RESEARCH CENTER
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FIELD

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Section Scientific Foundations

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AIRSEA Project-Team

3. Research Program

3.1. Introduction

Recent events have raised questions regarding the social and economic implications of anthropic alterations of the Earth system, i.e. climate change and the associated risks of increasing extreme events. Ocean and atmosphere, coupled with other components (continent and ice) are the building blocks of the Earth system. A better understanding of the ocean atmosphere system is a key ingredient for improving prediction of such events. Numerical models are essential tools to understand processes, and simulate and forecast events at various space and time scales. Geophysical flows generally have a number of characteristics that make it difficult to model them. This justifies the development of specifically adapted mathematical methods:

- Geophysical flows are strongly non-linear. Therefore, they exhibit interactions between different scales, and unresolved small scales (smaller than mesh size) of the flows have to be **parameterized** in the equations.
- Geophysical fluids are non closed systems. They are open-ended in their scope for including and dynamically coupling different physical processes (e.g., atmosphere, ocean, continental water, etc). **Coupling** algorithms are thus of primary importance to account for potentially significant feedback.
- Numerical models contain parameters which cannot be estimated accurately either because they are difficult to measure or because they represent some poorly known subgrid phenomena. There is thus a need for **dealing with uncertainties**. This is further complicated by the turbulent nature of geophysical fluids.
- The computational cost of geophysical flow simulations is huge, thus requiring the use of **reduced models, multiscale methods** and the design of algorithms ready for **high performance computing** platforms.

Our scientific objectives are divided into four major points. The first objective focuses on developing advanced mathematical methods for both the ocean and atmosphere, and the coupling of these two components. The second objective is to investigate the derivation and use of model reduction to face problems associated with the numerical cost of our applications. The third objective is directed toward the management of uncertainty in numerical simulations. The last objective deals with efficient numerical algorithms for new computing platforms. As mentioned above, the targeted applications cover oceanic and atmospheric modeling and related extreme events using a hierarchy of models of increasing complexity.

3.2. Modeling for oceanic and atmospheric flows

Current numerical oceanic and atmospheric models suffer from a number of well-identified problems. These problems are mainly related to lack of horizontal and vertical resolution, thus requiring the parameterization of unresolved (subgrid scale) processes and control of discretization errors in order to fulfill criteria related to the particular underlying physics of rotating and strongly stratified flows. Oceanic and atmospheric coupled models are increasingly used in a wide range of applications from global to regional scales. Assessment of the reliability of those coupled models is an emerging topic as the spread among the solutions of existing models (e.g., for climate change predictions) has not been reduced with the new generation models when compared to the older ones.

Advanced methods for modeling 3D rotating and stratified flows The continuous increase of computational power and the resulting finer grid resolutions have triggered a recent regain of interest in numerical methods and their relation to physical processes. Going beyond present knowledge requires a better understanding of numerical dispersion/dissipation ranges and their connection to model fine scales. Removing the leading order truncation error of numerical schemes is thus an active topic of research and each mathematical tool has to adapt to the characteristics of three dimensional stratified and rotating flows. Studying the link between discretization errors and subgrid scale parameterizations is also arguably one of the main challenges.

Complexity of the geometry, boundary layers, strong stratification and lack of resolution are the main sources of discretization errors in the numerical simulation of geophysical flows. This emphasizes the importance of the definition of the computational grids (and coordinate systems) both in horizontal and vertical directions, and the necessity of truly multi resolution approaches. At the same time, the role of the small scale dynamics on large scale circulation has to be taken into account. Such parameterizations may be of deterministic as well as stochastic nature and both approaches are taken by the AIRSEA team. The design of numerical schemes consistent with the parameterizations is also arguably one of the main challenges for the coming years. This work is complementary and linked to that on parameters estimation described in 3.4 .

Ocean Atmosphere interactions and formulation of coupled models State-of-the-art climate models (CMs) are complex systems under continuous development. A fundamental aspect of climate modeling is the representation of air-sea interactions. This covers a large range of issues: parameterizations of atmospheric and oceanic boundary layers, estimation of air-sea fluxes, time-space numerical schemes, non conforming grids, coupling algorithms ...Many developments related to these different aspects were performed over the last 10-15 years, but were in general conducted independently of each other.

The aim of our work is to revisit and enrich several aspects of the representation of air-sea interactions in CMs, paying special attention to their overall consistency with appropriate mathematical tools. We intend to work consistently on the physics and numerics. Using the theoretical framework of global-in-time Schwarz methods, our aim is to analyze the mathematical formulation of the parameterizations in a coupling perspective. From this study, we expect improved predictability in coupled models (this aspect will be studied using techniques described in 3.4). Complementary work on space-time nonconformities and acceleration of convergence of Schwarz-like iterative methods (see 7.1.2) are also conducted.

3.3. Model reduction / multiscale algorithms

The high computational cost of the applications is a common and major concern to have in mind when deriving new methodological approaches. This cost increases dramatically with the use of sensitivity analysis or parameter estimation methods, and more generally with methods that require a potentially large number of model integrations.

A dimension reduction, using either stochastic or deterministic methods, is a way to reduce significantly the number of degrees of freedom, and therefore the calculation time, of a numerical model.

Model reduction Reduction methods can be deterministic (proper orthogonal decomposition, other reduced bases) or stochastic (polynomial chaos, Gaussian processes, kriging), and both fields of research are very active. Choosing one method over another strongly depends on the targeted application, which can be as varied as real-time computation, sensitivity analysis (see e.g., section 7.3.1) or optimisation for parameter estimation (see below).

Our goals are multiple, but they share a common need for certified error bounds on the output. Our team has a 4-year history of working on certified reduction methods and has a unique positioning at the interface between deterministic and stochastic approaches. Thus, it seems interesting to conduct a thorough comparison of the two alternatives in the context of sensitivity analysis. Efforts will also be directed toward the development of efficient greedy algorithms for the reduction, and the derivation of goal-oriented sharp error bounds for non linear models and/or non linear outputs of interest. This will be complementary to our work on the deterministic reduction of parametrized viscous Burgers and Shallow Water equations where the objective is to obtain sharp error bounds to provide confidence intervals for the estimation of sensitivity indices.

Reduced models for coupling applications Global and regional high-resolution oceanic models are either coupled to an atmospheric model or forced at the air-sea interface by fluxes computed empirically preventing proper physical feedback between the two media. Thanks to high-resolution observational studies, the existence of air-sea interactions at oceanic mesoscales (i.e., at $\mathcal{O}(1km)$ scales) have been unambiguously shown. Those interactions can be represented in coupled models only if the oceanic and atmospheric models are run on the same high-resolution computational grid, and are absent in a forced mode. Fully coupled models

at high-resolution are seldom used because of their prohibitive computational cost. The derivation of a reduced model as an alternative between a forced mode and the use of a full atmospheric model is an open problem.

Multiphysics coupling often requires iterative methods to obtain a mathematically correct numerical solution. To mitigate the cost of the iterations, we will investigate the possibility of using reduced-order models for the iterative process. We will consider different ways of deriving a reduced model: coarsening of the resolution, degradation of the physics and/or numerical schemes, or simplification of the governing equations. At a mathematical level, we will strive to study the well-posedness and the convergence properties when reduced models are used. Indeed, running an atmospheric model at the same resolution as the ocean model is generally too expensive to be manageable, even for moderate resolution applications. To account for important fine-scale interactions in the computation of the air-sea boundary condition, the objective is to derive a simplified boundary layer model that is able to represent important 3D turbulent features in the marine atmospheric boundary layer.

Reduced models for multiscale optimization The field of multigrid methods for optimisation has known a tremendous development over the past few decades. However, it has not been applied to oceanic and atmospheric problems apart from some crude (non-converging) approximations or applications to simplified and low dimensional models. This is mainly due to the high complexity of such models and to the difficulty in handling several grids at the same time. Moreover, due to complex boundaries and physical phenomena, the grid interactions and transfer operators are not trivial to define.

Multigrid solvers (or multigrid preconditioners) are efficient methods for the solution of variational data assimilation problems. We would like to take advantage of these methods to tackle the optimization problem in high dimensional space. High dimensional control space is obtained when dealing with parameter fields estimation, or with control of the full 4D (space time) trajectory. It is important since it enables us to take into account model errors. In that case, multigrid methods can be used to solve the large scales of the problem at a lower cost, this being potentially coupled with a scale decomposition of the variables themselves.

3.4. Dealing with uncertainties

There are many sources of uncertainties in numerical models. They are due to imperfect external forcing, poorly known parameters, missing physics and discretization errors. Studying these uncertainties and their impact on the simulations is a challenge, mostly because of the high dimensionality and non-linear nature of the systems. To deal with these uncertainties we work on three axes of research, which are linked: sensitivity analysis, parameter estimation and risk assessment. They are based on either stochastic or deterministic methods.

Sensitivity analysis Sensitivity analysis (SA), which links uncertainty in the model inputs to uncertainty in the model outputs, is a powerful tool for model design and validation. First, it can be a pre-stage for parameter estimation (see 3.4), allowing for the selection of the more significant parameters. Second, SA permits understanding and quantifying (possibly non-linear) interactions induced by the different processes defining e.g., realistic ocean atmosphere models. Finally SA allows for validation of models, checking that the estimated sensitivities are consistent with what is expected by the theory. On ocean, atmosphere and coupled systems, only first order deterministic SA are performed, neglecting the initialization process (data assimilation). AIRSEA members and collaborators proposed to use second order information to provide consistent sensitivity measures, but so far it has only been applied to simple academic systems. Metamodels are now commonly used, due to the cost induced by each evaluation of complex numerical models: mostly Gaussian processes, whose probabilistic framework allows for the development of specific adaptive designs, and polynomial chaos not only in the context of intrusive Galerkin approaches but also in a black-box approach. Until recently, global SA was based primarily on a set of engineering practices. New mathematical and methodological developments have led to the numerical computation of Sobol' indices, with confidence intervals assessing for both metamodel and estimation errors. Approaches have also been extended to the case of dependent entries, functional inputs and/or output and stochastic numerical codes. Other types of indices and generalizations of Sobol' indices have also been introduced.

Concerning the stochastic approach to SA we plan to work with parameters that show spatio-temporal dependencies and to continue toward more realistic applications where the input space is of huge dimension with highly correlated components. Sensitivity analysis for dependent inputs also introduces new challenges. In our applicative context, it would seem prudent to carefully learn the spatio-temporal dependences before running a global SA. In the deterministic framework we focus on second order approaches where the sought sensitivities are related to the optimality system rather than to the model; i.e., we consider the whole forecasting system (model plus initialization through data assimilation).
All these methods allow for computing sensitivities and more importantly a posteriori error statistics.

