Preface

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Automata networks are discrete mathematical models rather easy to describe and to define that nevertheless admit richness and complexity in their dynamical behaviours. This gives them a specific ability to capture deep properties of natural phenomena, notably in physics and biology. Their intrinsic properties make them particularly appealing for both theoretical and applied studies. The broad framework of automata networks includes classical models such as cellular automata and Boolean networks, to name but a few. While cellular automata evolve on regular spaces where cells are governed by a common rule, Boolean networks evolve on general graphs where any node admits its own rule. While cellular automata are infinite by definition, Boolean networks are classically considered as finite. While cellular automata were introduced by von Neummann in the 1940's (based on works of Ulam) to study self-reproducing universal systems, Boolean networks were introduced by McCulloch and Pitts in the 1940's to study an analogy between human brains and universal computational machines. Despite these differences, cellular automata and Boolean networks are parts of automata networks and share for this reason fundamental qualitative properties that make them able to capture major features and intricacies of the real world: they are discrete models, in time and space, composed of entities (or cells, nodes, ...) that interact locally with each other over time. In that respect, automata networks are discrete dynamical systems that can be viewed as such from a purely mathematical point of view, or as models of computations from a theoretical computer science point of view, or as prediction or observability models of real phenomena from a modelling point of view. The articles in this volume illustrate this wide spectrum. They provide a good overview of recent developments and new results that reflect quite well the dynamism of the field.

This special issue was initiated at the 4th French-speaking meeting on *Interaction Networks – Foundations and Applications to Biology* that took

place at the CIRM in Marseilles in January 3rd-6th, 2017. This meeting was dedicated to Prof. Jacques Demongeot, on the occasion of his 70th birthday, a French physician and mathematician who is a pioneer in using discrete dynamical systems, in particular automata networks, in the framework of modelling complex biological systems. Moreover, in order to provide a more comprehensive presentation of the field, this special issue was not limited to articles related to talks given during the meeting (an international call for participations was widely distributed through multiple channels). A rigorous refereeing process resulted in eight papers accepted for this issue.

The first contribution is a tribute to Prof. Jacques Demongeot by Prof. Eric Goles.

The contribution of J. Demongeot and S. Sené[1] is not a standard article. It is rather a *manifesto* in favour of studying automata networks with less conventional update schedules, like the *block-parallel* one whose pertinence to model biological timers is notably emphasised on two genetic regulation networks.

The contribution of M. Gadouleau is a survey of known results on relations between the architecture (static view of the interaction between nodes) and the structure (or transition graph, the dynamical view of the trajectories between configurations) of finite automata networks with a given alphabet size. The focus is on three quantities: the minimum, average and maximum number of images, of periodic configurations and of fixed points.

The contribution of M. Chaves et al. deals with Boolean networks and presents a manner to analyse their dynamical behaviours by considering them as compositions, or rather feedback interconnections of modules. This modular vision provides a trustful method to construct a global asymptotic transition graph on the basis of modules local transition graphs.

The contribution of K. Perrot et al. provides a classification of the elementary cellular automata according to their sensitivity to specific fair and periodic update schedules defined as ordered partitions of the cell set, well known as block-sequential update schedules.

The contribution of T. Chatain et al. proposes to explore characteristics of Boolean networks through the formalism of Read Petri Nets (RPNs). Among the results presented, it develops several ideas about the encoding of the former into the latter, leading to the PSPACE-completeness of reachability problem, and about the synchronism sensitivity generalising known results to RPNs.

The contribution of D. Travisani et al. belongs to in the framework of biological modelling, that of *Clostridium difficile* infection that provokes chronic diarrhea. More precisely, by using a threshold Boolean network modelling the genetic control operated by *Clostridium difficile* infection, some

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[1]The refereeing of this paper was done properly and in a totally blind way w.r.t. S. Sené.

genetic regulations that could be targets of therapy are identified thanks to an evolutionary algorithm.

The contribution of E. De Maria et al. deals with the problem of learning parameters of spiking neural networks, by modelling the latter by means of timed automata (the neurons) and shared channels among them (the synaptic connections). The originality of using timed automata is validated theoretically, which leads to an algorithm for learning synaptic weight values so that a specific behaviour can emerge.

The contribution of P. Arrighi et al. is based on causal graph dynamics that constitute an extension of automata networks in the sense that the underlying architecture can vary. By adding some physics-like properties, computational results about reversibility are given that extend well-known similar results on cellular automata.

We would like to thank all the authors for the works that they share with us. Of course, we do not forget the rigorous efforts made by the referees that made this special issue possible. A warm thank you also to them.

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