Booklet of abstracts

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Contents

Invited talks

NeVAE: A Deep Generative Model for Molecular Graphs

Niloy Ganguly
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Deep generative models have been praised for their ability to learn smooth latent representation of images, text, and audio, which can then be used to generate new, plausible data. However, current generative models are unable to work with molecular graphs due to their unique characteristics—their underlying structure is not Euclidean or grid-like, they remain isomorphic under permutation of the nodes labels, and they come with a different number of nodes and edges. In this paper, we propose NeVAE, a novel variational autoencoder for molecular graphs, whose encoder and decoder are specially designed to account for the above properties by means of several technical innovations. In addition, by using masking, the decoder is able to guarantee a set of valid properties in the generated molecules. Experiments reveal that our model can discover plausible, diverse and novel molecules more effectively than several state of the art methods. Moreover, by utilizing Bayesian optimization over the continuous latent representation of molecules our model finds, we can also find molecules that maximize certain desirable properties more effectively than alternatives.

Neuronal Networks as Discrete Dynamical Systems and Dynamical Mechanisms of Information Routing in the Brain

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The collective spiking activity in the neuronal networks of our brain can be modeled in the form of pulse-coupled networks. They lead to complex discrete dynamical systems with peculiar behavior, e.g. a convergence to synchronized states in finite time - i.e. point attractors in phase space. In principle this can allow for fast switching between different states, yet the mechanisms that allow our brain to quickly switch between different information routing states have remained unclear.

It is our brain's ability to flexibly select relevant information and to route it along different paths, e.g. under selective attention, that constitutes part of its efficiency. How can it switch this routing so fast in a fraction of a second, if the neuronal connections can be reconfigured only slowly? We have recently uncovered a highly flexible mechanism which uses transient synchrony to dynamically rewire information paths in a few hundred milliseconds [1]. We show that models of cortical networks near the onset of oscillatory synchrony selectively route input signals despite the short duration of oscillatory bursts and the irregularity of neuronal firing. In multi-area networks with realistic anatomy we find that oscillatory gamma bursts spontaneously arise with matched timing and frequency and that they organize information flow by large-scale routing states.

Work in collaboration with A. Palmigiano, D. Battaglia, and F. Wolf.

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Topological determinants of excitation propagation and self-sustained activity on excitable networks

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Discrete models of excitable dynamics on graphs are an efficient framework for studying the interplay between network topology and dynamics. This topic is of practical relevance to diverse fields, ranging from neuroscience to engineering. In particular, we have investigated how a single excitation propagates through a random network as a function of the excitation threshold, that is, the relative amount of activity in the neighborhood required for the excitation of a node. We observe that two sharp transitions delineate a region of sustained activity. Using analytical considerations and numerical simulation, we show that these transitions originate from the presence of barriers to propagation and the excitation of topological cycles, respectively, and can be predicted from the network topology. Our findings are interpreted in the context of self-sustained activity in neural systems, which is a question of long-standing interest in computational neuroscience. Mathematical modeling of mechanical signaling in biological development.

Work done with M.-T. Hütt (Jacobs Univ., Bremen, Germany) and C. Hilgetag (Hamburg Univ., Germany & Boston Univ., USA).

Mathematical modeling of mechanical signaling in biological development

Roeland Merks

Leiden University, The Netherlands

To form patterns and shapes during embryonic development, cells must carefully coordinate their behavior. It has become increasingly clear that, alongside exchange of chemical signals, mechanical cell-cell signaling plays a prominent role in biological development. Mechanical signals are often mediated by the extracellular matrix (ECM), the fibrous and jelly materials secreted by the cells that act as mechanical support in many tissues. In this talk I will present mathematical modeling approaches for mechanical regulation of single cell behavior and collective cell behavior by the ECM, showing examples of single cell behavior, blood vessel development, and somitogenesis. After discussing examples involving isotropic contractile cells and isotropic extracellular matrix materials, I will show our more recent attempts to add more biological detail. In particular, I will discuss how focal adhesions, the cells' "hands" and "feet" by which they adhere to the matrix can help coordinate cellular responses to cell stiffness. Time permitting, I will also discuss anisotropic cell contraction, and our recent attempts to model fibrous ECMs. Altogether, our models help explain how local, cell-ECM interactions assist in coordinating cell behavior during multicellular patterning.

Population Genetics and Democratic Elections

Johannes Müller
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In recent years it became clear that the voter model can be used to model democratic elections. One point needs to be adapted: The Voter model on a connected, finite graph tends in the long run to an absorbing state, where only one opinion/party is left. Therefore, different forms of the noisy voter model have been introduced [1,2], where individuals choose with a certain probability one of the given opinions, without interaction with neighbours.

We propose a slightly different approach, based on the infinite allele model, that is well known in population genetics. With a certain probability, new groups are created, and old groups disappear. We show that this model (with slight adaptations to avoid opinions/parties with only few supporters) on a full graph has properties that are in line with election data from the US, Netherlands, France and Germany [3]. In the present talk we investigate the importance of the graph structure, with the aim to better understand mechanisms behind the variance in election data.

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3. Hösel, V., Müller, J. Tellier, A. (2019) *Universality of neutral models: decision process in politics*. Palgrave Comm., in press.

Joint work with Volker Hösel, TUM, and Aurelien Tellier, TU München.

From Pixelsex to Mathematical Socialism – confronting cellular automata with real (artistic) live

Tim Otto Roth
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Cellular automata (CA) modelling often applies a similar method like art history: visual analogies. Such analogies are made comparing a pattern generated in silico with patterns in vivo respectively in 'physica'. An inverse approach is to create physically automata and look for eventual implications of this real world implementation. In my presentation I will introduce a couple of my CA related artistic and composition works revealing a certain shift related to such a material translation by physico-mechanical apparatuses or human agents.

For instance I realized performances with musicians or dancers creating sound or spatiotemporal patterns reacting simply on their neighbours. Human actors reveal special forms of interferences as they can simply fail to execute correctly a neighbourhood rule. Such a failure is not necessarily aleatoric, but can show also certain patterns, as a recent project in India revealed creating hand knotted carpets according to CA rules – this was a very special social experiment at the very same time.

The most challenging task was to use automata for music composition. For a water organ I introduced a special way to analyse the dynamics of the agents: The activity of each pipe is translated into alternating water levels changing also the pipe's timbre and pitch. Last but not least I will report about some collateral effects of such an artistic approach playing for instance with asymmetric topologies or developing a new way to describe the dynamics and robustness of automata system complementary to the Wolfram classification.

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Future Mobility: Self-Organization, Inefficiencies and Paradoxa

Marc Timme
Chair for Network Dynamics, TU Dresden

Human mobility together with human-centric transport, the transport of the goods humans produce, use and discard fundamentally underlies all aspects of our modern society. How we work, how we spend our free time, how we consume goods and services, how we use and need energy, how we protect our health and ensure environmental sustainability. Besides the large number of challenges existing today, including to contain climate change, to avoid traffic grid locks and to reduce emissions, a vast range of technological innovations impinges on mobility systems today. I highlight how questions on human mobility open up a fascinating research field on self-organization processes described by statistical physics and nonlinear dynamics of coupled multi-dimensional systems. Models, simulations (and real world data) here bridge the regimes between few, discrete entities and infinite numbers of entities characterized, e.g., by continuous flows. First, I highlight why and how hysteresis persistently causes major inefficiencies across ride-hauling (taxis, ride sharing, etc.) systems. Second, I illustrate how ride pooling may enable smoother door-to-door service without the need of owning a private car, also illustrating a recent pilot project we organized. Finally, I point out how tech-enabled routing systems may be optimized not for fastest individual route but for overall effectiveness if the routes of many travelers collectively minimize the total time wasted. I am happy to discuss the long list of open questions on future mobility.

`http://networkdynamics.info`

This is work with Malte Schroeder, Philip Marszal, David Storch and others.

Contributed talks

Non-Markovian effects in discrete, individual-based reaction systems

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Many mechanisms have been developed for the purpose of explaining the formation of the various emergent structures in developmental biology. Two examples are the clock-wavefront mechanism for somite segmentation and Turing's reaction-diffusion equations for spontaneous pattern formation. At their heart, both of these models involve sets of discrete agents interacting with one another in a stochastic manner. Often, however, the intrinsic noise associated with the individual-based nature of the dynamics is neglected in favour of the use of simpler, deterministic equations, which are valid in the limit of infinite system size. Such an approach can ignore important noise-induced effects such as stochastic patterns, cycles or waves, which are not captured by deterministic equations and which can be non-negligible for the numbers of particles involved in biological systems.

The temptation to ignore noise becomes even greater when complicating factors such as non-Markovianity (memory effects) enter into the models. Such memory effects can arise, for example, as a result of delays in the production of mRNA or protein in gene regulatory systems or of non-Fickian (anomalous) diffusion in reaction-diffusion schemes. In these cases, conventional master equation techniques are no longer applicable and one has to resort to alternative approaches which take into account the memory effects in the system.