Parameter estimation Advanced parameter estimation methods are barely used in ocean, atmosphere and coupled systems, mostly due to a difficulty of deriving adequate response functions, a lack of knowledge of these methods in the ocean-atmosphere community, and also to the huge associated computing costs. In the presence of strong uncertainties on the model but also on parameter values, simulation and inference are closely associated. Filtering for data assimilation and Approximate Bayesian Computation (ABC) are two examples of such association.
Stochastic approach can be compared with the deterministic approach, which allows to determine the sensitivity of the flow to parameters and optimize their values relying on data assimilation. This approach is already shown to be capable of selecting a reduced space of the most influent parameters in the local parameter space and to adapt their values in view of correcting errors committed by the numerical approximation. This approach assumes the use of automatic differentiation of the source code with respect to the model parameters, and optimization of the obtained raw code.

AIRSEA assembles all the required expertise to tackle these difficulties. As mentioned previously, the choice of parameterization schemes and their tuning has a significant impact on the result of model simulations. Our research will focus on parameter estimation for parameterized Partial Differential Equations (PDEs) and also for parameterized Stochastic Differential Equations (SDEs). Deterministic approaches are based on optimal control methods and are local in the parameter space (i.e., the result depends on the starting point of the estimation) but thanks to adjoint methods they can cope with a large number of unknowns that can also vary in space and time. Multiscale optimization techniques as described in 7.2.1 will be one of the tools used. This in turn can be used either to propose a better (and smaller) parameter set or as a criterion for discriminating parameterization schemes. Statistical methods are global in the parameter state but may suffer from the curse of dimensionality. However, the notion of parameter can also be extended to functional parameters. We may consider as parameter a functional entity such as a boundary condition on time, or a probability density function in a stationary regime. For these purposes, non-parametric estimation will also be considered as an alternative.

Risk assessment Risk assessment in the multivariate setting suffers from a lack of consensus on the choice of indicators. Moreover, once the indicators are designed, it still remains to develop estimation procedures, efficient even for high risk levels. Recent developments for the assessment of financial risk have to be considered with caution as methods may differ pertaining to general financial decisions or environmental risk assessment. Modeling and quantifying uncertainties related to extreme events is of central interest in environmental sciences. In relation to our scientific targets, risk assessment is very important in several areas: hydrological extreme events, cyclone intensity, storm surges...Environmental risks most of the time involve several aspects which are often correlated. Moreover, even in the ideal case where the focus is on a single risk source, we have to face the temporal and spatial nature of environmental extreme events. The study of extremes within a spatio-temporal framework remains an emerging field where the development of adapted statistical methods could lead to major progress in terms of geophysical understanding and risk assessment thus coupling data and model information for risk assessment.

Based on the above considerations we aim to answer the following scientific questions: how to measure risk in a multivariate/spatial framework? How to estimate risk in a non stationary context? How to reduce dimension (see 3.3) for a better estimation of spatial risk?

Extreme events are rare, which means there is little data available to make inferences of risk measures. Risk assessment based on observation therefore relies on multivariate extreme value theory. Interacting particle systems for the analysis of rare events is commonly used in the community of computer experiments. An open question is the pertinence of such tools for the evaluation of environmental risk.
Most numerical models are unable to accurately reproduce extreme events. There is therefore a real need to develop efficient assimilation methods for the coupling of numerical models and extreme data.

3.5. High performance computing

Methods for sensitivity analysis, parameter estimation and risk assessment are extremely costly due to the necessary number of model evaluations. This number of simulations require considerable computational resources, depends on the complexity of the application, the number of input variables and desired quality of approximations. To this aim, the AIRSEA team is an intensive user of HPC computing platforms, particularly grid computing platforms. The associated grid deployment has to take into account the scheduling of a huge number of computational requests and the links with data-management between these requests, all of these as automatically as possible. In addition, there is an increasing need to propose efficient numerical algorithms specifically designed for new (or future) computing architectures and this is part of our scientific objectives. According to the computational cost of our applications, the evolution of high performance computing platforms has to be taken into account for several reasons. While our applications are able to exploit space parallelism to its full extent (oceanic and atmospheric models are traditionally based on a spatial domain decomposition method), the spatial discretization step size limits the efficiency of traditional parallel methods. Thus the inherent parallelism is modest, particularly for the case of relative coarse resolution but with very long integration time (e.g., climate modeling). Paths toward new programming paradigms are thus needed. As a step in that direction, we plan to focus our research on parallel in time methods.

New numerical algorithms for high performance computing Parallel in time methods can be classified into three main groups. In the first group, we find methods using parallelism across the method, such as parallel integrators for ordinary differential equations. The second group considers parallelism across the problem. Falling into this category are methods such as waveform relaxation where the space-time system is decomposed into a set of subsystems which can then be solved independently using some form of relaxation techniques or multigrid reduction in time. The third group of methods focuses on parallelism across the steps. One of the best known algorithms in this family is parareal. Other methods combining the strengths of those listed above (e.g., PFASST) are currently under investigation in the community.

Parallel in time methods are iterative methods that may require a large number of iteration before convergence. Our first focus will be on the convergence analysis of parallel in time (Parareal / Schwarz) methods for the equation systems of oceanic and atmospheric models. Our second objective will be on the construction of fast (approximate) integrators for these systems. This part is naturally linked to the model reduction methods of section (7.2.2). Fast approximate integrators are required both in the Schwarz algorithm (where a first guess of the boundary conditions is required) and in the Parareal algorithm (where the fast integrator is used to connect the different time windows). Our main application of these methods will be on climate (i.e., very long time) simulations. Our second application of parallel in time methods will be in the context of optimization methods. In fact, one of the major drawbacks of the optimal control techniques used in 3.4 is a lack of intrinsic parallelism in comparison with ensemble methods. Here, parallel in time methods also offer ways to better efficiency. The mathematical key point is centered on how to efficiently couple two iterative methods (i.e., parallel in time and optimization methods).

ARIC Project-Team

3. Research Program

3.1. Efficient approximation methods

3.1.1. Computer algebra generation of certified approximations

We plan to focus on the generation of certified and efficient approximations for solutions of linear differential equations. These functions cover many classical mathematical functions and many more can be built by combining them. One classical target area is the numerical evaluation of elementary or special functions. This is currently performed by code specifically handcrafted for each function. The computation of approximations and the error analysis are major steps of this process that we want to automate, in order to reduce the probability of errors, to allow one to implement "rare functions", to quickly adapt a function library to a new context: new processor, new requirements – either in terms of speed or accuracy.

In order to significantly extend the current range of functions under consideration, several methods originating from approximation theory have to be considered (divergent asymptotic expansions; Chebyshev or generalized Fourier expansions; Padé approximants; fixed point iterations for integral operators). We have done preliminary work on some of them. Our plan is to revisit them all from the points of view of effectivity, computational complexity (exploiting linear differential equations to obtain efficient algorithms), as well as in their ability to produce provable error bounds. This work is to constitute a major progress towards the automatic generation of code for moderate or arbitrary precision evaluation with good efficiency. Other useful, if not critical, applications are certified quadrature, the determination of certified trajectories of spatial objects and many more important questions in optimal control theory.

3.1.2. Digital Signal Processing

As computer arithmeticians, a wide and important target for us is the design of efficient and certified linear filters in digital signal processing (DSP). Actually, following the advent of MATLAB as the major tool for filter design, the DSP experts now systematically delegate to MATLAB all the part of the design related to numerical issues. And yet, various key MATLAB routines are neither optimized, nor certified. Therefore, there is a lot of room for enhancing numerous DSP numerical implementations and there exist several promising approaches to do so.

The main challenge that we want to address over the next period is the development and the implementation of optimal methods for rounding the coefficients involved in the design of the filter. If done in a naive way, this rounding may lead to a significant loss of performance. We will study in particular FIR and IIR filters.

3.1.3. Table Maker's Dilemma (TMD)

There is a clear demand for hardest-to-round cases, and several computer manufacturers recently contacted us to obtain new cases. These hardest-to-round cases are a precious help for building libraries of correctly rounded mathematical functions. The current code, based on Lefèvre's algorithm, will be rewritten and formal proofs will be done.

We plan to use uniform polynomial approximation and diophantine techniques in order to tackle the case of the IEEE quad precision, and analytic number theory techniques (exponential sums estimates) for counting the hardest-to-round cases.

3.2. Lattices: algorithms and cryptology

Lattice-based cryptography (LBC) is an utterly promising, attractive (and competitive) research ground in cryptography, thanks to a combination of unmatched properties:

- **Improved performance.** LBC primitives have low asymptotic costs, but remain cumbersome in practice (e.g., for parameters achieving security against computations of up to 2100 bit operations). To address this limitation, a whole branch of LBC has evolved where security relies on the restriction of lattice problems to a family of more structured lattices called *ideal lattices*. Primitives based on such lattices can have quasi-optimal costs (i.e., quasi-constant amortized complexities), outperforming all contemporary primitives. This asymptotic performance sometimes translates into practice, as exemplified by NTRUEncrypt.
- **Improved security.** First, lattice problems seem to remain hard even for quantum computers. Moreover, the security of most of LBC holds under the assumption that standard lattice problems are hard in the worst case. Oppositely, contemporary cryptography assumes that specific problems are hard with high probability, for some precise input distributions. Many of these problems were artificially introduced for serving as a security foundation of new primitives.
- **Improved flexibility.** The master primitives (encryption, signature) can all be realized based on worst-case (ideal) lattice assumptions. More evolved primitives such as ID-based encryption (where the public key of a recipient can be publicly derived from its identity) and group signatures, that were the playing-ground of pairing-based cryptography (a subfield of elliptic curve cryptography), can also be realized in the LBC framework, although less efficiently and with restricted security properties. More intriguingly, lattices have enabled long-wished-for primitives. The most notable example is homomorphic encryption, enabling computations on encrypted data. It is the appropriate tool to securely outsource computations, and will help overcome the privacy concerns that are slowing down the rise of the cloud.

We work on three directions, detailed now.

3.2.1. Lattice algorithms

All known lattice reduction algorithms follow the same design principle: perform a sequence of small elementary steps transforming a current basis of the input lattice, where these steps are driven by the Gram-Schmidt orthogonalisation of the current basis.

In the short term, we will fully exploit this paradigm, and hopefully lower the cost of reduction algorithms with respect to the lattice dimension. We aim at asymptotically fast algorithms with complexity bounds closer to those of basic and normal form problems (matrix multiplication, Hermite normal form). In the same vein, we plan to investigate the parallelism potential of these algorithms.

Our long term goal is to go beyond the current design paradigm, to reach better trade-offs between run-time and shortness of the output bases. To reach this objective, we first plan to strengthen our understanding of the interplay between lattice reduction and numerical linear algebra (how far can we push the idea of working on approximations of a basis?), to assess the necessity of using the Gram-Schmidt orthogonalisation (e.g., to obtain a weakening of LLL-reduction that would work up to some stage, and save computations), and to determine whether working on generating sets can lead to more efficient algorithms than manipulating bases. We will also study algorithms for finding shortest non-zero vectors in lattices, and in particular look for quantum accelerations.

