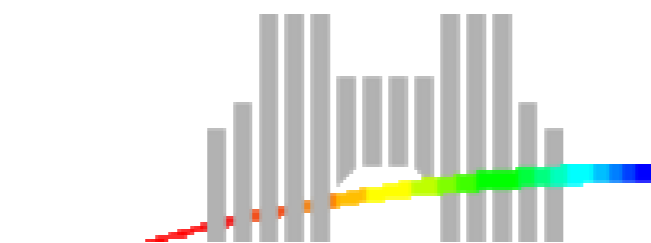




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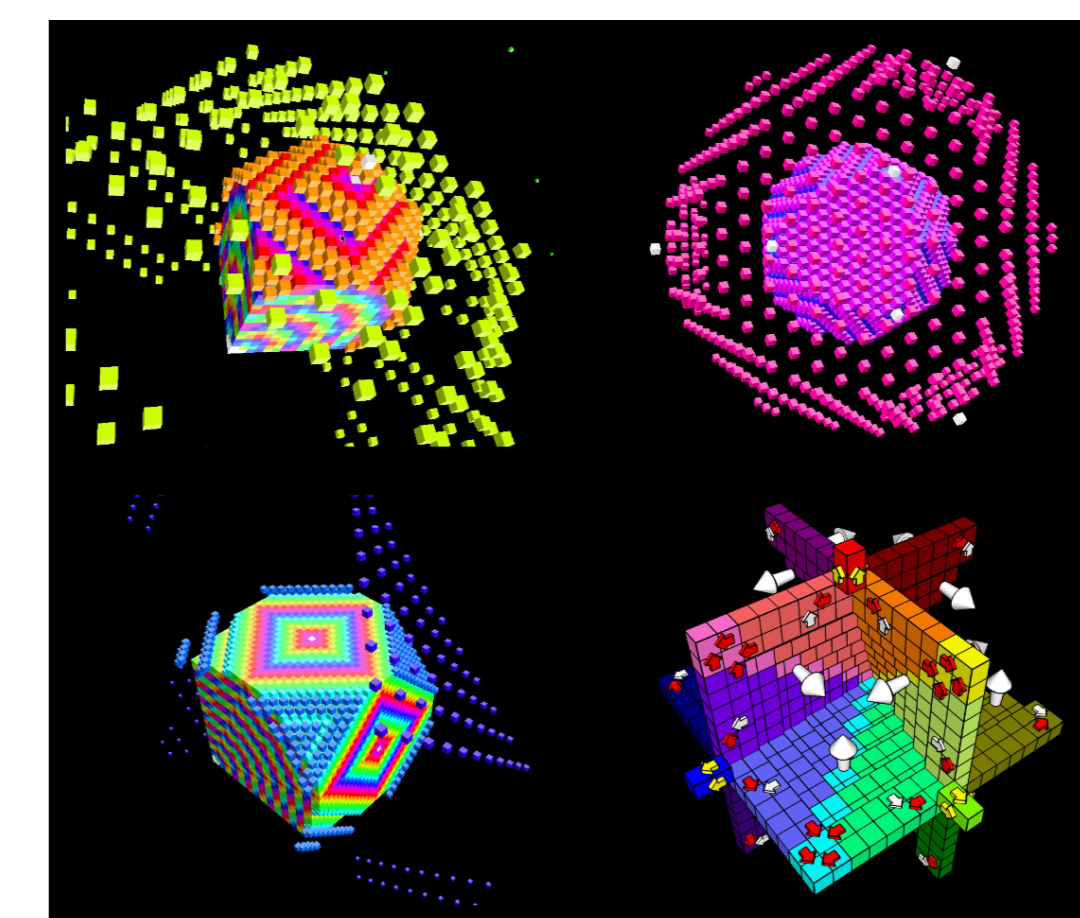
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MC2 : Modèles de Calcul et Complexité

Team objectives: We try to understand the power and limitations of **efficient algorithms**. Toward this end we design and analyze algorithms, and we obtain impossibility results (i.e., completeness results or whenever possible unconditional lower bounds).

Algorithms can be sequential, parallel, distributed, synchronous or asynchronous, deterministic, probabilistic or quantum. Besides computation time, one can try to optimize memory requirements or volume of data exchanged. In order to focus the attention on one (or a few) of these different aspects of computation, we study various **models of computation** such as, for example, synchronous and asynchronous cellular automata or quantum models of computation.

In our **complex systems** research we try to understand interactions between the microscopic and macroscopic levels. We pursue this goal both for idealized mathematical models such as cellular automata or boolean networks, and real systems such as gene regulation networks.



Cellular Automata, Tilings and Self-Assembly

A common theme to these 3 topics is the importance of discrete geometric structures within 2D or 3D Euclidean space.

Cellular automata are a longtime strength of the team. More recently, we have begun a **probabilistic analysis** of asynchronous cellular automata. We have studied two regimes: α -asynchronicity (i.i.d. updates with probability α) and full asynchronicity (1 update/step uniformly). In cellular automata, asynchronous behaviors differ drastically from their synchronous behaviors as witnessed by the relaxation time, i.e. the expected absorption time in final components of configurations. Some couplings with directed percolation were suspected from experimental studies about coalescence and were then formalized properly.