In this talk, I will discuss two examples where non-Markovianity is important in a noisy system (alluded to above): delays in the gene-regulatory networks related to somite segmentation, and noise-induced pattern formation in reaction-diffusion systems with subdiffusion. I will outline the path integral approach one can use to quantify the noise in non-Markovian discrete-particle systems. To demonstrate the applicability of the theory, I will discuss how an interplay between noise and subdiffusion can ameliorate the so-called 'fine-tuning' issue associated with Turing pattern formation [1]. I will also discuss how the combination of noise and delay can lead to the production of sustained cycles missed by deterministic models of the somite segmentation clock, and discuss the synchronisation, amplification and increase in coherence of such cycles with the strength of 'Delta-Notch' signalling strength between cells [2].

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Collective Estimation of Dynamic Signals in Cell Communities

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We introduce a framework for deriving the physical limit to the precision of estimation in cell populations. This limit is a result of intrinsic stochasticity of the chemical reactions used for the inference by cells as well as extrinsic noise due to the cell-to-cell variability. Our analysis is based on an intuitive order-parameter which can determine the quality of the estimation on each component of the system whose elements are connected through any arbitrary topology. We employ this analysis to study a simple model in which environmental signal is governed by a stochastic birth-death reaction and cells respond linearly to that. Our results indicate that cell to cell communication (modeled by molecule transport) significantly enhances the precision of estimation in the presence of the cell-to-cell variability while does not affect it, in the case of identical cells. The latter case seems to be due to an exact trade-off between the cross-correlation and MSE of estimation.

An exploration of two-dimensional Affine Continuous Cellular Automata rules solving the fixed-size density classification problem

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The density classification problem (DCP) originally appeared in [1, 2] relates to binary Cellular Automata (CA) and is straightforward to formulate. The goal is to define a CA that can decide whether an initial configuration contains more 1s than 0s. Such a solution needs to be valid irrespective of the number of cells. The output is to be given such that all cells get the majority state. Even though this problem is trivial for classical computers with global memory, it turns out to be very challenging for CAs, which are capable of local computation only. It has been shown that there exists no general solution to this problem valid for any dimension d [3].

Continuous Cellular Automata (CCA) can be seen as a generalization of CA, in which we still keep space and time discrete, but we consider that cell states can be taken from some infinite set. This process allows to construct for every binary CA some particular CCA (so-called Fuzzy CA) through an extension of the domain of the local rule. A further generalization of this idea is used in the definition of affine CCAs [4]. This kind of CCAs, apart from the Fuzzy CAs, is considered the simplest possible generalization, as the local rule is affine in each variable. It appears that ACCAs offer much more opportunities than the binary CAs they stem from.

Our previous work [5] presented results for the one-dimensional ACCAs solving the DCP. Now, we focus on ACCAs with the von Neumann neighborhood that can solve the DCP for a given two-dimensional grid size $N \times N$. As the problem is more complex in the two-dimensional case, we use differential evolution [6] as an optimization method that is able to find a set of ACCAs solving the DCP.

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Generating multi-state reversible and number-conserving cellular automata

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Reversible cellular automata (CAs) are of particular interest, since they can be used to simulate, for instance, gas or fluid dynamics. A CA is called reversible if its global rule can be reversed, which is possible only if every configuration has exactly one predecessor and exactly one successor. Determining whether a CA is reversible is an intricate task, but for one-dimensional automata there exist effective algorithms.

Number-conserving CAs (NCCAs) were exhaustively generated before for less than or equal to four states and it is known that there are exactly 5 binary NCCAs, exactly 144 ternary NCCAs and 89588 NCCAs with four states $\{0, 1, 2, 3\}$. From such lists, reversible CAs can be selected, but the size of the set of all NCCAs grows very rapidly. On the other hand, only quite trivial ways of constructing reversible NCCAs were proposed. We demonstrate a novel approach to construct rules that are both number-conserving and reversible. In this way, it is possible to get a comprehensive list of such CAs with five and six states, without generating all NCCAs.

We analyze this list and provide an interpretation for the rules generated. In this way, we obtain a construction method for reversible and number-conserving CAs with an arbitrarily large number of states.

Multiple scale phenomena in cell populations with realistic cell cycle time distributions

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Cell proliferation is typically incorporated into stochastic mathematical models of cell migration by assuming that cell divisions occur after an exponentially distributed waiting time. Experimental observations, however, show that this assumption is often far from the real cell cycle time distribution (CCTD). In this talk I will investigate if, and how, some features of the CCTD have an impact on typical macroscopic dynamics of the total cell population (travelling waves, cell cycle synchronisation). I will present a series of stochastic and deterministic age-structured models which can be used to explore this connection from an analytical prospective. Finally, I will discuss potential medical applications of these models to melanoma drug treatment optimisation and other extensions.

Bigraphical Meta-Modeling of Fog Computing-Based Systems

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Motivation

Fog computing is regarded as a facet of pervasive computing, whereby, computational resources are more rigorously hierarchically organized concerning the spatial structure [4]. Furthermore, location-awareness, device heterogeneity and low-latency are only some characteristics for applications of the Fog which makes it a non-trivial extension of the Cloud [5]. This computing paradigm will gain importance with the increasing employment of smart devices in our public buildings and the emergence of robotic co-working therein, where humans and robots must work together in uncontrolled environments. Equally for both application fields, the primary objective for software development is to reduce the development costs by allowing minimal transition and implementation time of the Fog application.

Consider the following smart building example, which exemplifies some key architectural points and the need for context-awareness. A smart building contains a multitude of sensors and actuators that measure several parameters and are continuously analyzed to adapt to the changing environment autonomously. For example, by automatically activating control mechanisms inside the building (e.g., turning the light on/off with regards to the time or presence of a resident). To clarify, smart buildings convey the notion that computing resources being aware of their surroundings (i.e., contexts). Furthermore, the constituents of a smart building are hierarchically structured (i.e., consisting of multiple floors, wings, gateways, services), thus, virtually and physically forming a chain of responsibility. In each hierarchy level computation shall be performed in a bounded context and propagated to the next handler to effectively reduce computation complexity. As a result, computation is performed relatively close to the user's end devices facilitating latency-sensitive applications. Thus, model-driven approaches also enable the transfer of formal methods to robot software effectively allowing robot applications to be certified and verified.

Problem

Modeling both static and dynamic aspects of fog computing-based systems becomes an arduous task imposed by the requirements of fog computing itself. Svorobej et al. [16], for example, expound several modeling challenges concerning the Fog and their participants, including application, infrastructure and network level modeling. These models are certainly not a single megamodel but rather a tower of models as indicated by Milner in [9]. In this regards, several algebraic theories for pervasive computing were proposed. On the one hand, formal frameworks specific to context-aware computing [15, 10, 6], on the other, process calculi such as mobile ambients, the π-calculus and the calculus of communicating systems (CCS), to mention but a few. Though some of these formal methods comprise necessary features such as composition, they are either rather rigid and to specific (e.g., fixed syntax, operations and semantics), equipped with weak equivalence classes, or do not scale well when composing a myriad of systems including different contexts.

Solution

Bigraphs, devised and refined by Milner and colleagues over the last decade [12, 8, 13, 11] are an intuitive, yet still young, mathematical framework for the modeling of complex distributed

systems employing contexts and mobility. The formalism not only resembles various theories [12] concerning mobile interaction (and thus, in fact, provides an unifying theory) but also compounds a theory of behavioral equivalence which is a congruence. So far, the theory has been successfully employed for modeling agent-based systems [14], context-aware systems [3, 7] and cyber-physical systems (CPS) [2].

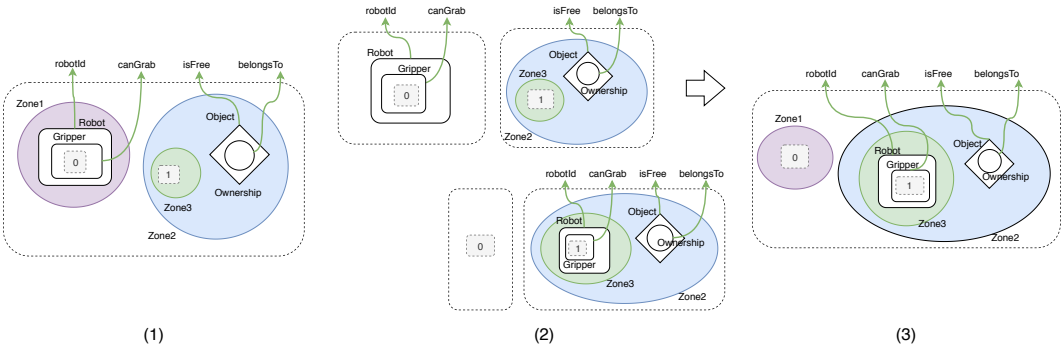

Figure 1: Example of a bigraph showing a Pick&Place robot. (a) The robot, equipped with a gripper, is located in "Zone1" and shall grab the object within another zone. (b) A reaction rule to describe the following dynamics: Robot moves into "Zone2" (i.e., collaboration zone). (c) The state after the transition. The robot moved into "Zone2" and is now ready for the takeover of the ownership and to grab the object.