We will implement and distribute all algorithmic improvements, e.g., within the fplll library. We are interested in high performance lattice reduction computations (see application domains below), in particular in connection with/continuation of the HPAC ANR project (algebraic computing and high performance consortium).

3.2.2. Lattice-based cryptography

Our long term goal is to demonstrate the superiority of lattice-based cryptography over contemporary public-key cryptographic approaches. For this, we will 1- Strengthen its security foundations, 2- Drastically improve the performance of its primitives, and 3- Show that lattices allow to devise advanced and elaborate primitives.

The practical security foundations will be strengthened by the improved understanding of the limits of lattice reduction algorithms (see above). On the theoretical side, we plan to attack two major open problems: Are ideal lattices (lattices corresponding to ideals in rings of integers of number fields) computationally as hard to handle as arbitrary lattices? What is the quantum hardness of lattice problems?

Lattice-based primitives involve two types of operations: sampling from discrete Gaussian distributions (with lattice supports), and arithmetic in polynomial rings such as $(\mathbb{Z}/q\mathbb{Z})[x]/(x^n+1)$ with n a power of 2. When such polynomials are used (which is the case in all primitives that have the potential to be practical), then the underlying algorithmic problem that is assumed hard involves ideal lattices. This is why it is crucial to precisely understand the hardness of lattice problems for this family. We will work on improving both types of operations, both in software and in hardware, concentrating on values of q and n providing security. As these problems are very arithmetic in nature, this will naturally be a source of collaboration with the other themes of the AriC team.

Our main objective in terms of cryptographic functionality will be to determine the extent to which lattices can help securing cloud services. For example, is there a way for users to delegate computations on their outsourced dataset while minimizing what the server eventually learns about their data? Can servers compute on encrypted data in an efficiently verifiable manner? Can users retrieve their files and query remote databases anonymously provided they hold appropriate credentials? Lattice-based cryptography is the only approach so far that has allowed to make progress into those directions. We will investigate the practicality of the current constructions, the extension of their properties, and the design of more powerful primitives, such as functional encryption (allowing the recipient to learn only a function of the plaintext message). To achieve these goals, we will in particular focus on cryptographic multilinear maps.

This research axis of AriC is gaining strength thanks to the recruitment of Benoit Libert. We will be particularly interested in the practical and operational impacts, and for this reason we envision a collaboration with an industrial partner.

3.2.3. Application domains

- Diophantine equations. Lattice reduction algorithms can be used to solve diophantine equations, and in particular to find simultaneous rational approximations to real numbers. We plan to investigate the interplay between this algorithmic task, the task of finding integer relations between real numbers, and lattice reduction. A related question is to devise LLL-reduction algorithms that exploit specific shapes of input bases. This will be done within the ANR DynA3S project.
- Communications. We will continue our collaboration with Cong Ling (Imperial College) on the use of lattices in communications. We plan to work on the wiretap channel over a fading channel (modeling cell phone communications in a fast moving environment). The current approaches rely on ideal lattices, and we hope to be able to find new approaches thanks to our expertise on them due to their use in lattice-based cryptography. We will also tackle the problem of sampling vectors from Gaussian distributions with lattice support, for a very small standard deviation parameter. This would significantly improve current schemes for communication schemes based on lattices, as well as several cryptographic primitives.
- Cryptanalysis of variants of RSA. Lattices have been used extensively to break variants of the RSA encryption scheme, via Coppersmith's method to find small roots of polynomials. We plan to work with Nadia Heninger (U. of Pennsylvania) on improving these attacks, to make them more practical. This is an excellent test case for testing the practicality of LLL-type algorithm. Nadia Heninger has a strong experience in large scale cryptanalysis based on Coppersmith's method (http://smartfacts.cr.yp.to/)

3.3. Algebraic computing and high performance kernels

The main theme here is the study of fundamental operations ("kernels") on a hierarchy of symbolic or numeric data types spanning integers, floating-point numbers, polynomials, power series, as well as matrices of all these. Fundamental operations include basic arithmetic (e.g., how to multiply or how to invert) common to all

such data, as well as more specific ones (change of representation/conversions, GCDs, determinants, etc.). For such operations, which are ubiquitous and at the very core of computing (be it numerical, symbolic, or hybrid numeric-symbolic), our goal is to ensure both high performance and reliability.

3.3.1. Algorithms

On the symbolic side, we will focus on the design and complexity analysis of algorithms for matrices over various domains (fields, polynomials, integers) and possibly with specific properties (structure). So far, our algorithmic improvements for polynomial matrices and structured matrices have been obtained in a rather independent way. Both types are well known to have much in common, but this is sometimes not reflected by the complexities obtained, especially for applications in cryptology and coding theory. Our goal in this area is thus to explore these connections further, to provide a more unified treatment, and eventually bridge these complexity gaps, A first step towards this goal will be the design of enhanced algorithms for various generalizations of Hermite-Padé approximation; in the context of list decoding, this should in particular make it possible to match or even improve over the structured-matrix approach, which is so far the fastest known.

On the other hand we will focus on the design of algorithms for certified computing. We will study the use of various representations, such as mid-rad for classical interval arithmetic, or affine arithmetic. We will explore the impact of precision tuning in intermediate computations, possibly dynamically, on the accuracy of the results (e.g. for iterative refinement and Newton iterations). We will continue to revisit and improve the classical error bounds of numerical linear algebra in the light of the subtleties of IEEE floating-point arithmetic.

Our goals in linear algebra and lattice basis reduction that have been detailed above in Section 3.2 will be achieved in the light of a hybrid symbolic-numeric approach.

3.3.2. Computer arithmetic

Our work on certified computing and especially on the analysis of algorithms in floating-point arithmetic leads us to manipulate floating-point data in their greatest generality, that is, as symbolic expressions in the base and the precision. Our aim here is thus to develop theorems as well as efficient data structures and algorithms for handling such quantities by computer rather than by hand as we do now. The main outcome would be a "symbolic floating-point toolbox" which provides a way to check automatically the certificates of optimality we have obtained on the error bounds of various numerical algorithms.

We will also work on the interplay between floating-point and integer arithmetics. Currently, small numerical kernels like an exponential or a 2×2 determinant are typically written using exclusively one of these two kinds of arithmetic. However, modern processors now have hardware support for both floating-point and integer arithmetics, often with vector (SIMD) extensions, and an important question is how to make the best use of all such capabilities to optimize for both accuracy and efficiency.

A third direction will be to work on algorithms for performing correctly-rounded arithmetic operations in medium precision as efficiently and reliably as possible. Indeed, many numerical problems require higher precision than the conventional floating-point (single, double) formats. One solution is to use multiple precision libraries, such as GNU MPFR, which allow the manipulation of very high precision numbers, but their generality (they are able to handle numbers with millions of digits) is a quite heavy alternative when high performance is needed. Our objective here is thus to design a multiple precision arithmetic library that would allow to tackle problems where a precision of a few hundred bits is sufficient, but which have strong performance requirements. Applications include the process of long-term iteration of chaotic dynamical systems ranging from the classical Henon map to calculations of planetary orbits. The designed algorithms will be formally proved.

Finally, our work on the IEEE 1788 standard leads naturally to the development of associated reference libraries for interval arithmetic. A first direction will be to implement IEEE 1788 interval arithmetic within MPFI, our library for interval arithmetic using the arbitrary precision floating-point arithmetic provided by MPFR: indeed, MPFI has been originally developed with definitions and handling of exceptions which are not compliant with IEEE 1788. Another one will be to provide efficient support for multiple-precision intervals,

in mid-rad representation and by developing MPFR-based code-generation tools aimed at handling families of functions.

3.3.3. High-performance algorithms and software

The algorithmic developments for medium precision floating-point arithmetic discussed above will lead to high performance implementations on GPUs. As a follow-up of the HPAC project (which ended in December 2015) we shall pursue the design and implementation of high performance linear algebra primitives and algorithms.

AVALON Project-Team

3. Research Program

3.1. Energy Application Profiling and Modelization

International roadmaps schedule to build exascale systems by the 2018 time frame. According to the Top500 list published in November 2013, the most powerful supercomputer is the Tianhe-2 platform, a machine with more than 3,000,000 cores. It consumes more than 17 MW for a maximum performance of 33 PFlops while the Defense Advanced Research Projects Agency (DARPA) has set to 20 MW the maximum energy consumption of an exascale supercomputer [40].

Energy efficiency is therefore a major challenge for building next generation large scale platforms. The targeted platforms will gather hundreds of million cores, low power servers, or CPUs. Besides being very important, their power consumption will be dynamic and irregular.

Thus, to consume energy efficiently, we aim at investigating two research directions. First, we need to improve the measure, the understanding, and the analysis of the large-scale platform energy consumption. Unlike approaches [41] that mix the usage of internal and external wattmeters on a small set of resources, we target high frequency and precise internal and external energy measurements of each physical and virtual resources on large scale distributed systems.

Secondly, we need to find new mechanisms that consume less and better on such platforms. Combined with hardware optimizations, several works based on shutdown or slowdown approaches aim at reducing energy consumption of distributed platforms and applications. To consume less, we first plan to explore the provision of accurate estimation of the energy consumed by applications without pre-executing and knowing them while most of the works try to do it based on in-depth application knowledge (code instrumentation [44], phase detection for specific HPC applications [49], etc.). As a second step, we aim at designing a framework model that allows interactions, dialogues and decisions taken in cooperation between the user/application, the administrator, the resource manager, and the energy supplier. While smart grid is one of the last killer scenarios for networks, electrical provisioning of next generation large IT infrastructures remains a challenge.

3.2. Data-intensive Application Profiling, Modeling, and Management

Recently, the term “Big Data” has emerged to design data sets or collections so large that they become intractable for classical tools. This term is most of the time implicitly linked to “analytics” to refer to issues such as curation, storage, search, sharing, analysis, and visualization. However, the Big Data challenge is not limited to data-analytics, a field that is well covered by programming languages and run-time systems such as Map-Reduce. It also encompasses data-intensive applications. These applications can be sorted into two categories. In High Performance Computing (HPC), data-intensive applications leverage post-petascale infrastructures to perform highly parallel computations on large amount of data, while in High Throughput Computing (HTC), a large amount of independent and sequential computations are performed on huge data collections.

