherlands, June 10, 11, 12, 2013)

This workshop took place on 10-12 June 2013 at EURANDOM—Math. and Computer Science Dpt, TU Eindhoven. It was organised by an interdisciplinary committee: Emilio Cirillo (La Sapienza U. di Roma, Italy), Nazim Fatès (Inria, Nancy, France), Roberto Fernández (Utrecht, The Netherlands), Pierre-Yves Louis (U. Poitiers, France), Roeland Merks (CWI, Amsterdam, The Netherlands), Francesca Nardi (TU Eindhoven, The Netherlands). Wioletta Ruszel (TU Delft, The Netherlands) and Cristian Spitoni (U. Utrecht, The Netherlands). Patty Koorn from EURANDOM helped as workshop officer.

The workshop aimed at exploring Probabilistic Cellular Automata (PCA) from the point of view of Statistical Mechanics, Probability Theory, Computational Biology, Computer Science and Discrete Dynamical Systems. The workshop's announcement was sent well in advance to different mailing-lists. A poster was sent out to a large list of potential interested contacts. A –very well indexed on the web– web page [1] gave an up-to-date information.

The scientific program featured 16 invited speakers, 10 contributed speakers. There were 14 long talks of 40 min, and 12 regular talks of 20 min. Two poster sessions were organised, each associated with a short presentation talk of 5 min (ca. 10 posters). One open problems session was organised. Two keynote speakers came from Australia and the USA. Detailed information can be found in the attached booklet (including the full list of the participants). It is downloadable [2].

The meeting was very well attended by 65 participants and 30% of female. Participants came mainly from The Netherlands, France, Italy, Germany and large part from Europe. Many young colleagues joint the meeting: 22% of the participants were PhD candidates and 19% were post-doctoral researchers. The diverse participants' backgrounds varied from probability theory, mathematical physics, computer science and computational biology at diverse levels. The three lunches, a welcome reception and social diner were organised and contributed to a nice contact atmosphere.

Different communities constituted an audience with a wide spectrum from theoretic, computational to more applied challenges. For the very first time at an international level, these communities were brought together. Speakers presented the state of the art from different interdisciplinary perspectives. Contributions shared review aspects, known literature, more recent research results, different communities' challenges, Presentations produced lively discussions at theoretical and applicative levels. Participants built new contacts. Their feed-back was very positive about the event. They expressed the interest in a follow-up workshop in two or three years.

Furthermore the workshop was financially supported by ESF–RGLIS, EURANDOM—TU Eindhoven, NWO Incidentele Steun, STAR, 3TU–AMI, University of Poitiers, TU Delft and University Utrecht. The organisers gratefully acknowledge the sponsors for their support.

There are ongoing discussions to publish a book at a graduate level on Probabilistic Cellular Automata from the point of view of Statistical Mechanics, Probability Theory, Computational Biology and Computer Science.

[1] `http://www.eurandom.nl/events/workshops/2013/PCA/PCA.html`
[2] `http://www.eurandom.nl/events/workshops/2013/PCA/PCA_Booklet.pdf`

EUROPEAN SCIENCE FOUNDATION

Probabilistic Cellular Automata: Theory, Applications and Future Perspectives

10-12 June 2013

EURANDOM, Eindhoven, The Netherlands

http://www.eurandom.nl/events

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Aims and Scope

Cellular Automata (CA) are discrete dynamical systems consisting of finite state cells (or agents/ individuals) that change simultaneously their states according to some local rules. Simple update rules may produce extremely complex behaviour. They have been used to model a wide range of physical phenomena including traffic flow, disease epidemics, invasion of populations...

Probabilistic Cellular Automata (PCA) are the generalization of CA since the updating rule is stochastic. Despite the applicative power of CA is clearly inherited by PCA, the stochastic updating rules make PCA a more flexible computational tool.

(P)CA build a bridge between probability, statistical mechanics, theoretical computer science and computational life–sciences. In recent years indeed there have been active research activities on the following three directions that we want to make interact:

1. statistical mechanics and probability (e.g. PCA as interacting particle system)
2. computer science and discrete dynamical systems (e.g. robustness of PCA when going from synchronous to asynchronous updating scheme)
3. computational (cell) biology (e.g. Cellular Potts Model and stability of emerging patterns).

This workshop aims at gathering scientists with different backgrounds but all sharing a common interest for PCA. We expect that the interaction between these different fields and approaches will produce cross-fertilisation both at theoretical and applicative levels, exchange of points of view and challenges, joint collaborations.

Organisers

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P.-Y. Louis thanks J. Attab from *Laboratoire de Mathématiques et Applications* (UMR 7348 Université de Poitiers & CNRS) for technical support concerning graphical issues.

Monday June, 10th

Please check the final schedule which will be available at the conference desk.

9:00–9:50 Registration and coffee/tea.

9:50–10:00 Opening by R. van der Hofstad, TU/e and scientific director of EURANDOM, and P.-Y. Louis for the organisers.