A bigraph is regarded as a superposition of two independent structures over a *signature* S—a *place graph* and a *link graph* of the form $B = \langle G^P, G^L \rangle$, where the former is used to model locality of nodes organized in hierarchies (i.e., participants of the Fog), the latter is used to describe relationships (i.e., connectivity or communication) between them. The reactions that may occur in a system (for modeling the dynamics of a system) is performed by composition of bigraphs or are modeled by *bigraphical reaction rules*. An example is depicted in Fig. 1. To emphasize, the semantics of a bigraph can be freely specified by reaction rules where the syntax is parameterized by its corresponding signature. By this, it has been shown that bigraphs resemble the π-calculus, mobile ambients, CCS and petri nets (see [13]). Further, they naturally convey the notion of contexts: A bigraph can be composed of contexts, that is to say, by a surrounding bigraph and an agent bigraph of the form $B = C \circ A$. Thus, behavior, contexts and agents of a Fog are independently modeled achieving separation of concerns.

Conclusion

We claim that bigraphs are a suitable framework supporting a hierarchical and modular description of real-world applications–two minimum necessary properties for the modeling of fog computing scenarios. With this contribution, we show, how intuitively a model for fog computing systems become which are composed of several contexts and agents with a constantly changing behavior.

In view of [1], it is yet to show if our model can be generalized to an explicit world model for smart rooms to facilitate and simplify the software development of human-robotic co-working applications, for example. This implies that the inclusion of context information must be supplied by the underlying world model to every constituent of a fog computing system. As a result, this makes them automatically smarter which in turn decreases the coupling and complexity of such systems.

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Forming Point Patterns by a Probabilistic Cellular Automata Rule

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The objective is to find a cellular automata rule that can form a 2D point pattern with a maximum number of points (black/blue 1-cells). The distance between any two points shall be at least one, i.e., points shall be separated by white/green 0-cells. A probabilistic rule was designed that can solve this task with asynchronous updating (random selection and random order) and cyclic boundary condition. The task is considered as a tiling problem, where point-tiles are used to cover the 0-space with overlaps. A point-tile consists of a black center pixel (the *kernel*) and 8 surrounding white pixels (forming the *hull*). The term *pixel* is used to distinguish the cells of a tile from the cells of a cellular automaton. For each of the 9 tile pixels (reference pixels) a so-called *template* is defined. In the rule application, the 9 templates are tested at the actual selected cell position. If all template pixels (except the central reference pixel) of a template match with the corresponding neighbors of the actual cell under consideration, the actual cell (more precisely its new state) is adjusted to the reference pixel's value. Otherwise the cell under consideration is set to a random value $\in \{0, 1\}$ with probability p_0 or left unchanged with probability $1-p_0$. The white pixels of the hulls are allowed to overlap. In order to evolve a maximum of points, the overlap between tiles has to be maximized. To do that, the number of template hits is counted. Depending on the hit-number additional noise is injected with certain probabilities. Thereby optimal patterns with the maximum number of points can be evolved (Fig. 1). The behavior and performance of the designed rule is evaluated for different parameter settings.

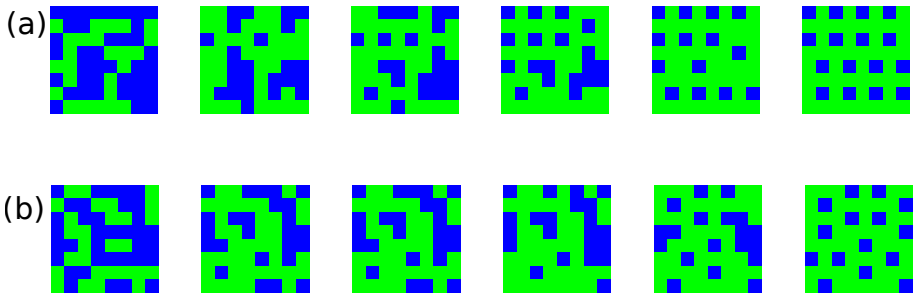

Figure 1: (a) Evolution of an 8 x 8 torus (initially random) to an optimal point pattern with 16 points. (b) Evolution to a near optimal point pattern with 15 points. Every 0-cell (green) is covered by at least two green hull pixels of the point-tiles.

Exact random sampling of connected graphs with a given degree sequence

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Center for System Biology Dresden

Sampling random graphs with various constraints is an essential tool for network analysis and modelling, but it is also challenging, each specific constraint requiring an individual approach. Here we consider random sampling from the set of connected realizations of a degree sequence. Most current methods for sampling with constrained degrees fall into two categories: rejection-based and Markov-chain Monte Carlo samplers, each with significant limitations and drawbacks. Recently, a new class of methods was proposed that can sample graphs with exact probabilities and generate the sampling weight together with each sample. However, the additional requirement of connectedness is important for many practical applications, such as computing certain network measures or simulating processes on the network. Unfortunately, imposing this requirement makes the classical approaches untenable. To solve this problem, we generalize and extend the newer class of sampling methods to effectively include the constraint of connectedness while maintaining its polynomial time efficiency. Further, we implement our new algorithm and demonstrate it on the sampling of connected networks with a power-law degree distribution.

Event-based model for digital oscillators

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Networks of coupled oscillators are ubiquitous in natural and artificial systems. In large electronic systems for example, the temporal coordination of spatially distributed components is essential for reliable operations. At high frequency or large spatial distribution, such coordination becomes a challenging task, e.g., due to inevitable signal transmission delays and crosstalk between signal transmission lines.

Here we study so called digital phase-locked loops (DPLLs), electronic feedback-loop circuits that can frequency lock to external periodic signals. DPLLs can therefore be entrained by a precise reference clock via a clock tree and play an essential role in the distribution of a time-reference in state-of-the-art electronics, e.g., mobile communications, indoor-navigation, and Systems-on-a-Chip. However, such hierarchical approaches to synchronization become complicated, or even impossible for large system sizes. Recently, the possibility to use mutually delay-coupled DPLL units has been explored, using a continuous phase-model description and an experimental prototype setup [1], [2]. This work has shown that self-organized synchronization is possible in such mutually delay-coupled DPLL networks. It is not clear however whether self-synchronization can also be achieved in the presence of noise. Therefore it is essential to understand how noise affects the dynamics in networks of coupled DPLLs.

We introduce a discrete dynamical model for delay-coupled DPLL networks. The digital signals of the DPLLs are therein represented by sets of discrete event-times. In this framework the introduction of noise in the form of timing-jitter comes in a natural way, as it can be directly implemented as the uncertainty of the signals' edge times. Time-delays in the system lead to simple shifts of these discrete event-times. Furthermore, the computational resources necessary to study large networks of such DPLL elements are greatly reduced due to the event-based nature of the underlying model. This enables the application of the tools of discrete dynamical systems theory.

The model is not restricted to the study of electronic oscillators as it governs the dynamics of coupled digital oscillators with signal transmission and processing delays in general. Due to its generic formulation it may be useful for studying the collective dynamics in a variety of analog-digital systems.

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Ferromagnetic and spin-glass-like transitions in nonequilibrium models with locally competing temperatures

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The possibility of the occurrence of the ferromagnetic and spin-glass-like transitions in spin models in contact with two thermal baths with different temperatures is discussed. The models comprise the Sherrington-Kirkpatrick model and the Ising model on random graphs with edges corresponding, with certain probability, to positive and negative exchange integrals. The spin flip rates are combinations of two Glauber rates at the two different temperatures, and the coefficients of this combination are probabilities of contact of the model with each thermal bath. Only in rare cases such nonequilibrium models with non-zero heat flux can be mapped onto equilibrium ones at certain effective temperature. Nevertheless, Monte Carlo simulations show that transitions from the paramagnetic to the ferromagnetic and spin-glass-like phases occur in all cases under study as the probability of the contact with each thermal bath is varied, and the phase diagrams resemble qualitatively those for the corresponding equilibrium models obtained with varying temperature. For both models theoretical calculations based on the mean-field approximation and the TAP equations predict correctly the location of the phase border between the paramagnetic and ferromagnetic phases, while in the case of the border between the paramagnetic and spin-glass-like phases only qualitative agreement between theoretical and numerical results is achieved. The obtained results can be interesting for modelling the opinion formation by means of the well-known majority-vote model on networks (which is equivalent to the Ising model in contact with two thermal baths, one with zero and the other one with infinite temperature) and related models.

"Pleasing" can improve indirect reciprocity under the hard condition of private, noisy and incomplete information

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Indirect Reciprocity is an important mechanism to enable cooperation, especially in humans. It is usually studied using agent-based simulations and dynamical analysis within a population of self-interested agents playing the donation game: a random agent is selected to pay a personal cost c, which grants benefit b to another randomly selected agent. As a cooperation problem, the benefit is assumed to be bigger than the cost (b>c). Hence, it is best for the population if every agent decides to take the cost, so the sum of wealth would increase with b-c>0 each interaction. However, in a perfectly cooperative population, an agent that never pays the cost (i.e. always defects) would achieve the best results, making the game a social dilemma. In order to maintain cooperation and prevent defection, agents may use strategies that are based on reputations and norms.