In the study of the combinatorics and the algorithmics of tilings, emphasis has been put on a recent self-assembly model introduced by bio-computer scientist E. Winfree (STOC 2000). In this model with **biochemistry** and **nanotechnology** flavors, tiles are squares with different types of glue on their sides which guide the way they aggregate. Some external parameters such as "temperature" modify the assembly. We could obtain size optimal and time optimal tiles sets for the construction of squares and later cubes. This is the only nontrivial 3D construction known as of today. In more classical settings, we have studied flip accessibility (sequences of local rearrangements) in lozenge tilings.

Algebraic Algorithms and Complexity

We have designed efficient algorithms for factoring sparse multivariate polynomials. This work has received a **distinguished paper award**.

In algebraic complexity we study algebraic versions of the **"P=NP ?" problem**:

- Valiant's problem: can the permanent of a matrix be evaluated in a polynomial number of arithmetic operations?
- The Blum-Shub-Smale problem: can the satisfiability of a system of polynomial equations (over the fields of real or complex numbers) be decided in a polynomial number of arithmetic operations and comparisons?

We have achieved a fairly good understanding of the relationships between these two problems and the classical "P=NP ?" problem. We have also obtained impossibility results in a restricted model (here, the graph-theoretic notion of **treewidth** plays an important role). Of course the general problems remain open! We are looking at promising approaches such as Mulmuley's Geometric Complexity Theory or the hardness versus randomness paradigm.

Quantum Computing

We have focused on quantum lower bounds, and in particular on quantum lower bounds for hidden subgroup problems. The hidden subgroup problem is an abstract framework in which most of the known "fast" quantum algorithms such as Shor's factoring algorithm can be cast. In this framework the algorithm has access to a **black-box function** f defined on a finite group G . This function is supposed to hide a subgroup $H \subseteq G$ in the sense that f is constant on each coset of H , and takes different values on different cosets. The goal of the quantum algorithm is to identify the hidden subgroup H by performing as few queries as possible to the black-box f .

We have obtained **optimal lower bounds** on the number of queries for all Abelian subgroups. Despite intensive work on lower bounds in the quantum computing community, this is still the only lower bound available for any hidden subgroup problem.

More recently, we have begun a systematic study of lower bounds for nonadaptive quantum algorithms. In this restricted model, a quantum algorithm must perform all of its queries to the black box simultaneously. This model is especially natural for hidden subgroup problems, since many of the known algorithms for such problems turn out to be nonadaptive.

Network Calculus

Network Calculus is a theory of deterministic queuing systems encountered in communications networks. Aiming at analyzing worst-case performance, it stores informations about the system in constraint functions which are combined thanks to special operators (mainly from $(\min, +)$ algebras) to output results. Though mathematical formulas exist for small but typical networks, little is known about the way to make the formulas effective with efficient algorithms and then to aggregate the computations to analyze large and complex networks.

With the perspective of offering an algorithmic toolbox and later an software, we have introduced a class of functions which is stable under Network Calculus operations. We have proposed algorithms to analyze complex networks with multiplexing and we have investigated some routing issues.

This is a new topic in team MC2, and it has already led to a **best-paper award** and industrial collaborations with **Onera** and **Thales**. The emphasis that we put on computational complexity analysis is rather new in the Network Calculus community. The challenge is to prove that this approach will be useful in the development of a concrete software tool.

Gene Regulatory Networks

We pursue this topic using theoretical and experimental approaches. Threshold networks are our main modeling paradigm: each node in the network represents a gene, each state variable is Boolean and represents the concentration of the gene's product. The weight on each edge represents the type and strength of the corresponding interaction. We have obtain some robustness results about the network's dynamics.

In collaboration with the plant reproduction lab at ENS Lyon, we have reconstructed the network corresponding to the first development stages of the flower of the **Ara-bidopsis plant**. The network's parameters were optimized by mathematical programming techniques in a collaboration with the LIX laboratory (Ecole Polytechnique).

A related event is the development of a general-purpose software platform for the simulation of complex systems. This platform has reached a level of maturity which makes it possible to create a **startup company**. The start-up is currently under incubation and should begin its operations around spring 2010.

Software Tools

- Software platform for complex systems simulation (E. Boix, J. Beltran, G. Chiquillo, A. Grignard, M. Morvan, M. Malaterre, R. Uribe).
- COINC - Computational Issues in Network Calculus (algorithmic contribution from E. Thierry).
- Cimula, a cellular automata analyzer (J.B. Rouquier, contribution from F. Becker).

Team members

- Permanent Researchers: Pascal KOIRAN (Professor, ENS Lyon), Natacha PORTIER (Associate Professor, ENS Lyon) Eric REMILA (Associate Professor, IUT Roanne), Eric THIERRY (Associate Professor, ENS Lyon).
- Engineers: Eric BOIX, Jorge BELTRAN, Gian CHIQUILLO, Arnaud GRIGNARD, Camilo LA ROTA, Mathieu MALATERRE, Ricardo URIBE.
- Doctoral Students: Irénée BRIQUEL, Bruno GRENET, Laurent JOUHET, Mathilde NOUAL, Julien ROBERT.