Session's chairman: R. van der Hofstad

10:00–10:40 Christian Maes, Physical modelling and MINEP for PCA

10:40–11:00 Piotr Slowinski, Probabilistic cellular automata with non–unique space–time phases

11:00–11:20 Coffee break

11:20–12:00 Emilio N.M. Cirillo, Metastable behaviour of reversible Probabilistic Cellular Automata

12:00–14:00 Lunch at University Club

Session's chairman: C. Spitoni

14:00–14:40 Paolo Dai Pra, Strategic interaction in trend–driven dynamics

14:40–15:00 Sylvain Sené, Non-linear threshold PCA in $\mathbb{Z}^2$: the central role of boundaries

15:00–15:20 Ida Minelli, Synchronisation via interacting reinforcement

15:20–15:40 Coffee break

15:40–16:20 Franco Bagnoli, Topological phase transitions in cellular automata

16:20–16:40 Poster flash session: F. Collet, C. Lancia, L. Taggi, H. Van Den Bosch

16:40–17:30 Poster session: F. Collet, C. Lancia, L. Taggi, H. Van Den Bosch

17:30–18:30 Welcome drinks at Eurandom lounge

19:00– Building closed

Tuesday June, 11th

Please check the final schedule which will be available at the conference desk.

Session's chairman: N. Fatès

9:00–9:40	Roeland Merks, Stochastic self-organization of branched organs: on the growth of blood vessels, glands, and kidneys
9:40–10:20	Kerry Landman, Modelling development and disease in our "second brain"
10:20–10:40	Coffee break
10:40–11:20	Yi Jiang, Angiogenesis in the Eye: the Good and the Bad
11:20–11:40	Carsten Mente, Individual cell dynamics in cellular automaton models
11:40–12:00	Nevena Maric, Fleming–Viot particle system driven by a random walk on naturals
12:00–14:00	Lunch at University Club

Session's chairman: P.-Y. Louis

14:00–14:40	Anja Voß–Böhme, PCA for modelling interacting cell systems
14:40–15:00	Fernando Peruani, Optimal noise maximizes collective motion in heterogeneous media
15:00–15:20	Pablo Arrighi, Stochastic Cellular Automata: Correlations, Decidability and Simulations
15:20–15:40	Coffee break
15:40–16:20	Danuta Makowiec, Pacemaker rhythm by cellular automata
16:20–16:40	Poster flash session: S. Boas, O. Bouré, J. Dorrestijn and D. Crommelin, M. Palm
16:40–17:30	Poster session: S. Boas, O. Bouré, J. Dorrestijn and D. Crommelin, M. Palm
18:30–	Conference dinner at restaurant "Vlijtig Liesje" (see Practical information for more details)

Wednesday June, 12th

Please check the final schedule which will be available at the conference desk.

Session's chairman: R. Merks

9:00–9:40	Jean Mairesse, Around Probabilistic Cellular Automata
9:40–10:20	Benedetto Scoppola, Equilibrium and non–equilibrium statistical mechanics by means of PCA
10:20–10:40	Coffee break
10:40–11:20	Damien Regnault, Several aspects of probabilistic cellular automata
11:20–11:40	Siamak Taati, Statistical equilibrium in deterministic cellular automata
11:40–12:00	Irène Marcovici, The envelope PCA, a tool for sampling the invariant measure of a PCA
12:00–14:00	Lunch at Zwarte Doos

Session's chairman: R. Fernández

14:00–14:40	Jean Bricmont, Phase transitions: from equilibrium models to PCA
14:40–15:00	Lucas Gérin, A connection between 2d percolation and the synchronous TASEP
15:00–15:20	Lise Ponselet, Phase transitions in PCA: erosion versus errors
15:20–15:40	Coffee break
15:40–16:20	Aernout van Enter, Anisotropic bootstrap percolation
16:20–17:30	Nazim Fatès, Modelling natural phenomena or computing, do we need to choose? On the landscape of randomness in cellular automata. Introduction to the open problems session and discussions
17:30–	Roberto Fernández Closing words
19:00–	Building closed

Long talk abstracts

Franco Bagnoli
Topological phase transitions in cellular automata
Cellular automata are successful modelling tools, but in many cases the classical regular lattice is not adequate to the problem under investigation. By changing the topology of the lattice, several interesting phenomena occurs. We illustrate an example of a phase transition that can be induced by a change in parameters or in the topology of the lattice. We show also how one can map the change in the topology onto the change in the parameters.

Jean Bricmont
Phase transitions: from equilibrium models to PCA
I will review some of the techniques used to prove the existence of phase transitions in equilibrium models and the problems that one encounters if one tries to extend those techniques to PCA.