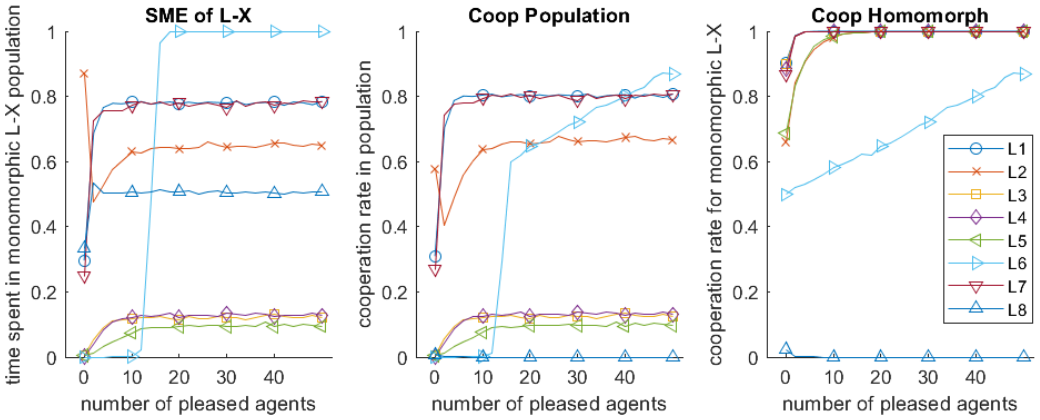
Reputation of the recipient determines how the potential donor should act (pay cost or not). Norms determine what reputations the acting agents will earn. A simple version of such a strategy may state: If the reputation of the recipient is good, then donate, otherwise defect; and: if an agent donates, he earns a good reputation, otherwise a bad one. It was shown that such simple strategies, whose norms only consider actions, cannot maintain stable cooperation, because agents refrain from punishing bad reputation (i.e. not donating) since they would earn a bad reputation themselves. More sophisticated norms consider also the current reputations of the donor and of the recipient. Each possible scenario (a good/bad donor cooperates/defects against a good/bad recipient) is linked to a resulting reputation (good/bad), leaving 256 possible norm combinations. An exhaustive search for successful norms showed that only eight can maintain stable cooperation. They are collectively referred to as the "leading-eight" but some are mentioned separately in the literature (e.g. L6 "stern judging" and L7 "staying") and some were argued to outperform the other eight, but these advantages appear very circumstantial.

Most previous studies on the subject assumed complete and shared information. That means that all agents always observe all actions and that they perceive them in the same way. There might be errors (noisy information), but they are done collectively. For example, an agent cooperates, but a rare error causes the action to seem as a defection, then all agents agree it is was a defection. More realistically however, information is not omnipresent but private. An agent can only access his own copy of the available information and each copy might be altered by errors independently. Also, an agent may not witness a certain action and therefore may lack information. This leads to severe disturbances. A single disagreement over the reputation of the recipient may lead to further disagreements over the subsequent reputation of the donor and so forth. Most leading-eight strategies fail to maintain stable cooperation under this condition.

We introduce a strategy to improve cooperation, called "pleasing". A pleasing agent keeps his own private opinion but acts in a way to match the expectations of others. He asked other agents for their opinion of the donor (i.e. himself) and recipient and chooses the action that will lead to his best possible subsequent reputation (i.e. that will lead the most agents to have a good opinion of him). To test this new strategy, we run agent-based simulations under private, noisy and incomplete information. Agents play either simple strategies: always cooperate (All-C) and always defect (All-C); or a sophisticated strategy based on norms (leading-eight, L-X). In addition to the strategies described in the literature (see table), L-X try to please other L-X agents with the new method.

We will examine evolutionary success of the pleasing L-X agents by computing how likely a single L-X can invade a finite population of simple agents (i.e. fixation probability in a Moran process) and vice versa. Together with the fixation probabilities of All-C in a population of All-D and vice versa, we compute the time spent in the state of homomorphic L-X population under the constraint of rare mutations (selection-mutation equilibrium), a common measure of evolutionary success. We also simulate the cooperation rates during these monomorphic states and consequently compute the cooperation rate in the population as a whole, the second important marker of success. We tested these for varying numbers of pleased agents to see, how efficient the strategy can be.

Norms of the	L1	L2	L3	L4	L5	L6	L7	L8
Leading-eight								
Good cooperates with Good	g	g	g	g	g	g	g	g
Good cooperates with Bad	g	b	g	g	b	b	g	b
Bad cooperates with Good	g	g	g	b	g	b	b	b
Bad cooperates with Bad	g	g	g	g	g	g	g	g
Good defects against Good	b	b	b	b	b	b	b	b
Good defects against Bad	g	g	g	g	g	g	g	g
Bad defects against Good	b	b	b	b	b	b	b	b
Bad defects against Bad	b	b	g	g	g	g	b	b



Figures show results for populations of 50 agents and a medium parameter setting (cost c=1, benefit b=5, observation chance q=0.9 & error rate $\epsilon = 0.05$). For two leading-eight strategies (L1 and L7), even pleasing just a few other agents highly increases the evolutionary success of these strategies and the cooperation rate in the population. Four other strategies were improved as well, whereas L2 ("consistent standing") lost some stability against All-C, which lowered its formerly outstanding evolutionary success (for no probing). The strategy L6 ("stern judging") was able to completely dominate populations against All-C and All-D if it pleased enough agents, which in turn led to the highest cooperation rates in the population. Our work shows that pleasing can highly improve evolutionary stability and cooperation. It also shows that this strategy can be very efficient and works even if only a few agents are pleased. Since we combined the strategy with the existing leading-eight, it further highlighted more distinctions between them. Lastly, trying to please all others with our strategy is a close approximation of the best possible action. Our results show that even acting ideally all the time may not solve the problem of private, noisy and incomplete information entirely.

Unstructured input enhances sequence memory in recurrent model of cortex through spike-timing dependent plasticity

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An unresolved issue of cortical development is whether internally generated activity plays a role in preparing the cortex for sensory input [1]. We here focus on the development of sequence memory, a prerequisite for prediction and procedural learning. We use a recurrent neural network model equipped with homeostatic and spike-timing-dependent plasticity [2], which has been shown to perform motor control [3] and visual sequence replay [4] when learning from structured input. We show that even unstructured input shapes the model network such that it can memorize sequences it has never before experienced. Moreover, we find that such pre-learning with unstructured input speeds up later sequence learning. Importantly, pre-learning requires both, homeostasis and spike-timing-dependent plasticity (STDP). The key mechanism of learning from both structured and unstructured input is the emergence of a few strong and directed synapses per neuron due to STDP. These foster temporal chains of activity, which can be harnessed to memorize unknown sequences. This mechanism may contribute to fast emergence of complex behavior after birth or offer an explanation why some mammals do not open their eyes immediately after birth but rely on internally generated activity instead.

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Process of network fragmentation – inverting rules of aggregation

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An aggregation of a network is a topic that was heavily investigated during the last decades with its burst after discovering the phenomenon of percolation in the Erdős–Rényi random networks. Since that time, a lot of different rules have been described and tested resulting in different behaviors of order parameters of the system (e.g. the size of the largest cluster). These aggregation rules can be, for instance, the constant kernel, the product kernel or the Achlioptas–like rules. On the other hand, the process of network fragmentation is not so popular in research, though, it occurs not much less often in nature than the aggregation. Having different aggregation rules, a catchy idea is to find such rules of fragmentation, that would be strictly inverse to their aggregation "mirror" rules, and to test whether they behave in the same way or not, once starting from the set of unconnected nodes, and, other time, from the fully connected network. However, finding the inverse – mirror – rules turns out to be tricky.

The example of problem can be as following. In the Achlioptas aggregation [1], we have two rules: the *min* rule (selecting smaller clusters with higher probability, preventing enlargement of the percolation cluster) and the *max* rule (selecting the larger clusters with higher probability, forcing the percolation cluster to grow). Now, we can imagine such network fragmentation rules that they are (by deleting appropriate links) more likely to destroy the percolation cluster (say the rule *f1*) or that they are more likely to retain the percolation cluster (say *f2*). Is the rule *f1* the inverse of the rule *max*, and the rule *f2* is the reverse rule *min*? Or maybe the opposite? It looks like we just have to make an appointment here, which rule we accept as the reverse of which one. An interesting way of dealing with this problem has been described previously in [2] where the authors proposed stepping back and forth in time to simulate the fragmentation process inverse to the Achlioptas aggregation. Unfortunately, the real systems do not step back or forth in time just to try the next step, thus, we should look for more straightforward framework of finding unique inverse rules.

Let's have another example, this time of the constant kernel. In this kernel, the clusters are always merged with the same probability. However, if we would like to perform the fragmentation process with the rule strictly reverse to the constant kernel rule, how should we remove the links? How to come up with and define a process that will be the exact inversion of joining clusters with constant probability?

In the case of random linking in the network (classical ER percolation), there is no doubt that the rule of fragmentation unambiguously inverse to the aggregation is random deleting of the links. In general, however, it seems that there is no obvious way to determine a single and unique rule of fragmentation that is inverse of the given aggregation rule. In addition, if we want to get the rule of fragmentation, we have to invent it. Then, how to prove that for a given rule of aggregation, an invented fragmentation rule is the only possible rule that can be invented?