These two types of data-intensive applications (HTC and HPC) raise challenges related to profiling and modeling that the Avalon team proposes to address. While the characteristics of data-intensive applications are very different, our work will remain coherent and focused. Indeed, a common goal will be to acquire a better understanding of both the applications and the underlying infrastructures running them to propose the best match between application requirements and infrastructure capacities. To achieve this objective, we will extensively rely on logging and profiling in order to design sound, accurate, and validated models. Then, the proposed models will be integrated and consolidated within a single simulation framework (SIMGRID). This will allow us to explore various potential “what-if?” scenarios and offer objective indicators to select interesting infrastructure configurations that match application specificities.

Another challenge is the ability to mix several heterogeneous infrastructures that scientists have at their disposal (*e.g.,* Grids, Clouds, and Desktop Grids) to execute data-intensive applications. Leveraging the aforementioned results, we will design strategies for efficient data management service for hybrid computing infrastructures.

3.3. Resourc-Agnostic Application Description Model

When programming in parallel, users expect to obtain performance improvement, whatever the cost is. For long, parallel machines have been simple enough to let a user program them given a minimal abstraction of their hardware. For example, MPI [43] exposes the number of nodes but hides the complexity of network topology behind a set of collective operations; OpenMP [47] simplifies the management of threads on top of a shared memory machine while OpenACC [46] aims at simplifying the use of GPGPU.

However, machines and applications are getting more and more complex so that the cost of manually handling an application is becoming very high [42]. Hardware complexity also stems from the unclear path towards next generations of hardware coming from the frequency wall: multi-core CPU, many-core CPU, GPGPUs, deep memory hierarchy, etc. have a strong impact on parallel algorithms. Hence, even though an abstract enough parallel language (UPC, Fortress, X10, etc.) succeeds, it will still face the challenge of supporting distinct codes corresponding to different algorithms corresponding to distinct hardware capacities.

Therefore, the challenge we aim to address is to define a model, for describing the structure of parallel and distributed applications that enables code variations but also efficient executions on parallel and distributed infrastructures. Indeed, this issue appears for HPC applications but also for cloud oriented applications. The challenge is to adapt an application to user constraints such as performance, energy, security, etc.

Our approach is to consider component based models [50] as they offer the ability to manipulate the software architecture of an application. To achieve our goal, we consider a "compilation" approach that transforms a resource-agnostic application description into a resource-specific description. The challenge is thus to determine a component based model that enables to efficiently compute application mapping while being tractable. In particular, it has to provide an efficient support with respect to application and resource elasticity, energy consumption and data management. OpenMP runtime is a specific use case that we target.

3.4. Application Mapping and Scheduling

This research axis is at the crossroad of the Avalon team. In particular, it gathers results of the three other research axis. We plan to consider application mapping and scheduling through the following three issues.

3.4.1. Application Mapping and Software Deployment

Application mapping and software deployment consist in the process of assigning distributed pieces of software to a set of resources. Resources can be selected according to different criteria such as performance, cost, energy consumption, security management, etc. A first issue is to select resources at application launch time. With the wide adoption of elastic platforms, *i.e.,* platforms that let the number of resources allocated to an application to be increased or decreased during its execution, the issue is also to handle resource selection at runtime.

The challenge in this context corresponds to the mapping of applications onto distributed resources. It will consist in designing algorithms that in particular take into consideration application profiling, modeling, and description.

A particular facet of this challenge is to propose scheduling algorithms for dynamic and elastic platforms. As the amount of elements can vary, some kind of control of the platforms must be used accordingly to the scheduling.

3.4.2. Non-Deterministic Workflow Scheduling

Many scientific applications are described through workflow structures. Due to the increasing level of parallelism offered by modern computing infrastructures, workflow applications now have to be composed not only of sequential programs, but also of parallel ones. New applications are now built upon workflows with conditionals and loops (also called non-deterministic workflows).

These workflows can not be scheduled beforehand. Moreover cloud platforms bring on-demand resource provisioning and pay-as-you-go billing models. Therefore, there is a problem of resource allocation for non-deterministic workflows under budget constraints and using such an elastic management of resources.

Another important issue is data management. We need to schedule the data movements and replications while taking job scheduling into account. If possible, data management and job scheduling should be done at the same time in a closely coupled interaction.

3.4.3. Security Management in Cloud Infrastructure

Security has been proven to be sometimes difficult to obtain [48] and several issues have been raised in Clouds. Nowadays virtualization is used as the sole mechanism to secure different users sharing resources on Clouds. But, due to improper virtualization of all the components of Clouds (such as micro-architectural components), data leak and modification can occur. Accordingly, next-generation protection mechanisms are required to enforce security on Clouds and provide a way to cope with the current limitation of virtualization mechanisms.

As we are dealing with parallel and distributed applications, security mechanisms must be able to cope with multiple machines. Our approach is to combine a set of existing and novel security mechanisms that are spread in the different layers and components of Clouds in order to provide an in-depth and end-to-end security on Clouds. To do it, our first challenge is to define a generic model to express security policies.

Our second challenge is to work on security-aware resource allocation algorithms. The goal of such algorithms is to find a good trade-off between security and unshared resources. Consequently, they can limit resources sharing to increase security. It leads to complex trade-off between infrastructure consolidation, performance, and security.

BEAGLE Project-Team

3. Research Program

3.1. Introduction

As stated above, the research topics of the BEAGLE Team are centered on the modelisation and simulation of cellular processes. More specifically, we focus on two specific processes that govern cell dynamics and behavior: Evolution and Biophysics. This leads to two main topics: computational cell biology and models for genome evolution.

3.2. Computational Cell Biology

BEAGLE contributes computational models and simulations to the study of cell signaling in prokaryotic and eukaryotic cells, with a special focus on the dynamics of cell signaling both in time and in space. Importantly, our objective here is not so much to produce innovative computer methodologies, but rather to improve our knowledge of the field of cell biology by means of computer methodologies.

This objective is not accessible without a thorough immersion in experimental cell biology. Hence, one specificity of BEAGLE is to be closely associated inside each research project with experimental biology groups. For instance, all the current PhD students implicated in the research projects below have strong interactions with experimenters, most of them conducting experiments themselves in our collaborators' labs. In such a case, the supervision of their PhD is systematically shared between an experimentalist and a theoretician (modeler/computer scientist).

Standard modeling works in cell biochemistry are usually based on mean-field equations, most often referred to as "laws of mass-action". Yet, the derivation of these laws is based on strict assumptions. In particular, the reaction medium must be dilute, perfectly-mixed, three-dimensional and spatially homogeneous and the resulting kinetics are purely deterministic. Many of these assumptions are obviously violated in cells. As already stressed out before, the external membrane or the interior of eukaryotic as well as prokaryotic cells evidence spatial organization at several length scales, so that they must be considered as non-homogeneous media. Moreover, in many case, the small number of molecule copies present in the cell violates the condition for perfect mixing, and more generally, the "law of large numbers" supporting mean-field equations.

When the laws-of-mass-action are invalidated, individual-based models (IBM) appear as the best modeling alternative to evaluate the impact of these specific cellular conditions on the spatial and temporal dynamics of the signaling networks. We develop Individual-Based Models to evaluate the fundamental impact of non-homogeneous space conditions on biochemical diffusion and reaction. More specifically, we focus on the effects of two major sources of non-homogeneity within cells: macromolecular crowding and non-homogeneous diffusion. Macromolecular crowding provides obstacles to the diffusive movement of the signaling molecules, which may in turn have a strong impact on biochemical reactions [45]. In this perspective, we use IBM to renew the interpretation of the experimental literature on this aspect, in particular in the light of the available evidence for anomalous subdiffusion in living cells. Another pertinent source of non-homogeneity is the presence of lipid rafts and/or caveolae in eukaryotic cell membranes that locally alter diffusion. We showed several properties of these diffusion gradients on cells membranes. In addition, combining IBMs and cell biology experiments, we investigate the spatial organization of membrane receptors in plasmic membranes and the impact of these spatial features on the initiation of the signaling networks [49]. More recently, we started to develop IBMs to propose experimentally-verifiable tests able to distinguish between hindered diffusion due to obstacles (macromolecular crowding) and non-homogeneous diffusion (lipid rafts) in experimental data.

The last aspect we tackle concerns the stochasticity of gene expression. Indeed, the stochastic nature of gene expression at the single cell level is now a well established fact [55]. Most modeling works try to explain this stochasticity through the small number of copies of the implicated molecules (transcription factors, in particular). In collaboration with the experimental cell biology group led by Olivier Gandrillon at the Centre de Génétique et de Physiologie Moléculaire et Cellulaire (CGPhyMC, UMR CNRS 5534), Lyon, we study how stochastic gene expression in eukaryotic cells is linked to the physical properties of the cellular medium (e.g., nature of diffusion in the nucleoplasm, promoter accessibility to various molecules, crowding). We have already developed a computer model whose analysis suggests that factors such as chromatin remodeling dynamics have to be accounted for [51]. Other works introduce spatial dimensions in the model, in particular to estimate the role of space in complex (protein+ DNA) formation. Such models should yield useful insights into the sources of stochasticity that are currently not explained by obvious causes (e.g. small copy numbers).

3.3. Models of genome evolution

Classical artificial evolution frameworks lack the basic structure of biological genome (i.e. a double-strand sequence supporting variable size genes separated by variable size intergenic sequences). Yet, if one wants to study how a mutation-selection process is likely (or not) to result in particular biological structures, it is mandatory that the effect of mutation modifies this structure in a realistic way. We have developed an artificial chemistry based on a mathematical formulation of proteins and of the phenotypic traits. In our framework, the digital genome has a structure similar to prokaryotic genomes and a non-trivial genotype-phenotype map. It is a double-stranded genome on which genes are identified using promoter-terminator- like and start-stop-like signal sequences. Each gene is transcribed and translated into an elementary mathematical element (a "protein") and these elements - whatever their number - are combined to compute the phenotype of the organism. The Aevol (Artificial EVOLution) model is based on this framework and is thus able to represent genomes with variable length, gene number and order, and with a variable amount of non-coding sequences (for a complete description of the model, see [63]).