Emilio N.M. Cirillo
Metastable behaviour of reversible Probabilistic Cellular Automata
Metastability is a relevant phenomenon in many different applied sciences. Its full mathematical description is quite recent and still incomplete. In this framework Probabilistic Cellular Automata pose challenging problems and show unexpected behaviours. In this talk some results will be reviewed.

Paolo Dai Pra
Strategic interaction in trend–driven dynamics
We propose a stochastic dynamics in which N agents update their state simultaneously but not independently. At each time step agents aim at maximizing their individual payoff, depending on their action, on the global trend of the system and on a random noise. In the limit of infinitely many agents, a law of large numbers is obtained; the limit dynamics consist in an implicit dynamical system, possibly multiple valued. For a special model, we determine the phase diagram for the long time behaviour of these limit dynamics and we show the existence of a phase, where a locally stable fixed point coexists with a locally stable periodic orbit.

Andreas Deutsch

Analysing emergent behaviour in cellular automaton models of cancer invasion (cancelled)

While molecular biology methods are required for a better characterization and identification of individual cancer cells, mathematical modelling and computer simulation is needed for investigating collective effects of cancer invasion. Here, we demonstrate how lattice-gas cellular automaton (LGCA) models allow for an adequate description of individual cancer cell behaviour [1]. We will then show how analysis of the LGCA models allows for prediction of emerging properties (in particular of the invasion speed) [2]. Furthermore, we propose that the transition to invasive phenotypes can be explained on the basis of the microscopic "Go or Grow" mechanism (migration/proliferation dichotomy) and oxygen shortage, i.e., hypoxia, in the environment of a growing tumour. We test this hypothesis again with the help of a lattice–gas cellular automaton. Finally, we use our LGCA models for the interpretation of data from in vitro glioma cancer cell invasion assays [3].

[1] A. Deutsch, S. Dormann, Cellular Automaton Modelling of Biological Pattern Formation: Characterization, Applications, and Analysis.
Birkhäuser, Boston, 2005.

[2] H. Hatzikirou, D. Basanta, M. Simon, K. Schaller, A. Deutsch, Go or Grow: the key to the emergence of invasion in tumour progression?
Math. Med. Biol. **29** (1), 49–65, 2012.

[3] M. Tektonidis, H. Hatzikirou, A. Chauviere, M. Simon, K. Schaller, A. Deutsch, Identification of intrinsic mechanisms for glioma invasion.
J. Theor. Biol. **287**, 131–147, 2011.

Aernout van Enter

Anisotropic bootstrap percolation

Bootstrap percolation models are Cellular Automata with probabilistic initial conditions. We discuss some results and open problems on the influence of anisotropy on properties of bootstrap percolation models in two and three dimensions. In particular we discuss finite–size scaling behaviour and sharp thresholds.
Joint work with Tim Hulshof, Anne Fey, Hugo Duminil–Copin.

Kerry Landman

Modelling development and disease in our "second brain"

The enteric nervous system (ENS) in our gastrointestinal tract, nicknamed the "second brain", is responsible for normal gut function and peristaltic contraction. Embryonic development of the ENS involves the colonization of the gut wall from one end to the other by a population of proliferating neural crest cells. Failure of these cells to invade the whole gut results in the relatively common, potentially fatal condition known as Hirschsprung disease (HSCR). Probabilistic cellular automata models provide insight into the colonization process at both the individual cell–level and population–level. Our models generate experimentally testable predictions, which have subsequently been confirmed. These results have important implications for HSCR and highlight the significance of stochastic effects.

Christian Maes

Physical modelling and MINEP for PCA

Being interested in describing and understanding physical phenomena one is often confronted with the question what effective models to choose as sufficiently realistic. That is true in general when taking serious models of interacting particle systems such as probabilistic cellular automata (PCA). What specifies the dynamical ensemble when moving outside thermodynamic equilibrium? We propose to consider the condition of local detailed balance and to introduce the frenetic contribution as a freedom in waiting time distributions. We then show that the minimum entropy production principle (MINEP) in general fails for PCA.

Jean Mairesse

Around Probabilistic Cellular Automata

In this introductory talk, I will first survey how PCA appear in various contexts ranging from combinatorics, to statistical physics and theoretical computer science. I will focus on two problems: the ergodicity of positive rates PCA, and the density classification.

Danuta Makowiec

Pacemaker rhythm by cellular automata

The sinoatrial node is the primary pacemaker of the heart. Nodal dysfunction can lead to a variety of pathological clinical syndromes. Although the basic mechanisms underlying the self-excitation of each individual nodal cell are accepted, there is still a lot of controversy on how the cells organize themselves to produce the periodic signal, which is strong enough to drive the contraction of the heart tissue.