The idea of this work is finding such a method (framework), which will allow to determine rules of fragmentation inverse to the given rules of aggregation in a simple way (immediately and unambiguously). The feature of this idea lies in the appropriate placement of holes (i.e. removing links) in the network, starting from a fully connected network. Thinking of holes as of objects is well known, e.g. in semiconductor physics. Thus, the term *putting holes* will mean exactly the same as deleting links in our work but it is simply convenient to think of it in such a manner as the fragmentation process is then mirror to the aggregation. If we now take the rule X of aggregation, but instead of putting links to the unconnected nodes, we will start in accordance with the X rule to put holes in a completely connected network, so then we will perform the fragmentation process with the rule unambiguously inverse (*in the sense of holes*) to the aggregation rule of X.

We will show that studying the pairs of aggregation and their inverse fragmentation rules results in unexpected behaviors and uncovers very interesting properties.

As an illustrative example, let's take the following rule. The nodes of higher degree will have higher probability of choice, and the nodes of lower degree will have lower probability of being chosen to create a link. In other words, the probability of putting a link is proportional to $(k+1)(m+1)$, where k and m are degrees of nodes. Therefore, we prefer large nodes. The addition of

unity results from the fact that a node with a zero degree cannot have a zero probability of being chosen. The results of this example are presented in Figure 1 and Figure 2.

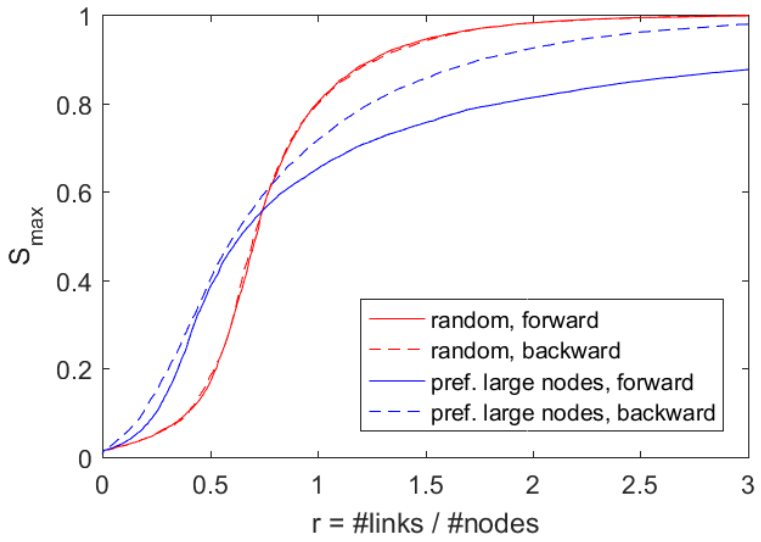

Figure 1: The graph shows the behavior of the *Preferred large nodes* rule in the aggregation and fragmentation process (128 nodes, 100 runs). For comparison, the rules of the random rule are also plotted. In this case, the rule *Preferred large nodes* causes that the largest cluster size (S_{max}), at the beginning, grows faster than in the case of the random rule (similar behavior as in the case of the Achlioptas max rule). The *forward* curve is aggregation, the *backward* curve is fragmentation.

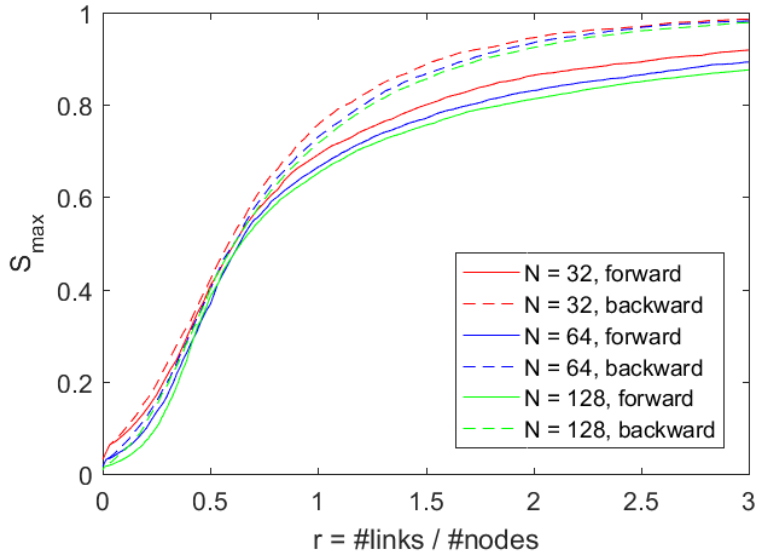

Figure 2: The illustration of the finite-size scaling problem on the *Preferred large nodes* rule. The largest cluster size patterns behave differently depending on the size of the system. Three curves are plotted for aggregation (for 32, 64 and 128 nodes) and three for fragmentation. They do not converge leading to the conclusion that this specific rule is not identical when considering the *forward* (aggregation) and *backward* (fragmentation) process.

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Timed automata in modeling of atrial electrophysiology

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A timed automata real-time framework is considered as a model of human right atrium. The idea of the model is shown in Fig. 1. A single timed automaton allows to simulate efficiently the electrophysiology of a single cardiac cell. The specific architecture of the right atrium is reconstructed by a special organization of cells on 2D grid. For the model details see [1]. With this framework one can model both the alternations in the structure of inter cellular connections and the impairment of the contraction strength of an individual cell.

It occurs that simulation results can be confronted with rhythms of heart contractions recorded on the patients after heart transplantation. Accordingly, different hypothesis about a given patient tissue degradation can be issued basing on a simple ECG measurement, namely the Holter recording.

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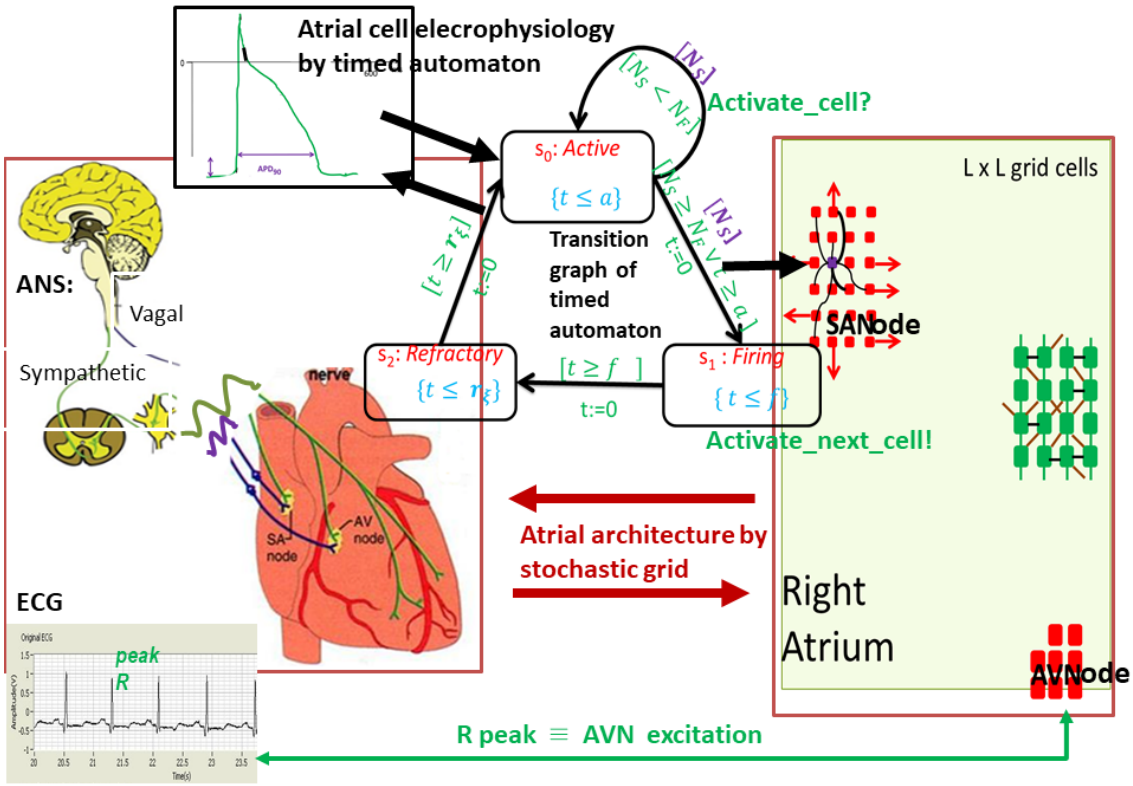

Figure 1: From a healthy heart (regulated by autonomic nervous system (ANS) consisting of two branches: sympathetic and vagus nerve) to the heart after heart transplantation (where nerves of ANS are cut off) and resulting ECG signal, then to the right atrium model (on a stochastic grid) and back. The intervals between consecuitive heart contractions (R peaks on ECG) are simulated by the AVnode excitation times. A timed automaton mimics the atrial cell elecrophysiology.