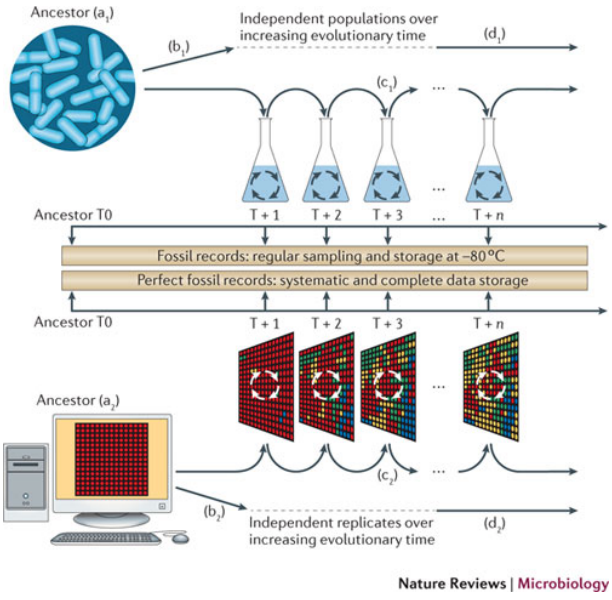

Figure 1. Parallel between experimental evolution and artificial evolution

As a consequence, this model can be used to study how evolutionary pressures like the ones for robustness or evolvability can shape genome structure [64], [61], [62], [71]. Indeed, using this model, we have shown that genome compactness is strongly influenced by indirect selective pressures for robustness and evolvability. By genome compactness, we mean several structural features of genome structure, like gene number, amount of non functional DNA, presence or absence of overlapping genes, presence or absence of operons [64], [61], [72]. More precisely, we have shown that the genome evolves towards a compact structure if the rate of spontaneous mutations and rearrangements is high. As far as gene number is concerned, this effect was known as an error-threshold effect [54]. However, the effect we observed on the amount of non functional DNA was unexpected. We have shown that it can only be understood if rearrangements are taken into account: by promoting large duplications or deletions, non functional DNA can be mutagenic for the genes it surrounds.

We have extended this framework to include genetic regulation (R-Aevol variant of the model). We are now able to study how these pressures also shape the structure and size of the genetic network in our virtual organisms [47], [46], [48],[29]. Using R-Aevol we have been able to show that (i) the model qualitatively reproduces known scaling properties in the gene content of prokaryotic genomes and that (ii) these laws are not due to differences in lifestyles but to differences in the spontaneous rates of mutations and rearrangements [46]. Our approach consists in addressing unsolved questions on Darwinian evolution by designing controlled and repeated evolutionary experiments, either to test the various evolutionary scenarios found in the literature or to propose new ones. Our experience is that "thought experiments" are often misleading: because evolution is a complex process involving long-term and indirect effects (like the indirect selection of robustness and evolvability), it is hard to correctly predict the effect of a factor by mere thinking. The type of models we develop are particularly well suited to provide control experiments or test of null hypotheses for specific evolutionary scenarios. We often find that the scenarios commonly found in the literature may not be necessary, after all, to explain the evolutionary origin of a specific biological feature. No selective cost to genome size was needed to explain the evolution of genome compactness [64], and no difference in lifestyles and environment was needed to explain the complexity of the gene regulatory network [46]. When we unravel such phenomena in the individual-based simulations, we try to build "simpler" mathematical models (using for instance population genetics-like frameworks) to determine the minimal set of ingredients required to produce the effect. Both approaches are complementary: the individual-based model is a more natural tool to interact with biologists, while the mathematical models contain fewer parameters and fewer ad-hoc hypotheses about the cellular chemistry.

At this time, simulating the evolution of large genomes during hundreds of thousands of generation with the Aevol software can take several weeks or even months. It is worse with R-aevol, where we not only simulate mutations and selection at the evolutionary timescale, but also simulate the lifetime of the individuals, allowing them to respond to environmental signals. Previous efforts to parallelize and distribute Aevol had yielded limited results due to the lack of dedicated staff on these problems. Since September 2014, we have been improving the performance of (R-)Aevol. Thanks to the ADT Aevol, one and a half full time engineers work on improving Aevol and especially to parallelize it. Moreover, we are working to formalize the numerical computation problems with (R-)Aevol to use state-of-the-art optimization techniques from the HPC community. It ranges from dense and sparse matrix multiplication and their optimizations (such as Tridiagonal matrix algorithm) to using new generation accelerator (Intel Xeon Phi and NVidia GPU). However, our goal is not to become a HPC nor a numerical computation team but to work with well-established teams in these fields, such as through the Joint Laboratory for Extreme-Scale Computing, but also with Inria teams in these fields (e.g. ROMA, Avalon, Corse, Storm, DataMove). By doing so, (R-)Aevol simulations will be faster, allowing us to study more parameters in a shorter time. Furthermore, we will also be able to simulate more realistic population sizes, that currently do not fit into the memory of a single computer.

In 2016 we have improved both the quality and the performance of the code. We are currently investigating advance usage of OpenMP to be able to offload part of our execution to accelerator. In particular, we are currently evaluating the performance of the OpenMP version of Aevol on Xeon Phi KNL and on NVidia GPU. In collaboration with the Avalon team and with the help of a shared internship (Mehdi Ghesh), we have build a benchmark for ordinary differential equation (ODE). This benchmark is based on a representative sample of the ODEs (formalizing the genetic network) found within the R-Aevol model. Thanks to this benchmark,

we can compare different ODE solvers and methods. Furthermore, researchers working on ODE solvers and methods could use it to evaluate the quality of their approach. We are now working with Avalon team on an algorithm that will automatically choose at runtime the best fitting solver and method (from a performance and a quality of results point of view). Through this collaboration, we have also extended the execo experimental engine [59] to support Aevol and R-Aevol. By doing so, we have now a complete automatic workflow to conduct large scale campaign experiments with thousands of different parameters of our model and use the resources of distributed platform (Grid'5000, CC-IN2P3 and a dedicated cluster).

Since 2014, we are also working on a second model of genome evolution.This new model, developed by the team within the Evoevo european Project, encompasses not only the gene regulation network (as R-aevol does) but also the metabolic level [8]. It allows us to have a real notion of resources and thus to have more complex ecological interactions between the individuals. To speed up computations, the genomic level is simplified compared to aevol, as a chromosome is modelled as a sequence of genes and regulatory elements and not as a sequence of nucleotides. Both models are thus complementary.

Little has been achieved concerning the validation of these models, and the relevance of the observed evolutionary tendencies for living organisms. Some comparisons have been made between Avida and experimental evolution [65], [58], but the comparison with what happened in a long timescale to life on earth is still missing. It is partly because the reconstruction of ancient genomes from the similarities and differences between extant ones is a difficult computational problem which still misses good solutions for every type of mutations, in particular the ones concerning changes in the genome structure.

There exist good phylogenic models of punctual mutations on sequences [56], which enable the reconstruction of small parts of ancestral sequences, individual genes for example [66]. But models of whole genome evolution, taking into account large scale events like duplications, insertions, deletions, lateral transfer, rearrangements are just being developped [74], [52]. Integrative phylogenetic models, considering both nucleotide subsitutions and genome architectures, like Aevol does, are still missing.

Partial models lead to evolutionary hypotheses on the birth and death of genes [53], on the rearrangements due to duplications [44], [73], on the reasons of variation of genome size [60], [67]. Most of these hypotheses are difficult to test due to the difficulty of *in vivo* evolutionary experiments.

To this aim, we develop evolutionary models to reconstruct the history of organisms from the comparison of their genome, at every scale, from nucleotide substitutions to genome organisation rearrangements. These models include large-scale duplications as well as loss of DNA material, and lateral gene transfers from distant species. In particular we have developed models of evolution by rearrangements [68], methods for reconstructing the organization of ancestral genomes [69], [50], [70], or for detecting lateral gene transfer events [43], [10]. It is complementary with the Aevol development because both the model of artificial evolution and the phylogenetic models we develop emphasize on the architecture of genomes. So we are in a good position to compare artificial and biological data on this point.

We improve the phylogenetic models to reconstruct ancestral genomes, jointly seen as gene contents, orders, organizations, sequences. It requires integrative models of genome evolution, which is desirable not only because they will provide a unifying view on molecular evolution, but also because they will shed light onto the relations between different kinds of mutations, and enable the comparison with artificial experiments from models like Aevol.

Based on this experience, the BEAGLE team contributes individual-based and mathematical models of genome evolution, in silico experiments as well as historical reconstruction on real genomes, to shed light on the evolutionary origin of the complex properties of cells.

BIPOP Project-Team

3. Research Program

3.1. Dynamic non-regular systems

nonsmooth mechanical systems, impacts, friction, unilateral constraints, complementarity problems, modeling, analysis, simulation, control, convex analysis

Dynamical systems (we limit ourselves to finite-dimensional ones) are said to be *non-regular* whenever some nonsmoothness of the state arises. This nonsmoothness may have various roots: for example some outer impulse, entailing so-called *differential equations with measure*. An important class of such systems can be described by the complementarity system

$$\begin{cases} \dot{x} = f(x,u,\lambda)\,, \\ 0 \le y \perp \lambda \ge 0\,, \\ g(y,\lambda,x,u,t) = 0\,, \\ \text{re-initialization law of the state } x(\cdot), \end{cases} \tag{1}$$

where $\perp$ denotes orthogonality; u is a control input. Now (1) can be viewed from different angles.

- Hybrid systems: it is in fact natural to consider that (1) corresponds to different models, depending whether $y_i = 0$ or $y_i > 0$ (y_i being a component of the vector y). In some cases, passing from one mode to the other implies a jump in the state x; then the continuous dynamics in (1) may contain distributions.
- Differential inclusions: $0 \le y \perp \lambda \ge 0$ is equivalent to $-\lambda \in \mathrm{N}_K(y)$, where K is the nonnegative orthant and $\mathrm{N}_K(y)$ denotes the normal cone to K at y. Then it is not difficult to reformulate (1) as a differential inclusion.
- Dynamic variational inequalities: such a formalism reads as $\langle \dot{x}(t) + F(x(t),t), v - x(t)\rangle \ge 0$ for all $v \in K$ and $x(t) \in K$, where K is a nonempty closed convex set. When K is a polyhedron, then this can also be written as a complementarity system as in (1).

Thus, the 2nd and 3rd lines in (1) define the modes of the hybrid systems, as well as the conditions under which transitions occur from one mode to another. The 4th line defines how transitions are performed by the state x. There are several other formalisms which are quite related to complementarity. See [7], [8], [15] for a survey on models and control issues in nonsmooth mechanical systems.

3.2. Nonsmooth optimization

optimization, numerical algorPierre-Brice Wieber.ithm, convexity, Lagrangian relaxation, combinatorial optimization.

Here we are dealing with the minimization of a function f (say over the whole space R^n), whose derivatives are discontinuous. A typical situation is when f comes from dualization, if the primal problem is not strictly convex – for example a large-scale linear program – or even nonconvex – for example a combinatorial optimization problem. Also important is the case of spectral functions, where $f(x) = F(\lambda(A(x)))$, A being a symmetric matrix and λ its spectrum.

For these types of problems, we are mainly interested in developing efficient resolution algorithms. Our basic tool is bundling and we act along two directions:

- To explore application areas where nonsmooth optimization algorithms can be applied, possibly after some tayloring. A rich field of such application is combinatorial optimization, with all forms of relaxation.
- To explore the possibility of designing more sophisticated algorithms. This implies an appropriate generalization of second derivatives when the first derivative does not exist, and we use advanced tools of nonsmooth analysis.