Approach based on Greenberg-Hastings cellular automata is redrafted to take account of the essential characteristics of both the physiology of a nodal cell and the known facts about the organization between cells. So, the model is based on cells that cycle

through firing, refractory and activity stages. If sufficiently many neighbours of a cell are firing then a cell jumps directly from the activity stage to firing stage, or prolong its refractory stage. These interactions cause the cell synchronize their stages, as in the real pacemaker tissue. The neighbourhood connections are created by a stochastic wrinkling algorithm to make the network of interactions three dimensional and heterogeneous. The synchronization in the system is studied by Kuramoto order parameters. We show that these parameters lead to the consistent description of the system stationary states, that is quantify frequencies emerging in the system. Finally, we will use the model to explain some changes that occur due to ageing in the human pacemaker.

Roeland Merks

Stochastic self-organization of branched organs: on the growth of blood vessels, glands, and kidneys

Morphogenesis, the formation of biological shape and pattern during embryonic development, is a topic of intensive experimental investigation, so the participating cell types and molecular signals continue to be characterized in great detail. Yet this data only partly tells biologists how molecules and cells interact dynamically to construct a biological tissue. Probabilistic Cellular Automata are a great help in analysing the mechanisms of biological morphogenesis. I will discuss some recent developments on a lattice-based, stochastic model for the formation of blood vessel networks (Merks et al. PLoS Comput Biol 2008), which is based on the cellular Potts model. In this model, we have identified a stochastic mechanism for branching growth that, in a modified form, may play a key role in the formation of branched organs of epithelial origin, e.g., mammary glands and kidneys. I will discuss this model in detail and conclude by suggesting some interesting continuum and stochastic mathematical problems that our simulations suggest.

Markus Owen

Hybrid multiscale and partial differential equation models for cancer immunotherapy (cancelled)

Cancer is a heterogeneous disease governed by interconnected processes at multiple spatial and temporal scales. For example, variations in vascular density and blood flow within tumours can have significant effects on nutrient distributions. In addition, such heterogeneities can have significant implications for the delivery and efficacy of drugs and other therapies. We have developed multiscale mathematical models for vascular tumour growth, based upon an extended cellular automata model for cell populations overlaid with networks of blood vessels and the distributions of nutrients, cytokines and therapies [1]. We have used these models to predict the efficacy of novel hypoxia-targeted macrophage-based therapies, conventional therapies, and combination therapies. We find that combination therapies can be highly synergistic, depending on their relative timing, but that host tissue and tumour variability can have important implications for thera-

peutic efficacy [2]. We have also begun to explore the relationships between our hybrid cellular automaton models and more traditional partial differential equation models.

[1] M.R. Owen, T. Alarcón, P.K. Maini, and H.M. Byrne, Angiogenesis and vascular remodelling in normal and cancerous tissues.
J. Math. Biol. **58**, 689–721, 2009.

[2] M.R. Owen, I.J. Stamper, M. Muthana, G.W. Richardson, J. Dobson, C.E. Lewis, and H.M. Byrne, Mathematical modelling predicts synergistic antitumor effects of combining a macrophage–based, hypoxia–targeted gene therapy with chemotherapy.
Cancer Res. **71** (8), 2826–37, 2011.

Damien Regnault
Several aspects of probabilistic cellular automata
From the point of view of a computer scientist, deterministic cellular automata are known as a parallel computation model. Different studies have introduced randomness in this model by considering probabilistic transitions. In this talk, I will present the different motivations of these studies as well as the current results and open questions.

Benedetto Scoppola
Equilibrium and non–equilibrium statistical mechanics by means of PCA
The aim of this talk is to introduce a class of PCA with some interesting features:
1) the equilibrium measure of the PCA tends to the Gibbs measure of Ising model in the thermodynamical limit.
2) In certain cases it is possible to introduce a unified description of reversible (equilibrium statistical mechanics) and irreversible dynamics (non equilibrium statistical mechanics).
3) Some cases are solved by exact computations.
Joint work with Elisabetta Scoppola and Paolo Dai Pra.

Anja Voß–Böhme
PCA for modelling interacting cell systems
Understanding the mechanisms that control tissue organization during development belongs to the most fundamental goals in developmental biology. Quantitative approaches and mathematical models are essential to deduce the consequences of existing morphogenetic hypotheses, thus providing the basis for experimental testing and theoretical understanding. One approach to questions concerning patterning in developing organisms is to consider tissues as huge populations of cells which behave according to certain rules that depend on their genetic programs and inner structure as well as the states and actions of directly neighbouring cells. Then, tissue organization can be understood as emergent behaviour that results from local intercellular interaction. PCA provide a spatiotemporal modelling framework to describe and analyse interacting cell populations. They have been successfully applied to study characteristic collective cell behaviours that result from

specific cellular interaction rules. However, there are considerable differences in the construction of these models. While cell differentiation, cell death and proliferation can be covered by classical PCA rules, a proper implementation of cell motility is challenging. In the talk, we will compare exemplary PCA models where one cell occupies one lattice node to spatially more resolved models, such as the CPM. We will expose the mechanistic structures of these models and discuss their implications for analysis and knowledge gain.