The Known (ex ante) and the Unknown (ex post): The Common Structure of Science in Nature, Technology, Economics and Society

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Why are universities teaching the knowledge of yesterday, when students need the knowledge of tomorrow? Is teaching the past useful for the future? The reason for teaching the known past is the hope that some parts of today's knowledge will still be valid in the future. These parts of knowledge are the V-elements of science. Of course, in the future students will also encounter new and unknown things; these are the U-elements of science. Accordingly, science will consist of the interaction W (V, U) of known V- and unknown U-elements. W (V, U) is the general structure of all sciences, we teach the known and valid (V) and we do research for the unknown (U). In social sciences, we call the known elements ex ante and the unknown elements ex post. In natural sciences, we have conservative systems that we may calculate, and not-conservative systems that we cannot fully calculate. Mathematics has solvable and unsolvable elements: we have exact and not-exact differentials, path independent Riemann and path dependent Stokes integrals, real constraints and statistical distributions, linear and non-linear differential equations, known rules and unknown cellular automata. By relating the (U, V) elements of natural and social sciences to the (U, V) elements of mathematics, natural and social sciences obtain the same 'hard' structure in calculus, stochastic theory, complexity and chaos theory. Moreover, the common mathematical structure leads to corresponding fields, models and equations: economics corresponds to physics, social science to chemistry, business to engineering, politics to material science and opinion formation to crystal growth. The resulting laws W (U, V) confirm, complement or replace the present models in natural, technical, economic and social science, and they are applied to present day problems by calculation and simulation: the rising gap between rich and poor, the refugee problem in Europe, the US presidential elections, the Brexit.

Evolution of artificial living creatures with Cartesian Genetic Programming

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Cartesian Genetic Programming (CGP) is an evolutionary algorithm, inspired by the rules of biological evolution, that can be used to evolve computer programs. Programs in CGP are encoded as a network of nodes. Each node is assigned a function (which can be different for each node) that processes input values supplied to the node. Functions and connections between nodes are determined using a simple algorithm of evolution. In contrast to the traditional approach employed in genetic algorithms, the size of each generation in CGP is very small (only four children and one parent program, which results in faster evolution) and subsequent generations are created solely via the application of the mutation operator (there is no crossover). CGP is very universal and can be used to solve a variety of different problems.

In our work, we apply CGP to a semi-biological problem — that is we try to evolve "brains" of artificial living creatures. The creatures, which are an idealised and heavily simplified models of animals, use springs and rigid bodies as their main building blocks. Springs act as muscles and can be contracted by the CGP evolved brain. Each creature has a number of sensors (for example, it can tell whether it is touching the ground). CGP programs process the data acquired from the sensors and decide which muscles, if any, should be contracted at a given time. The goal of the evolutionary algorithm is to create programs that allow creatures to walk in a two-dimensional virtual environment. As such, we try to solve a biological optimisation problem. Each newly evolved program (that is, each generation of creatures) is supposed to be more adapted to walk in the environment than the previous one. Our results indicate that Cartesian Genetic Programming is well suited for this task.

Pattern formation, condensation, and swarming of polar and nematic-aligning particles

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Several types of organisms are known to come together, self-organize, create spatial patterns, and migrate together as a population. The coordinated movement of individuals, known as swarming, has been successfully modeled as the result of pairwise polar interactions between individuals, which favors de parallel reorientation of particles' velocities. The collective movement of elongated, rod-shaped bacteria, on the other hand, has been modeled through nematic interactions which, contrary to polar interactions, not only favors parallel alignment of velocities, but antiparallel alignment as well.

In this talk, we use lattice-gas cellular automata (LGCA) models to study the collective phenomena of velocity aligning particles. First, we construct models of zero-range polar and nematic aligning particles. We characterize the order-disorder transitions, as well as particle condensation numerically. Furthermore, we derive a continuous macrioscopic description of the particle population for both alignment mechanisms. We show that the derived macroscopic models agree qualitatively with lattice-gas simulations, though large particle fluctuations in the lattice-gas model likely prevent quantitative agreement.

Secondly, we define a model of persistent, nematic aligning particles, where individuals interact with one another through nematic interactions, but exhibit persistent motion when in isolation. We find that the collective behavior of the population is heavily dependent on the strength of the particle interaction, and the degree of persistence of individual particles.

What is the Optimal Railway Network?

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We present a straightforward algorithm to optimise a railway network. Starting from some assumptions and a basic understanding of the mathematics, we show that the network can be optimised by considering only network structures such as circuits. The algorithm is applied to an abstraction of the British railway network, which concludes with a novel proposal for the structure of the optimal railway network.

Model description

Consider an idealised model of a railway, where trains leave stations as soon as possible, and the frequency of train departures is as high as possible. We add the following crucial condition: trains scheduled to depart must wait for all arriving trains before departing. Let $x_i(k)$ represent the k^{th} departure time at station S_i. Then, given our conditions, the future timetable of the simple railway network of Fig. 1 is given by the following recurrence relation.

$$x_1(k+1) = \max(x_1(k)+2, x_2(k)+5) \quad (1)$$
$$x_2(k+1) = \max(x_1(k)+3, x_2(k)+3)\ . \quad (2)$$

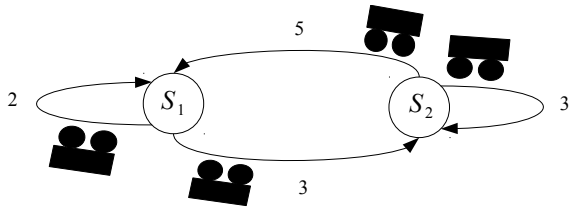

Figure 1: Simple railway network with two stations, one train on each track.

By making operator transforms $\max \mapsto \oplus$ and $+ \mapsto \otimes$, this system is linearised, which takes us to the realm of *max-plus algebra* (MPA). Such a system has been well-studied for the railway application in [1], where the intimate link between eigenvalues of the network adjacency matrix, railway performance, and network structure has been highlighted.

Here, we build on this idea to optimise the British railway network. We present an algorithm that takes only a standard understanding of MPA, following which the optimisation steps are grounded solely in the study of circuits in the network. A fundamental theorem of MPA says that, in a strongly connected network such as the railway, the eigenvalue is unique and determined by the circuit(s) with the largest average weight. Thus, critical circuits in the network are those circuits that comprise the longest average round-trip time λ, which also represents average inter-departure times. Reducing λ therefore addresses the aim of maximising the frequency of departures; our algorithm achieves this by identifying such circuits and incrementally adding dummy stations on them. Subsequently, new critical circuits are identified, and the process is repeated until desired.

Thus, we strategically add nodes and edges, enlarging circuits along the way so as to reduce their λ value. Ultimately, this produces a one-way ring layout as optimal (see Fig. 2). Indeed, this allows stations to wait only for one train before departures, though it looks impractical; for instance, to travel from London Euston to Oxford in the south, it seems one would have to go through Edinburgh, a futile diversion to the north. However, the additional nodes (the dummy stations) in this layout represent platforms within stations, and the dashed edges represent walks between these platforms. This is what produces the impracticality illusion; we have in fact split London Euston into multiple substations, i.e., platforms.

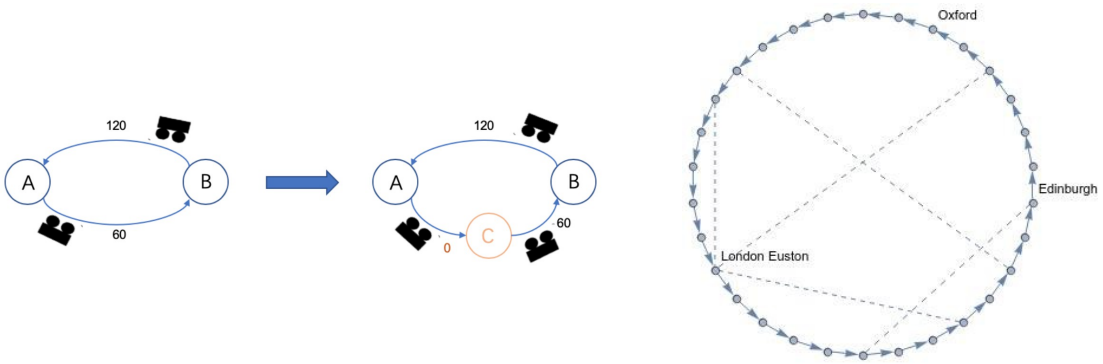

Figure 2: Left: Adding a dummy station enlarges a circuit and reduces its average weight: from $\lambda = (180)/2 = 90$ to $\lambda = 180/3 = 60$. Right: the optimal railway network is a one-way ring?

Implications

Max-plus algebra has been proposed as a useful modelling tool for optimising railway timetables in [1] as well as for the scheduling in certain biological applications and manufacturing processes [2, 3]. However, there has been minimal focus on the structure of the network. Here we show that we can optimise the railway structure at little cost. We envisage beneficial discussions with experts at SOLSTICE 2019 to further this research, particularly in terms of wider implications and other applications; does this ring network arise in biological networks and manufacturing?

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Number-conserving cellular automata in one dimension

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In a number-conserving cellular automaton, each cell contains a finite number of particles, depending on its state. When the automaton evolves, these particles move according to a transition rule, and none of them is destroyed or created.