$\Longrightarrow$*The optimization scientific activity in BIPOP is no longer existing after Jérôme Malick left BIPOP to lead the DAO team in the Laboratoire Jean Kuntzman.*

CHROMA Team

3. Research Program

3.1. Introduction

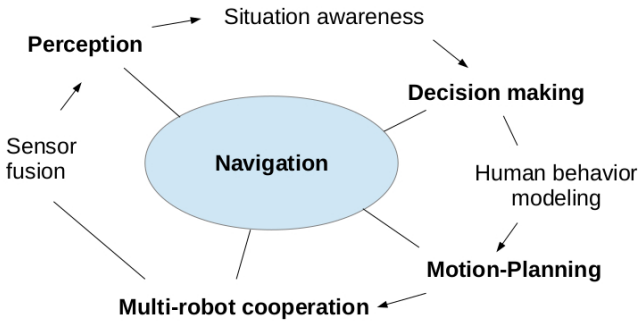

Figure 1. Research themes of the team and their relation

The Chroma team aims to deal with different issues of autonomous mobile robotics : perception, decision-making and cooperation. Figure 1 schemes the different themes and sub-themes investigated by Chroma.

We present here after our approaches to address these different theme of research, and how they combine to contribute to the general problem of robotic navigation. Chroma pays particular attention to current challenges that are autonomous navigation in highly dynamic environments populated by humans and cooperation in (large) multi-robot systems. These challenges are common with other major robotic laboratories/teams in the world, such as Autonomous Systems Lab at ETH Zurich, Robotic Embedded Systems Laboratory at USC, KIT [0] (Prof Christoph Stiller lab and Prof Ruediger Dillmann lab), UC Berkeley, Vislab Parma (Prof. Alberto Broggi), iCeiRA [0] laboratory in Taipei. Chroma is collaborating at various levels (visits, postdocs, research projects, common publications, etc.) with most of these laboratories, see Sections 9.3 and 9.4 .

3.2. Perception and Situation Awareness

Participants: Christian Laugier, Agostino Martinelli, Jilles S. Dibangoye, Anne Spalanzani, Olivier Simonin.

Robust perception in open and dynamic environments populated by human beings is an open and challenging scientific problem. Traditional perception techniques do not provide an adequate solution for these problems, mainly because such environments are uncontrolled [0] and exhibit strong constraints to be satisfied (in particular high dynamicity and uncertainty). This means that **the proposed solutions have to simultaneously take into account characteristics such as real time processing, temporary occultations, dynamic changes or motion predictions**.

[0] Karlsruhe Institut fur Technologie
[0] International Center of Excellence in Intelligent Robotics and Automation Research.
[0] partially unknown and open

Figure 2. Illustrations of the HSBOF model and experiment with the Zoe car

3.2.1. Bayesian perception

Context and previous work. Perception is known to be one of the main bottleneck for robot motion autonomy, in particular when navigating in open and dynamic environments is subject to strong real-time and uncertainty constraints. Traditional object-level solutions [0] still exhibit a lack of efficiency and of robustness when operating in such complex environments. In order to overcome this difficulty, we have proposed in the scope of the former e-Motion team, a new paradigm in robotics called "Bayesian Perception". The foundation of this approach relies on the concept of "Bayesian Occupancy Filter (BOF)" initially proposed in the PhD thesis of Christophe Coué [42] and further developed in the team [58] [0].

The basic idea is to combine a Bayesian filter with a probabilistic grid representation of both the space and the motions, see illustration Fig. 2 . This new approach can be seen as an extension for uncertain dynamic scenes, of the initial concept of "Occupancy Grid" proposed in 1989 by Elfes [0]. It allows the filtering and the fusion of heterogeneous and uncertain sensors data, by taking into account the history of the sensors measurements, a probabilistic model of the sensors and of the uncertainty, and a dynamic model of the observed objects motions.

In the scope of the Chroma team and of several academic and industrial projects, we went on with the development and the extension under strong embedded implementation constraints, of our Bayesian Perception concept. This work has already led to the development of more powerful models and more efficient implementations, e.g. the *HSBOF*[0] approach [76] and the *CMCDOT*[0] framework [84] which is still under development.

Current and future work address the extension of this model and its software implementation.

Objective — Extending the Bayesian Perception paradigm to the object level — We aim at defining a complete framework extending the Bayesian Perception paradigm to the object level. The main objective is to be simultaneously more robust, more efficient for embedded implementations, and more informative for the subsequent scene interpretation step.

We propose to integrate in a robust way higher level functions such as multiple objects detection and tracking or objects classification. The idea is to avoid well known object level detection errors and data association problems, by simultaneously reasoning at the *grid level* and at the *object level* by extracting / identifying / tracking / classifying clusters of dynamic cells (first work has been published in [84]).

[0] object recognition based on image processing
[0] The *Bayesian programming formalism* developed in e-Motion, pioneered (together with the contemporary work of Thrun, Burgards and Fox [94]) a systematic effort to formalize robotics problems under Probability theory –an approach that is now pervasive in Robotics.
[0] A. Elfes."Occupancy grids: A probabilistic framework for robot perception and navigation", Ph.D. dissertation, Carnegie Mellon University, Pittsburgh, USA, 1989.
[0] Hybrid Sampling Bayesian Occupancy Filter
[0] Conditional Monte Carlo Dense Occupancy Tracker

Software development : new approaches for software / hardware integration The objective is to improve the efficiency of the approach (by exploiting the highly parallel characteristic of our approach), while drastically reducing important factors such as the required memory size, the size of the hardware component, its price and the required energy consumption. This work is absolutely necessary for studying *embedded solutions* for the future generation of mobile robots and autonomous vehicles.

3.2.2. Situation Awareness and Prediction

Context. Prediction of the evolution of the perceived actors is an important ability required for navigation in dynamic and uncertain environments, in particular to allow on-line safe decisions. We have recently shown that an interesting property of the Bayesian Perception approach is to generate short-term conservative [0] predictions on the likely future evolution of the observed scene, even if the sensing information is temporary incomplete or not available [76]. But in human populated environments, estimating more abstract properties (e.g. object classes, affordances, agents intentions) is also crucial to understand the future evolution of the scene.

Objective We aim to develop an integrated approach for "Situation Awareness & Risk Assessment" in complex dynamic scenes involving multiples moving agents (e.g vehicles, cyclists, pedestrians ...), whose behaviors are most of the time unknown but predictable.

Our approach relies on combining machine learning to build a model of the agent behaviors and generic motion prediction techniques (Kalman-based, GHMM [98], Gaussian Processes [92]). A strong challenge of prediction in multiple moving agents environments is to take into consideration the interactions between the different agents (traffic participants). Existing interaction-aware approaches estimate exhaustively the intent of all road users [59], assume a cooperative behavior [88], or learn the policy model of drivers using supervised learning [50]. In contrast, we adopt a *planning-based motion prediction approach*, which is a framework to predict human behavior [102], [56][27]. Planning-based approaches assume that humans, when they perform a task, they do so by minimizing a cost function that depends on their preferences and the context. Such a cost function can be obtained, for example, from demonstrations using *Inverse Reinforcement Learning* [75], [36]. This constitutes an intuitive approach and, more importantly, enables us to overcome the limitations of other approaches, namely, high complexity [59], unrealistic assumptions [88], and overfitting [50]. We have recently demonstrated the predictive potential of our approach in [26].

Towards an On-line Bayesian Decision-Making framework. The team aims at building a general framework for perception and decision-making in multi-robot/vehicle environments. The navigation will be performed under both dynamic and uncertainty constraints, with contextual information and a continuous analysis of the evolution of the probabilistic collision risk (see above). Results have recently been obtained in cooperation with Renault and Berkeley, by using the "Intention / Expectation" paradigm and Dynamic Bayesian Networks; these results have been published in [60], [61] and patented.

We are currently working on the generalization of this approach, in order to take into account the dynamics of the vehicles and multiple traffic participants. The objective is to design a new framework, allowing to overcome the shortcomings of rules-based reasoning approaches usually showing good results [64] [49], but leading to a lack of scalability and long terms predictions. Our research work is carried out through several cooperative projects (Toyota, Renault, project Prefect of IRT Nanoelec, European project ECSEL Enable-S3) and related PhD theses.

3.2.3. Robust state estimation (Sensor fusion)

Context. In order to safely and autonomously navigate in an unknown environment, a mobile robot is required to estimate in real time several physical quantities (e.g., position, orientation, speed). These physical quantities are often included in a common state vector and their simultaneous estimation is usually achieved by fusing the information coming from several sensors (e.g., camera, laser range finder, inertial sensors). The problem of fusing the information coming from different sensors is known as the *Sensor Fusion* problem and it is a fundamental problem which plays a major role in robotics.

[0] i.e. when motion parameters are supposed to be stable during a small amount of time

Objective. A fundamental issue to be investigated in any sensor fusion problem is to understand whether the state is observable or not. Roughly speaking, we need to understand if the information contained in the measurements provided by all the sensors allows us to carry out the estimation of the state. If the state is not observable, we need to detect a new observable state. This is a fundamental step in order to properly define the state to be estimated. To achieve this goal, we apply standard analytic tools developed in control theory together with some new theoretical concepts we introduced in [68] (concept of continuous symmetry). Additionally, we want to account the presence of disturbances in the observability analysis.

Our approach is to introduce general analytic tools able to derive the observability properties in the nonlinear case when some of the system inputs are unknown (and act as disturbances). We recently obtained a simple analytic tool able to account the presence of unknown inputs [71], which extends a heuristic solution derived by the team of Prof. Antonio Bicchi [40] with whom we collaborate (Centro Piaggio at the University of Pisa).

Fusing visual and inertial data. A special attention is devoted to the fusion of inertial and monocular vision sensors (which have strong application for instance in UAV navigation). The problem of fusing visual and inertial data has been extensively investigated in the past. However, most of the proposed methods require a state initialization. Because of the system nonlinearities, lack of precise initialization can irreparably damage the entire estimation process. In literature, this initialization is often guessed or assumed to be known [38], [63], [46]. Recently, this sensor fusion problem has been successfully addressed by enforcing observability constraints [51], [52] and by using optimization-based approaches [62], [45], [66], [53], [74]. These optimization methods outperform filter-based algorithms in terms of accuracy due to their capability of relinearizing past states. On the other hand, the optimization process can be affected by the presence of local minima. We are therefore interested in a deterministic solution that analytically expresses the state in terms of the measurements provided by the sensors during a short time-interval.

For some years we explore deterministic solutions as presented in [69] and [70]. Our objective is to improve the approach by taking into account the biases that affect low-cost inertial sensors (both gyroscopes and accelerometers) and to exploit the power of this solution for real applications. This work is currently supported by the ANR project VIMAD [0] and experimented with a quadrotor UAV. We have a collaboration with Prof. Stergios Roumeliotis (the leader of the MARS lab at the University of Minnesota) and with Prof. Anastasios Mourikis from the University of California Riverside. Regarding the usage of our solution for real applications we have a collaboration with Prof. Davide Scaramuzza (the leader of the Robotics and Perception group at the University of Zurich) and with Prof. Roland Siegwart from the ETHZ.