Yi Jiang

Angiogenesis in the Eye: the Good and the Bad

Angiogenesis, or blood vessel growth from existing ones, is an important physiological process that occur during development, wound healing, as well as diseases such as cancer and diabetes. I will report our recent progress in modelling angiogenesis in the eye in two scenarios. The good refers to healthy blood vessel growth in the retina in mouse embryos, which is a perfect experimental model for understanding the molecular mechanism of angiogenesis.The bad is the pathological blood vessel growth in age related macular degeneration, which is the leading cause of vision loss in the elderly and a looming epidemic in our ageing society. We develop cell–based, multiscale models that include intracellular, cellular, and extracellular scale dynamics, and show that biomechanics of cell–cell and cell–matrix interactions play crucial roll in determining the dynamics of blood vessel growth initiation as well as vascular network formation. Such models show great potential as in silico Petri–dishes for predictive studies of mechanisms as well as therapies.

Regular talk abstracts

Pablo Arrighi
Stochastic Cellular Automata: Correlations, Decidability and Simulations
This talk introduces a simple formalism for dealing with deterministic, non-deterministic and stochastic cellular automata in an unified and composable manner. This formalism allows for local probabilistic correlations, a feature which is usually not present in standard definitions. We show that this feature allows for strictly more behaviours (for instance, surjective number conserving stochastic cellular automata are shown to require local stochastic correlation). We show also show that several problems which seem deceptively simple in the standard definitions, become undecidable, even in $1D$. Still, $1D$ stochastic cellular automata have much simpler behaviours: we show how to solve some problems that become undecidable in dimension higher than two. Armed with this formalism, we extend the notion of intrinsic simulation between deterministic cellular automata, to the non-deterministic and stochastic settings. We then provide explicit tools to prove or disprove the existence of such a simulation between two stochastic cellular automata, even if the intrinsic simulation relation is shown to be undecidable in dimension two and higher. The key result behind this is the characterization of equality of stochastic global maps by the existence of a coupling between the random sources. Finally, we then prove that there is a universal non-deterministic cellular automaton, but no universal stochastic cellular automaton. Yet we provide stochastic cellular automata achieving optimal partial universality.
The talk is based on upon an extended version of http://arxiv.org/abs/1208.2763.
Joint work with Nicolas Schabanel and Guillaume Theyssier.

Nazim Fatès
Modelling natural phenomena or computing, do we need to choose?
On the landscape of randomness in cellular automata.
Introduction to the open problems session.

Lucas Gérin
A connection between 2d percolation and the synchronous TASEP
The aim of this talk is to describe a connection between the geometry of the $2d$ percolation infinite cluster, an important object in statistical mechanics, and the discrete–time and synchronous TASEP, a $1d$ interacting particle system modelling non–equilibrium phenomena (and which is quite known in the PCA community). We will point out some consequences and possible extensions.
Joint work with A. L. Basdevant, N. Enriquez, and J.–B. Gouéré.

Irène Marcovici

The envelope PCA, a tool for sampling the invariant measure of a PCA

We propose a perfect sampling algorithm for the invariant measure of an ergodic PCA. A PCA is a finite state space Markov chain. Therefore, coupling from the past from all possible initial configurations provides a basic perfect sampling procedure. But it is a very inefficient one since the number of configurations is exponential. Here, the contribution consists in simplifying the procedure. We define a new PCA on an extended alphabet, called the envelope PCA (EPCA). We obtain a perfect sampling procedure for the original PCA by running the EPCA on a single initial configuration. Our algorithm does not assume any monotonicity property of the local rule.
Joint work with A. Busic and J. Mairesse.

Nevena Marić

Fleming–Viot particle system driven by a random walk on naturals

Random walk on naturals with negative drift and absorption at 0, when conditioned on survival, has uncountably many invariant measures (quasi–stationary distributions, *qsd*) ν_c. We study a Fleming–Viot (FV) particle system driven by this process. In this particle system there are N particles where each particle evolves as the random walk described above. As soon as one particle is absorbed, it reappears, choosing a new position according to the empirical measure at that time. Between the absorptions, the particles move independently of each other. Our focus is in the relation of empirical measure of the FV process with *qsd*'s of the random walk. Firstly, mean normalized densities of the FV unique stationary measure converge to the minimal *qsd*, ν_0, as N goes to infinity. Moreover, every other *qsd* of the random walk $(\nu_c, c > 0)$ corresponds to a metastable state of the FV particle system.