In 1991, Hattori and Takesue found a necessary and sufficient condition that the transition rule of a one-dimensional cellular automaton is number-conserving. With it, one can find number-conserving transition rules, but only by searching the space of all rules. I will introduce two related methods with which one can construct number-conserving rules directly.

The constructions use the concept of *particle flow*. This is the function that expresses the number of particles that cross the boundary between two cells in terms of a finite neighbourhood of these cells. Up to a few remaining choices in some cases, a number-conserving rule is determined by its particle flow.

The first construction of number-conserving rules involves a sequence of choices that impose increasingly stronger restrictions on the particle flow. The sequence ends when a single flow is specified. All particle flows and therefore all number-conserving rules can be found in this way.

The second construction is based on an order structure in the set of particle flows: The maximum and minimum of two flows are again particle flows. The set of all flow functions has the structure of a distributive lattice. There is a subset of particle flows such that all other flows can be expressed as the maximum of a subset of these functions. This subset of "minimal" flows can be specified explicitly and from it, all flows can be constructed.

The first construction provides a classification for number-conserving rules. The second lets one specify the rules in a more informative form than Wolfram numbers.

Isometries of the hypercube: a tool for logical regulatory networks analysis

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Biological processes are complex systems controlled by underlying gene regulatory networks [1]. Boolean networks are discrete dynamical systems used in systems biology to model the dynamics of intracellular networks and interpret the emergence of cellular behaviors [2].

We consider a boolean Finite Dynamical System (FDS) S: a map from the hypercube $\{0,1\}^n$ to itself, with n the number of genes. Each boolean variable x_i states for the discrete expression of gene g_i (present/absent), and boolean vectors $x \in \{0,1\}^n$ are the states of the system. From S, we can compute the corresponding regulatory graph $\mathcal{RG}(S)$ (oriented and signed), consisting in all activations and inhibitions (edges with sign $+$, resp. $-$) between genes (nodes). If a gene has at least one regulator, we describe the conditions for its activation by logical rules involving all its regulators [3, 4]. Function S encodes the dynamics, but updating rules still have to be precised to describe the trajectories of the system. Most commun updating policies are the synchronous one, where all components update simultaneously, and the asynchronous one, supposing that only one component can update at a time. The synchronous trajectories are iterations of S; the asynchronous dynamics is non deterministic (a state may have several successors), and its trajectories follow the edges of the hypercube.

Properties of S and of the asynchronous State Transition Graph (the directed graph representing the asynchronous trajectories) can be interpreted as biological features (e.g. multistability and cellular differentiation, cyclical attractors and homeostasis; cf [5, 6]). However, the exploration of all the trajectories is a challenging task because of the combinatorial explosion. A way to approach this problem is to exploit the links between regulatory graphs and dynamics (FDS). Clearly, a unique regulatory graph is associated to each FDS S, whereas several FDS correspond to the same regulatory graph. We propose here to characterize the regulatory graphs corresponding to classes of dynamics related to each others by symmetries of the hypercube.

Given S a boolean FDS and f a symmetry of the hypercube, we consider the conjugated dynamics $\phi_f(S) = f \circ S \circ f^{-1}$ (see for instance [7, 8]). Clearly, $\phi_f(S)$ preserves the dynamical properties of S [9]. We compare their respective regulatory graphs $\mathcal{RG}(S)$ and $\mathcal{RG}(\phi_f(S))$, and their logical rules. The regulatory graphs of two conjugated FDS S and $\phi_f(S)$ are similar: our study proves that they have the same topology (nodes are renumbered); edges may switch their signs, but signs of circuits remain unchanged. Their logical rules may also be modified; for example, logical operators OR and AND may be interchanged between two conjugated FDS, but not OR and XOR. Hence, the set of symmetries of the hypercube defines classes of boolean FDS, gathering all the conjugates $\phi_f(S)$ of a given boolean FDS S, in other words gathering all the isometric FDS. Thus, we classify the set of boolean FDS on the basis of those isometries, and emphasize their common features through regulatory graphs and logical rules.

We can then restrict the dynamical analysis of all the boolean FDS to one representative per class, and thereby considerably restrict the dynamical analysis of all the boolean FDS.

As an illustration, we study boolean dynamics of well-known motifs - isolated circuits [10], chorded circuits [11] and flower graphs [12] - through the choice of an appropriate representative FDS.

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Generating Non-linear Codes for Multi-bit Symbol Error Correction using Cellular Automata

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Error Correcting Codes and cryptography go hand in hand since the security of cryptosystems depends heavily on their resilience against attacks such as fault attacks. In fault attacks, faults are induced into the cryptographic implementations which cause errors. These errors can be exploited to reveal the internal working of cryptosystems. Recently, in order to make systems fault-resistant, researchers have been using error correcting codes (ECC). In general, the existing schemes mostly encounter only one or two faults being injected, Single Error Correcting (SEC), Double Error Detecting (DED) hamming codes have important applications in building fault-tolerant systems.

Cellular Automata (CA) have been explored as efficient crypto-primitives as well as to generate error correcting codes. The random sequences generated by both linear and nonlinear CA are exploited in symmetric key cryptosystems. A number of research works are available in literature where CA is used to generate error correcting codes. In earlier works, CA is mainly used in bit error correction [3]. In general, the existing work assume only one or two faults are injected and hence, SEC-DED is effective. However, in the practical scenario, when fault is injected by a laser beam or using a clock glitch, multiple bits get infected. The situation thus demands detection/correction of multi-bit errors instead of SEC-DE [2].

AES, the block cipher standard also performs byte operations during encryption. So, corruption of one byte is more likely to happen due to injection of one bit to eight bit faults. So, to make AES secure against fault attacks, detection and correction of multi-bit errors are more relevant than SEC-DED codes. Previously, linear CA have been used in ECC for errors in bytes [1]. Here we try to apply non-linear CA in generating multi-bit symbol error correcting codes which may be successfully used in cryptosystems.

Linear CA generating linear codes is of very little use in cryptography as they provide little to no security when used as a component in a cryptosystem. Linear components are very easily breached by numerous attacks. A non-linear component in a cryptosystem - for instance, an s-box in block ciphers or a random sequence generator in stream ciphers - is what makes the system or cipher secure. Non-linear error correcting codes can therefore provide security to a cryptosystem by being used as a non-linear cryptoprimitive. These non-linear crypto-primitives are mainly useful in memory units of cryptographic devices which are vulnerable to fault-injection attacks. On using nonlinear cellular automata (NLCA) in generating error correcting codes, the nonlinearity as well as the randomness of NLCA can be exploited as the crypto-primitives.

In our work, we try to apply non-linear error correcting codes to detect and correct multi-bit errors where the number of faults are restricted to one or two symbols in an N-bit message. The size of the multi-bit symbols can be variable. We denote this variable size as m (m = 8 for a Byte). We restrict the block length of information bytes to N, where $N < (2^m - 1)$.

We begin with a m-cell maximum-length CA, i.e, with a cycle length of $2^m - 1$ and inject non-linearities at specific points of the CA in order to retain its maximum-length property. Let $T_{NL}[x]$ denote the operation of applying the non-linear CA on a multi-bit symbol x once. Further, $T^k_{NL}[x]$ denotes the CA being applied to the m-bit symbol k times.

Now, the checksymbols can be generated by running the NLCA for N cycles, while sequentially feeding the N information bytes. The method of generating the checksymbols is analogous to the computation of checkbytes in earlier research work, but the main point of difference being that earlier, linear CA were used which made it impractical for use in the cryptographic context. In order to implement single symbol error correction and double symbol error detection we need to calculate three check symbols. So with S as the seed (the initial state of the NLCA), the checksymbols C_0, C_1 and C_2 are given by -

$$C_O = P_{N-1} \oplus P_{N-2} \oplus P_{N-3} \oplus ... \oplus P_0$$

$$C_1 = P_{N-1} \oplus T_{NL}[P_{N-2}] \oplus T^2_{NL}[P_{N-3}] \oplus ... \oplus T^{N-1}_{NL}[P_0]$$

$$C_1 = P_{N-1} \oplus T^2_{NL}[P_{N-2}] \oplus T^4_{NL}[P_{N-3}] \oplus ... \oplus T^{2(N-1)}_{NL}[P_0]$$

where $P = [P_O, P_1, ..., P_{N-2}, P_{N-l}]$ denotes the message or plaintext P as a concatenation of $N-1$ m-bit symbols. To generate check byte C_O, the information bytes are simply EXOR-ed. For generating checksymbols C_1 and C_2, we can employ two m-cell maximum length group NLCAS.