3.3. Navigation and cooperation in dynamic environments

Participants: Olivier Simonin, Anne Spalanzani, Jilles S. Dibangoye, Christian Laugier, Laetitia Matignon, Fabrice Jumel, Jacques Saraydaryan.

In his reference book *Planning algorithms*[0] S. LaValle discusses the different dimensions that made the motion-planning problem complex, which are the number of robots, the obstacle region, the uncertainty of perception and action, and the allowable velocities. In particular, it is emphasized that complete algorithms require at least exponential time to deal with multiple robot planning in complex environments, preventing them to be scalable in practice (p. 320). Moreover, dynamic and uncertain environments, as human-populated ones, expand this complexity.

In this context, we aim at **scale up decision-making in human-populated environments and in multi-robot systems, while dealing with the intrinsic limits of the robots (computation capacity, limited communication)**.

3.3.1. Motion-planning in human-populated environment

[0] Navigation autonome des drones aériens avec la fusion des données visuelles et inertielles, lead by A. Martinelli, Chroma.
[0] Steven M. LaValle, Planning Algorithms, Cambridge University Press, 2006.

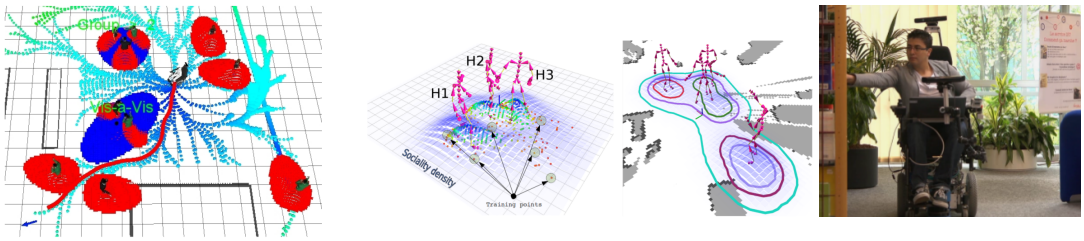

Figure 3. Illustrations of a. the Risk-RRT planning b. the human interaction space model c. experiment with the wheelchair.

Context. Motion planning in dynamic and human-populated environments is a current challenge of robotics. Many research teams work on this topic. We can cite the Institut of robotic in Barcelone [44], the MIT [37], the Autonomous Intelligent Systems lab in Freiburg [41], or the LAAS [77]. In Chroma, we explore different issues : **integrating the risk (uncertainty) in planning processes, modeling and taking into account human behaviors and flows.**

Objective We aim to give the robot some socially compliant behaviors by anticipating the near future (trajectories of mobile obstacle in the robot's surroundings) and by integrating knowledge from psychology, sociology and urban planning. In this context, we will focus on the following 3 topics.

Risk-based planning. Unlike static or controlled environments [0] where global path planning approaches are suitable, dealing with highly dynamic and uncertain environments requires to integrate the notion of risk (risk of collision, risk of disturbance). This risk can be computed by methods proposed in the section 3.2.2 . Then, we examine how motion planning approaches can integrate this risk in the generation and selection of the paths. An algorithm called RiskRRT was proposed in the eMotion team. This algorithm plans goal oriented trajectories that minimize the risk estimated at each instant. It fits environments that are highly dynamic and adapts to a representation of uncertainty [90] (see Figure 3 .a for illustration). Now, we aim to extend this principle to be adapted to various risk evaluation methods (proposed in 3.2) and various situation (highways, urban environments, even in dense traffic or in crowds).

Sharing the physical space with humans. Robots are expected to share their physical space with humans. Hence, robots need to take into account the presence of humans and to behave in a socially acceptable way. Their trajectories must be safe but also predictable, that is why they must follow social conventions, respecting proximity constraints, avoiding people interacting or joining a group engaged in conversation without disturbing. For this purpose, we proposed earlier to integrate some knowledge from the psychology domain (i.e. proxemics theory), see figure 3 .b. We aim now to integrate semantic knowledge [0] and psycho-social theories of human behavior [00] in the navigation framework we have developed for a few years (i.e. the Risk-based navigation algorithms [48], [90], [97]). These concepts were tested on our automated wheelchair (see figure 3 .c) but they have and will be adapted to autonomous cars, telepresence robots and companion robots. This work is currently supported by the ANR Valet, the TENSIVE project and the Associated team Sampen (with Iceira Lab, Taipei).

[0]known environment without uncertainty
[0]B. Kuipers, The Spatial Semantic Hierarchy, Artificial Intelligence, Volume 119, Issues 1–2, May 2000, Pages 191-233
[0]Gibson, J. (1977). The theory of affordances, in Perceiving, Acting, and Knowing. Towards an Ecological Psychology. Number eds Shaw R., Bransford J. Hoboken,NJ: John Wiley & Sons Inc.
[0]Hall, E. (1966). The hidden dimension. Doubleday Anchor Books.

Mapping human flows. We investigate the problem of modeling recurring human displacements to improve robots navigation in such dense populated environments. It has been shown that such recurring behaviours can be mapped from spatial-temporal observations, as in [95]. In this context we address the problem of mapping human flows from robot(s) perception. We started to propose counting-based mapping models [30] that contain motion probabilities in the grid cells. Then such a grid can be exploited to define path-planning functions (eg. A* based) that take into account the probability to encounter humans in opposite direction. We also aim at demonstrating the efficiency of the approach whith real robots evolving in dense human-populated environments.

3.3.2. Decision Making in Multi-robot systems

Context. A central challenge in Chroma is to define **decision-making algorithms that scale up to large multi-robot systems**. This work takes place in the general framework of Multi-Agent Systems (MAS). The objective is to compute/define agent behaviors that provide cooperation and adaptation abilities. Solutions must also take into account the agent/robot computational limits.

We can abstract the challenge in three objectives :
i) mastering the complexity of large fleet of robots/vehicles (scalability),
ii) dealing with limited computational/memory capacity
iii) building adaptive solutions (robustness).

Combining Decision-theoretic models and Swarm intelligence.

Over the past few years, our attempts to address multi-robot decision-making are mainly due to Multi-Agent Sequential Decision Making (MA-SDM) and Swarm Intelligence (SI). MA-SDM builds upon well-known decision-theoretic models (e.g., Markov decision processes and games) and related algorithms, that come with strong theoretical guarantees. In contrast, the expressiveness of MA-SDM models has limited scalability in face of realistic multi-robot systems [0], resulting in computational overload. On their side, SI methods, which rely on local rules – generally bio-inspired – and relating to Self-Organized Systems [0], can scale up to multiple robots and provide robustness to disturbances, but with poor theoretical guarantees [0]. Swarm models can also answer to the need of designing tractable solutions [89], but they remain not geared to express complex realistic tasks or to handle (point-to-point) communication between robots. This motivates our work to go beyond these two approaches and to combine them.

First, we plan to investigate **incremental expansion mechanisms in anytime decision-theoretic planning**, starting from local rules (from SI) to complex strategies with performance guarantees (from MA-SDM) [43]. This methodology is grounded into our research on anytime algorithms, that are guaranteed to stop at anytime while still providing a reliable solution to the original problem. It further relies on decision theoretical models and tools including: Decentralized and Partially Observable Markov Decision Processes and Games, Dynamic Programming, Distributed Reinforcement Learning and Statistical Machine Learning.

Second, we plan to extend the SI approach by considering **the integration of optimization techniques at the local level**. The purpose is to force the system to explore solutions around the current stabilized state – potentially a local optimum – of the system. We aim at keeping scalability and self-organization properties by not compromising the decentralized nature of such systems. Introducing optimization in this way requires to measure locally the performances, which is generally possible from local perception of robots (or using learning techniques). The main optimization methods we will consider are Local Search (Gradient Descent), Distributed Stochastic Algorithm and Reinforcement Learning. We have shown in [96] the interest of such an approach for driverless vehicle traffic optimization. In 2016, we started a new PHD in collaboration with the VOLVO Group to deal with global-local optimization for goods distribution using a fleet of autonomous vehicles.

[0] Martin L. Puterman, Markov Decision Processes; Stuart Russell and Peter Norvig, Artificial Intelligence - A Modern Approach
[0] D. Floreano and C. Mattiussi, Bio-Inspired Artificial Intelligence - Theories, Methods, and Technologies, MIT Press, 2008.
[0] S. A. Brueckner, G. Di Marzo Serugendo, A. Karageorgos, R. Nagpal (2005). Engineering Self-Organising Systems, Methodologies and Applications. LNAI 3464 State-of-the-Art Survey, Springer book.

Both approaches must lead to **master the complexity** inherent to large and open multi-robot systems. Such systems are prone to combinatorial problems, in term of state space and communication, when the number of robots grows. To cope with this complexity we started to develop a methodology which relies on incrementally refining the environment representation while the robots perform their tasks.

Mastering the computational cost involved in cooperative decision-making relies also on building heuristics. We explore how exact (global) solutions can be decentralized in local computation allocated to group of robots or to each robot. We started to apply this methodology to dynamic problems such as the patrolling of moving persons (see [87]).

Beyond this methodological work, we aim to evaluate our models on benchmarks from the literature, by using simulation tools as a complement of robotic experiments. This will lead us to develop simulators, allowing to deploy thousands of humans and robots in constrained environments.

Towards adaptive connected robots.

Mobile robots and autonomous vehicles are becoming more connected to one another and to other devices in the environment (concept of cloud of robots [0] and V2V/V2I connectivity in transportation systems). Such robotic systems are open systems as the number of connected entities is varying dynamically. Network of robots brought with them new problems, as the need of (online) adaption to changes in the system and to the variability of the communication.

In Chroma, we address the problem of adaptation by considering machine learning techniques and local mechanisms as discussed above (SI models). More specifically we investigate the problem of maintaining the connectivity between robots which perform dynamic version of tasks such as patrolling, exploration or transportation, i.e. where the setting of the problem is constinuously changing and growing (see [25]).

Robot fleets should be able to adapt their behavior and organisation to communication limits and variation. It has been shown that wireless communication are very changing in time and space [65]. So we explore how robots can optimize their behaviors by perceiving and learning the quality of their communication in the environment. In Lyon, the CITI Lab. conducts research in many aspects of telecommunication, from signal theory to distributed computation. In this context, Chroma develops cooperations with the Inria team Urbanet [25] (wireless communication protocols) and with the Dynamid team [19] (middlleware and cloud aspects), that we wish to reinforce in the next years.

[0] see for instance the first International Workshop on Cloud and Robotics, 2016.