Carsten Mente

Individual cell dynamics in cellular automaton models of interacting cell systems

Lattice–gas cellular automaton (LGCA) models have proven successful in the analysis of collective behaviour arising from populations of moving and interacting cells. Examples of collective cell behaviour at a macroscopic level include the formation of cell density patterns and the dynamics of moving cell fronts. However, important microscopic observables which emerge as a consequence of collective cell behaviour, especially individual cell trajectories, can not be simulated and analysed with LGCA models so far since these models cannot distinguish individual cells. Here, we introduce an extension of the classical LGCA model, which allows labelling and tracking of individual cells. We name these extended LGCA models "individual–based lattice–gas cellular automata" (IB–LGCA). Furthermore, we derive stochastic differential equations (SDE) corresponding to specific IB–LGCA models, which permit the investigation of individual cell trajectories and the

approximate description of IB–LGCA models by systems of SDEs. This approach allows computationally efficient simulations and analytical treatment of individual cell trajectories in populations of interacting cells. Finally, we present IB–LGCA examples demonstrating the analysis of individual cell trajectories in populations of interacting cells: random cell motion and the motion of cells exposed to an external gradient.

Ida Minelli

Synchronization via interacting reinforcement

We consider a system of urns of Polya–type, with balls of two colours; the reinforcement of each urn depends both on the content of the same urn and on the average content of all urns. We show that the urns synchronize almost surely, in the sense that the fraction of balls of a given colour converges almost surely, as the time goes to infinity, to the same limit for all urns. A normal approximation for a large number of urns is also obtained.

Fernando Peruani

Optimal noise maximizes collective motion in heterogeneous media

We study the effect of spatial heterogeneity on the collective motion of self–propelled particles (SPPs). The heterogeneity is modelled as a random distribution of either static or diffusive obstacles, which the SPPs avoid while trying to align their movements. We find that such obstacles have a dramatic effect on the collective dynamics of usual SPP models. In particular, we report about the existence of an optimal (angular) noise amplitude that maximizes collective motion. We also show that while at low obstacle densities the system exhibits long–range order, in strongly heterogeneous media collective motion is quasi–long–range and exists only for noise values in between two critical noise values, with the system being disordered at both, large and low noise amplitudes. Since most real system have spatial heterogeneities, the finding of an optimal noise intensity has immediate practical and fundamental implications for the design and evolution of collective motion strategies.

Lise Ponselet

Phase transitions in PCA: erosion versus errors

We consider a class of probabilistic cellular automata (PCA) of interest both in statistical physics and in computer science. They are perturbations of cellular automata (CA) that have the property of eroding blocks of impurities in an almost homogeneous configuration. A stochastic perturbation turns the CA into PCA by admitting errors in the states of the cells with some probability distribution. If the erosion is sufficient to correct the effects of errors, the PCA process can have several stationary states, providing an example of non-equilibrium phase transition. We study some properties of these stationary states when the probability of errors is small.

Sylvain Sené

Nonlinear threshold PCA in $\mathbb{Z}^2$: the central role of boundaries

The general question of the influence of the environment on dynamical systems has already been widely studied in the past decades. One of the best known example comes from mathematical physics and is that of the characterisation of phase transitions in the classical Ising Model, shown by Dobrushin and Ruelle independently. However, this question remains of particular interest in other contexts, closer to theoretical computer science and biology. For instance, now that cellular automata, and more generally automata networks, are more and more studied as dynamical systems to model and analyse the dynamics of biological regulation networks, such as genetic networks, going further in the understanding of the substantial influence of their environment actually is important. In this presentation, to make a step in this direction, I propose to tackle from a theoretical point of view the question of the structural instability (in the sense of Thom) of a particular class of two-dimensional finite threshold Boolean cellular automata when the latter are subjected to distinct fixed boundary instances. More precisely, focusing on a non-linear probabilistic version of the classical threshold function governing the evolution of formal neural networks, I will show the existence of a necessary condition under which attractive cellular automata of this form become boundary sensitive, i.e., a condition without which a cellular automaton hits the same asymptotic dynamical behaviour whatever its boundary conditions are. Then will be given an explicit formula for this necessary condition, whose sufficiency will be highlighted by simulations.

Keywords: Threshold Boolean PCA, non-linearity, boundary sensitivity.

Piotr Słowiński

Probabilistic cellular automata with non–unique space–time phases

I will use space–time phases to describe some properties of probabilistic cellular automata (PCA). Space–time phases are probability distributions over state as a function of space and time that arise from initial probabilities in the past. In particular, I will focus on PCA with non–unique phase and show how space–time phases can be used to analyse emergence in such systems. To illustrate the most interesting phenomena I will use numerical demonstration. Furthermore, I will present examples of emergence in PCA used in ecology and economy.

The research is supported by the Alfred P. Sloan Foundation (New York).

Joint work with R.S. MacKay.

Siamak Taati

Statistical equilibrium in deterministic cellular automata

Some deterministic cellular automata have long been observed to demonstrate thermodynamic behaviour: starting from a random configuration, they undergo a transient dynamics until they reach a state of macroscopic equilibrium. An example is the Ising cellular automaton which can be seen as a deterministic and microscopically reversible variant of a Gibbs sampler (or a micro–canonical sampler). I will discuss some results and open problems regarding (approach to) macroscopic equilibrium in reversible (and more generally surjective) cellular automata.