Now we assume that the errors have occurred at the i^{th} and j^{th} symbols and the erroneous symbols generated are denoted by E_i and E_j. Let C'_O, C'_1 and C'_2 be the checksymbols generated on the receiver's end. The receiver, from the two sets of checksymbols available to him, can generate the following signature symbols -

$$S_0 = C_0 \oplus C'_0 = E_i \oplus E_j$$

$$S_1 = C_1 \oplus C'_1 = T^i_{NL}[E_i] \oplus T^j_{NL}[E_j]$$

$$S_2 = C_2 \oplus C'_2 = T^{2i}_{NL}[E_i] \oplus T^{2j}_{NL}[E_j]$$

The error symbols may be detected using this signature. If S_0, S_1 and S_2 are all 0, then evidently, no errors were introduced in the message P. However, if only one of the signature symbols, S_e ($e = 0$, 1 or 2) results in 0 while the other two are non-zero, then only the checksymbol C_e has an error. If more than one of the signature symbols are non-zero, then we must find an x such that $T^x_{NL}[S_0] = S_1$ and $T^{2x}_{NL}[S_0] = S_2$. The error has then occurred in the $(N-1-x)^{th}$ m-bit symbol. If x cannot be found, then more than 2 errors have occurred.

This work has immense potential for use in practical cryptosystems in order to achieve resilience against fault attacks in both public-key as well as private-key cryptography. There is scope for further research work in this domain.

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A new lattice-gas cellular automaton model explains plasticity of breast cancer invasion

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Plasticity of cancer invasion and metastasis depends on the ability of cancer cells to switch between collective invasion modes and single cell dissemination, under the control of cadherin-mediated cell-cell junctions [1]. E-cadherin is considered a tumor suppressor, the downregulation of which causes single-cell scattering in 2D environments. In clinical samples, however, E-cadherin expressing and deficient tumors both invade collectively and metastasize equally, implicating additional mechanisms controlling cell-cell cooperation and dissemination [2].
Using a lattice-gas cellular automaton model [3, 4] incorporating E-cadherin mediated cell-cell adhesion and physical confinement by the extracellular matrix (ECM), we identify cell jamming by 3D tissue boundaries as the dominant physical mechanism which supports collective invasion irrespective of the composition and stability of cell-cell junctions. In particular, we predict that downregulation of E-cadherin only allows single cell escape under conditions of locally high ECM porosity. Model predictions are validated in spatially defined organotypic culture and using intravital microscopy in breast cancer in mice. Our findings reveal that steric hinderance by 3D tissue can substitute for cadherin-dependent cell-cell cooperation and dictates cell jamming and unjamming in complex environments.

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A discrete model of interactions between the respiratory and cardiovascular systems

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The respiratory sinus arrhythmia (RSA) is a variation in time between consecutive heart contractions (so-called RR-intervals) caused by the network of complex interactions between the cardiovascular and the respiratory systems. In a healthy man, the RSA means shortening of RR-intervals during inspiration and elongation of RR-intervals during expiration. In the following we ask if a two-state model of the respiration: inspiration and expiration, allows to identify the RSA, and also to determine variations in systolic blood pressure (SBP) and/or diastolic blood pressure (DBP).

Our analysis proves an asymmetry in distribution of RR-intervals in inspiration and expiration phase in signals recorded in the healthy people, but it does not provide a significant distinction in SBP and DBP. However a strong difference is observed in the distribution of increments of SBP and DBP (ΔSBP and ΔDBP). Moreover, our simplified model of the respiration was enough to find differences in the variations of RR-intervals, SBP and DBP between the healthy people and the hypertensive patients, see Fig. 1, what suggests a different organization of the cardiovascular-respiratory interactions in the hypertensive patients.

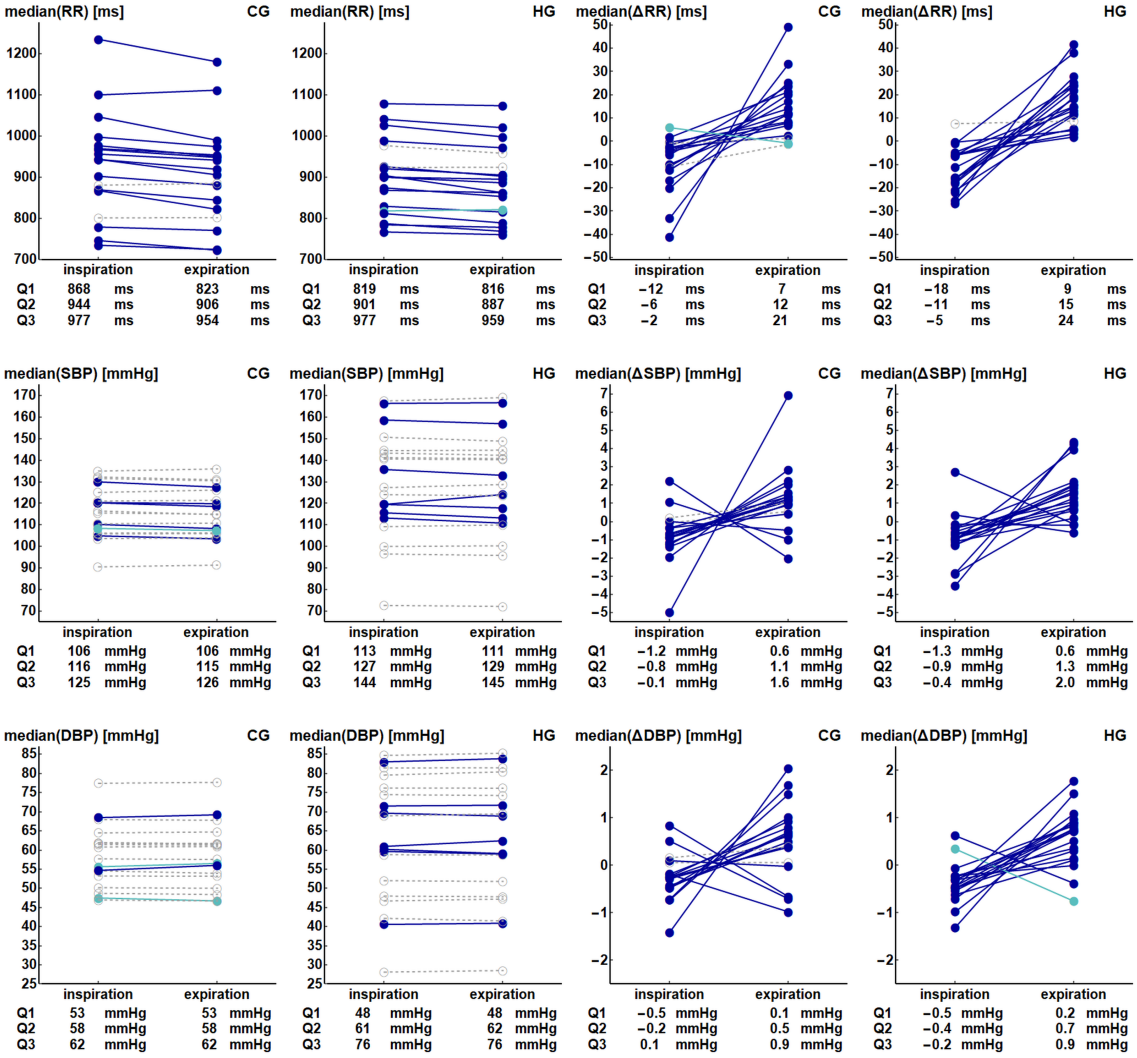

Figure 1: Medians for all analyzed signals. Medians for RR, SBP and DBP signals and their differences ΔRR, ΔSBP and ΔDBP are calculated from the data split into inspiration and expiration phase. CG – the healthy people group, HG – the hypertensive patients group.

The split-and-perturb decomposition of number-conserving cellular automata

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Number-conserving (or density-conserving) cellular automata (CAs) are of particular interest to mathematicians, computer scientists and physicists, as they can serve as models of physical phenomena obeying some conservation law. In higher dimensions, a very popular neighborhood used in modeling physical phenomena is the von Neumann neighborhood. Unfortunately, studying multidimensional CAs with this kind of neighborhood is not easy, because this neighborhood is not a Cartesian product of one-dimensional neighborhoods (in contrast to the Moore neighborhood). For this reason, for $d > 1$, the problem of number conservation in d-dimensional CAs with the von Neumann neighborhood has been poorly researched and understood so far, which results in a lack of theoretical background for the models used.

The family of d-dimensional number-conserving CAs with the von Neumann neighborhood not only depends on d but also on the considered state set Q. Until now, finding all number-conserving CAs for $d > 1$ was basically impossible – even for small Q. It is connected with the double exponential complexity of the problem: if the dimension is d, then the number of cells forming the von Neumann neighborhood equals $2d+1$, thus there are $|Q|^{|Q|^{2d+1}}$ CAs in this case. Even having some necessary and sufficient condition specifying whether the CA given is a number-conserving one, we are not able to check each of these $|Q|^{|Q|^{2d+1}}$ CAs.

We propose a new approach to study such CAs that works in any dimension d and for any set of states Q. Essentially, the local rule of a CA is decomposed into two parts: a *split function* and a *perturbation*. This decomposition is unique and, moreover, the set of all possible split functions has a very simple structure, while the set of all perturbations forms a linear space and is therefore very easy to describe in terms of a basis. We show how this approach allows to find all number-conserving CAs in many cases of d and Q. In particular, we can find all three-dimensional number-conserving CAs with three states, which until now was beyond the capabilities of computers. Moreover, the decomposition theorem turns out to be a convenient tool also for proving some general properties concerning number-conserving CAs and allows to revisit some unresolved questions in the field.

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