Joint work with Jarkko Kari.

Short talk and poster abstracts

Sonja E. M. Boas

Lumen formation during angiogenesis: A unifying computational model

Blood vessel development (angiogenesis) is important during embryogenesis and for many processes throughout our entire lifespan, such as wound healing and also tumor growth. New blood vessels hollow (lumen formation) to allow blood perfusion. Despite decades of experimental research, two alternative lumen formation hypotheses are still debated. The vacuolation hypothesis originally suggests that a lumen forms intra-cellularly by fusion of vesicles into vacuoles and this view was extended to extracellular lumen formation by exocytosis of vacuoles. The cell-cell repulsion hypothesis assumes that lumens initiate by active repulsion of adjacent cells and are expanded by cell shape changes. We use a multi-scale, agent-based model to compare and study both hypotheses. The model is based on the Cellular Potts Model, which allows explicit modelling of cell shape and of the adhesive properties of cells. To model the mechanisms of lumen formation and cell membrane polarization, specialized Cellular Potts domains and biased random walkers represent sub-cellular detail, including membrane proteins and vesicles. These vesicles fuse into larger intracellular vacuoles. During a simulation, endothelial cells in a branched vessel polarize their cell membrane and form lumens by vacuolation or by cell-cell repulsion. Based on the simulation results, we propose a plausible third hypothesis for lumen formation: The combination of vacuolation and cell-cell repulsion in the same vessel is more robust in lumen formation.

Acknowledgements: We thank the Indiana University and the Biocomplexity Institute for providing the CC3D modelling environment.

Olivier Bouré

Using robustness to study the metastable behaviours of a discrete model of swarming

Studies in biology are increasingly interested in cellular automata to simulate natural phenomena with simple models. But do they also take into account the robustness of their behaviour? We consider this issue in the scope of a lattice-gas model of swarming, which has been shown to display a phase transition between an ordered and a disordered phase. Using a method based on robustness, we observe that the organised phase may result in several qualitatively different patterns, and show that some aspects of the behaviour depend on specific attributes of the model's definition, such as the cellular lattice or the synchronous scheme.

Francesca Collet

The role of disorder in the dynamics of critical fluctuations of mean field

We aim at analysing how the disorder affects the fluctuation dynamics for two different types of interacting particle system: the Curie–Weiss and Kuramoto model. The models under consideration are a collection of spins and rotators respectively. They both are subject to a mean field interaction and embedded in a site–dependent, i.i.d. random environment. As the number of particles goes to infinity their limiting dynamics become deterministic and exhibit phase transition. The main result concerns the fluctuations around this deterministic limit at the critical point in the thermodynamic limit. From a qualitative point of view, it indicates that when disorder is added spin and rotator systems belong to two different classes of universality, which is not the case for the homogeneous models (i.e., without disorder).

The poster is based on a joint work with Paolo Dai Pra, University of Padova.

Jesse Dorrestijn and Daan Crommelin

Modelling clouds with PCA

For climate and atmosphere models, the parametrisation (or representation) of clouds and convection is of great importance. Climate and weather prediction models have too coarse resolutions to resolve these processes, therefore they must be represented in a simplified way. An emerging approach is the use of cellular automata (CA) to represent clouds, convection and other sub-grid processes, thanks to their random character combined with the ability to self–organize into spatial structures. As clouds and convection interact with the atmospheric circulation, the CA are coupled to the partial differential equations (PDEs) that model the atmospheric flow. In a recent study, we used data of high–resolution convection simulations to construct a PCA emulating the development of convective clouds (Dorrestijn et al. 2013). Statistical inference for PCA is a key element in this approach.

Carlo Lancia

Ising Waves on 2D Torus for totally asymmetric Ising model

In this short talk I will present an irreversible, asymmetric PCA dynamics for the Ising model on a 2D Torus. The model is a variant of the PCA dynamics recently studied in [1]. Despite the irreversibility of the dynamics, the stationary distribution of such a PCA has the same form as in [1]. Therefore, under suitably conditions the invariant measure is Gibbsian in the thermodynamic limit. By means of numerical simulations I will show that for opportune choices of the parameters the standard Ising droplets undergo a peculiar change, and transform into Ising waves.

References:

[1] P. Dai Pra, B. Scoppola and E. Scoppola, Sampling from a Gibbs Measure with Pair Interaction by Means of PCA, JSP 149:4, 722–737 (2012)

Joint work with B. Scoppola.

Margriet Palm

A parameter sensitivity analysis to identify cell properties for tip cells in a cellular Potts model of blood vessel formation

Computational, cell-based models can be used to study blood vessel formation. New blood vessels form by cells that sprout from existing vessels. These sprouts grow and connect, and thereby form a vascular network. A sprout consists of a tip cell that leads the sprout and stalk cells that form the sprout body. In most computational models vascular networks form without distinct tip and stalk cells. This raises the question why it matters that there are both tip and stalk cells during blood vessel formation. We study how tip cells affect the morphology of vascular networks using a model, based on the cellular Potts model, of blood vessel formation. In this model we assign different parameter values to a fixed subset of the cells: the tip cells. Because we do not know what parameters should differ for tip and stalk cells, we perform a parameter sensitivity analysis in which we analyse how the model parameters affect tip cell location and network morphology. In this manner we identified a range of values for a single parameter for which tip cells occupy sprout tips and affect network morphology. We assumed that the subset of tip cells was fixed. In reality, however, tip cells inhibit their neighbours from becoming tip cells and thereby regulate the number and location of tip cells. This so-called tip cell selection is added to our model by determining cell type based on the cell types of neighbouring cells. Using this tip cell selection model and the previously identified tip cell parameter values, we can study how tip cells and tip cell selection affect the morphology of vascular networks.

Ioana Niculescu

t.b.a

Explaining many biological phenomena require a multiscale approach in which the cell is often the natural level of separation between the intracellular regulatory mechanisms and the emerging tissue level. For many tissue level phenomena, the internal mechanism that generates a certain cell behaviour may not be that important, as long as morphodynamically the cells behave realistic enough to serve the purpose of the model trying to explain those phenomena. Cell migration is a vital process in morphogenesis, tissue repair, disease fighting but also disease progression. We propose a phenomenological model for cell migration based on the CPM framework, that bypasses the complex internal mechanism that drives the cell to move. We show that this simple and computational light method can be calibrated to fit many migration-shape deformation patterns (morphodynamics) including the amoeboid and keratocyte-like migration. The method is suited for random as well as directional migration and is easily applied in the context of crowded multicellular and heterogeneous tissue where cells need to interact.

Lorenzo Taggi

Lower bounds for critical probabilities in oriented percolation with arbitrary neighbours

Directed site percolation can be interpreted as a probabilistic cellular automaton undergoing an "absorbing" phase transition. I consider the generalization of this stochastic process to arbitrary (translation invariant) neighbourhood in the one-dimensional lattice. Each choice of the neighbourhood can be related to a different "modified" two–dimensional oriented percolation problem. I discuss the dependence of the critical probabilities on the neighbourhood, I provide lower bounds for the critical probabilities and I relate them to a specific aspect of the dynamics: taking into account that sets of "absorbed" states can dynamically merge one with the other, the lower bound is improved.

Hanne Van Den Bosch

Majority voter PCA and its mean field approximation

Mean field models are often used to obtain qualitative information on phase transitions. However they do not necessarily behave in a same way as finite range models. We try to find a class of PCAs that tend to a mean field model in a suitable limit. Using contour methods we prove the existence of a phase transition in a model interpolating between PCAs with finite range couplings and a mean field model.

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Practical information

Location: EURANDOM, Mathematics and Computer Science Dpt, Technische Universiteit Eindhoven, Den Dolech 2, 5612 AZ Eindhoven, The Netherlands.

EURANDOM is located on the campus of Eindhoven University of Technology, in the brand new TU/e Metaforum building (4th floor) (about the building). The university is located at 10 minutes walking distance from Eindhoven main railway station.

The conference will be held at the Eindhoven Technical University. The TU/e is a relatively young university. It was founded some 50 years ago and is situated in the southern part of The Netherlands in the city of Eindhoven, well known as the hometown of the giant in Electronics, the Philips Company, and the famous football club, PSV Eindhoven. The TU/e intends to be a research driven, design oriented university of technology at an international level, with the primary objective of providing young people with an academic education within the "engineering science & technology" domain.

The mission of EURANDOM is to foster research in the stochastic sciences and their applications by a visitor exchange and workshops program. EURANDOM acts as an international meeting point for researchers in the various areas of stochastics and takes initiatives for collaborative research at a national as well as a European level.

Conference room: Metaforum Building MF11&12. The meeting–room is equipped with a data projector, an overhead projector, a projection screen and a blackboard. Please note that speakers and participants making an oral presentation are kindly requested to bring their own laptop or their presentation on a memory stick.

Pay attention:

The Metaforum Building is closed after 19:00. No exit possible after this time.

Computers: In the EURANDOM library/lounge, you will find two computers with Internet. Feel free to use them. Please do not install additional programmes. WiFi is available; if you have not registered before arrival, you can do so now by filling in the enclosed form and hand it over to the secretariat (Patty Koorn). Another possibility is to use the available eduroam connection with the login of your institution (https://www.eduroam.org/).

Lunches: Organised on campus

Conference dinner: Tuesday June 11, 18.30h,
Dinner for speakers, organisers and for participants, who have indicated they will join the dinner. You can go on foot to restaurant "Vlijtig Liesje", Ten Hagestraat 7, Eindhoven, phone number +31 (0)40 2370101 (see enclosed route description)

Questions If you have any questions, please come to Patty's office (MF 4.081) or ask one of the organisers.