COMPSYS Team

3. Research Program

3.1. Architecture and Compilation Trends

The embedded system design community is facing two challenges:

- The complexity of embedded applications is increasing at a rapid rate.
- The needed increase in processing power is no longer obtained by increases in the clock frequency, but by increased parallelism.

While, in the past, each type of embedded application was implemented in a separate appliance, the present tendency is toward a universal hand-held object, which must serve as a cell-phone, as a personal digital assistant, as a game console, as a camera, as a Web access point, and much more. One may say that embedded applications are of the same level of complexity as those running on a PC, but they must use a more constrained platform in terms of processing power, memory size, and energy consumption. Furthermore, most of them depend on international standards (e.g., in the field of radio digital communication), which are evolving rapidly. Lastly, since ease of use is at a premium for portable devices, these applications must be integrated seamlessly to a degree that is unheard of in standard computers.

All of this dictates that modern embedded systems retain some form of programmability. For increased designer productivity and reduced time-to-market, programming must be done in some high-level language, with appropriate tools for compilation, run-time support, and debugging. This does not mean however that all embedded systems (or all of an embedded system) must be processor based. Another solution is the use of field programmable gate arrays (FPGA), which may be programmed at a much finer grain than a processor, although the process of FPGA "programming" is less well understood than software generation. Processors are better than application-specific circuits at handling complicated control and unexpected events. On the other hand, FPGAs may be tailored to just meet the needs of their application, resulting in better energy and silicon area usage. It is expected that most embedded systems will use a combination of general-purpose processors, specific processors like DSPs, and FPGA accelerators (or even low-power GPUs). Such a combination DSP+FPGA is already present in recent versions of the Atom Intel processor.

As a consequence, parallel programming, which has long been confined to the high-performance community, must become the common place rather than the exception. In the same way that sequential programming moved from assembly code to high-level languages at the price of a slight loss in performance, parallel programming must move from low-level tools, like OpenMP or even MPI, to higher-level programming environments. While fully-automatic parallelization is a Holy Grail that will probably never be reached in our lifetimes, it will remain as a component in a comprehensive environment, including general-purpose parallel programming languages, domain-specific parallelizers, parallel libraries and run-time systems, back-end compilation, dynamic parallelization. The landscape of embedded systems is indeed very diverse and many design flows and code optimization techniques must be considered. For example, embedded processors (micro-controllers, DSP, VLIW) require powerful back-end optimizations that can take into account hardware specificities, such as special instructions and particular organizations of registers and memories. FPGA and hardware accelerators, to be used as small components in a larger embedded platform, require "hardware compilation", i.e., design flows and code generation mechanisms to generate non-programmable circuits. For the design of a complete system-on-chip platform, architecture models, simulators, debuggers are required. The same is true for multicores of any kind, GPGPU ("general-purpose" graphical processing units), CGRA (coarse-grain reconfigurable architectures), which require specific methodologies and optimizations, although all these techniques converge or have connections. In other words, embedded systems need all usual aspects of the process that transforms some specification down to an executable, software or hardware. In this wide range of topics, Compsys concentrated on the code optimizations aspects (and the associated analysis) in this transformation chain, restricting to compilation (transforming a program to a program) for embedded

processors and programmable accelerators, and to high-level synthesis (transforming a program into a circuit description) for FPGAs.

Actually, it is not a surprise to see compilation and high-level synthesis getting closer (in the last 10 years now). Now that high-level synthesis has grown up sufficiently to be able to rely on place-and-route tools, or even to synthesize C-like languages, standard techniques for back-end code generation (register allocation, instruction selection, instruction scheduling, software pipelining) are used in HLS tools. At the higher level, programming languages for programmable parallel platforms share many aspects with high-level specification languages for HLS, for example the description and manipulations of nested loops, or the model of computation/communication (e.g., Kahn process networks and its many "streaming" variants). In all aspects, the frontier between software and hardware is vanishing. For example, in terms of architecture, customized processors (with processor extensions as first proposed by Tensilica) share features with both general-purpose processors and hardware accelerators. FPGAs are both hardware and software as they are fed with "programs" representing their hardware configurations.

In other words, this convergence in code optimizations explains why Compsys studied both program compilation and high-level synthesis, and at both front-end and back-end levels, the first one acting more at the granularity of memories, transfers, and multiple cores, the second one more at the granularity of registers, system calls, and single core. Both levels must be considered as they interact with each other. Front-end optimizations must be aware of what back-end optimizations will do, as single core performance remain the basis for good parallel performances. Some front-end optimizations even act directly on back-end features, for example register tiling considered as a source-level transformation. Also, from a conceptual point of view, the polyhedral techniques developed by Compsys are actually the symbolic front-end counterpart, for structured loops, of back-end analysis and optimizations of unstructured programs (through control-flow graphs), such as dependence analysis, scheduling, lifetime analysis, register allocation, etc. A strength of Compsys was to juggle with both aspects, the first one based on graph theory with SSA-type optimizations, the other on polyhedra representing loops, and to exploit the correspondence between both. This has still to be exploited, for applying polyhedral techniques to more irregular programs. Besides, Compsys had a tradition of building free software tools for linear programming and optimization in general, as needed for our research.

3.1.1. Compilation and Languages Issues in the Context of Embedded Processors, "Embedded Systems", and Programmable Accelerators

Compilation is an old activity, in particular back-end code optimizations. The development of embedded systems was one of the reasons for the revival of compilation activities as a research topic. Applications for embedded computing systems generate complex programs and need more and more processing power. This evolution is driven, among others, by the increasing impact of digital television, the first instances of UMTS networks, and the increasing size of digital supports, like recordable DVD, and even Internet applications. Furthermore, standards are evolving very rapidly (see for instance the successive versions of MPEG). As a consequence, the industry has focused on programmable structures, whose flexibility more than compensates for their larger size and power consumption. The appliance provider has a choice between hard-wired structures (Asic), special-purpose processors (Asip), (quasi) general-purpose processors (DSP for multimedia applications), and now hardware accelerators (dedicated platforms – such as those developed by Thales or the CEA –, or more general-purpose accelerators such as GPUs or even multicores, even if these are closer to small HPC platforms than truly embedded systems). Our cooperation with STMicroelectronics, until 2012, focused on investigating the compilation for specialized processors, such as the ST100 (DSP processor) and the ST200 (VLIW DSP processor) family. Even for this restricted class of processors, the diversity is large, and the potential for instruction level parallelism (SIMD, MMX), the limited number of registers and the small size of the memory, the use of direct-mapped instruction caches, of predication, generated many open problems. Our goal was to contribute to their understanding and their solutions.

An important concept to cope with the diversity of platforms is the concept of *virtualization*, which is a key for more portability, more simplicity, more reliability, and of course more security. This concept – implemented at low level through binary translation and just-in-time (JIT) compilation [0] – consists in hiding the architecture-

dependent features as long as possible during the compilation process. It has been used for a while for servers such as HotSpot, a bit more recently for workstations, and now for embedded computing. The same needs drive the development of intermediate languages such as OpenCL to, not necessarily hide, but at least make more uniform, the different facets of the underlying architectures. The challenge is then to design and compile high-productivity and high-performance languages [0] (coping with parallelism and heterogeneity) that can be ported to such intermediate languages, or to architecture-dependent runtime systems. The offloading of computation kernels, through source-to-source compilation, targeting back-end C dialects, has the same goals: to automate application porting to the variety of accelerators.

For JIT compilation, the compactness of the information representation, and thus its pertinence, is an important criterion for such late compilation phases. Indeed, the intermediate representation (IR) is evolving not only from a target-independent description to a target-dependent one, but also from a situation where the compilation time is almost unlimited (cross-compilation) to one where any type of resource is limited. This is one of the reasons why static single assignment (SSA), a sparse compact representation of liveness information, became popular in embedded compilation. If time constraints are common to all JIT compilers (not only for embedded computing), the benefit of using SSA is also in terms of its good ratio pertinence/storage of information. It also enables to simplify algorithms, which is also important for increasing the reliability of the compiler. In this context, our aim has been, in particular, to develop exact or heuristic solutions to *combinatorial* problems that arise in compilation for VLIW and DSP processors, and to integrate these methods into industrial compilers for DSP processors (mainly ST100, ST200, Strong ARM). Such combinatorial problems can be found in register allocation, opcode selection, code placement, when removing the SSA multiplexer functions (known as ϕ functions). These optimizations are usually done in the last phases of the compiler, using an assembly-level intermediate representation. As mentioned in Sections 2.3 and 2.4 , we made a lot of progress in this area in our past collaborations with STMicroelectronics (see also previous activity reports). Through the Sceptre and Mediacom projects, we first revisited, in the light of SSA, some code optimizations in an aggressive context, to develop better strategies, without eliminating too quickly solutions that may have been considered as too expensive in the past. Then we exploited the new concepts introduced in the aggressive context to design better algorithms in a JIT context, focusing on the speed of algorithms and their memory footprint, without compromising too much on the quality of the generated code.

Our recent research directions were more focused on programmable accelerators, such as GPU and multicores, but still considering *static* compilation and without forgetting the link between high-level (in general at source-code level) and low-level (i.e., at assembly-code level) optimizations. They concerned program analysis (of both sequential and parallel specifications), program optimizations (for memory hierarchies, parallelism, streaming, etc.), and also the link with applications, and between compilers and users (programmers). Polyhedral techniques play an important role in these directions, even if control-flow-based techniques remain in the background and may come back at any time in the foreground. This is also the case for high-level synthesis, as exposed in the next section.

3.1.2. Context of High-Level Synthesis and FPGA Platforms

High-level synthesis has become a necessity, mainly because the exponential increase in the number of gates per chip far outstrips the productivity of human designers. Besides, applications that need hardware accelerators usually belong to domains, like telecommunications and game platforms, where fast turn-around and time-to-market minimization are paramount. When Compsys started, we were convinced that our expertise in compilation and automatic parallelization could contribute to the development of the needed tools.

[0] *Aggressive compilation* consists in allowing more time to implement more complete and costly solutions: compilation time is less relevant than execution time, size, and energy consumption of the produced code, which can have a critical impact on the cost and quality of the final product. The application is usually cross-compiled, i.e., compiled on a powerful platform distinct from the target processor. *Just-in-time compilation*, on the other hand, corresponds to compiling applets on demand on the target processor. The code can be uploaded or sold separately on a flash memory. Compilation is performed at load time and even dynamically during execution. The optimization heuristics, constrained by time and limited resources, are far from being aggressive. They must be fast but smart enough.

[0] For examples of such languages, see the keynotes event we organized in 2013: http://labexcompilation.ens-lyon.fr/hpc-languages.

Today, synthesis tools for FPGAs or ASICs come in many shapes. At the lowest level, there are proprietary Boolean, layout, and place-and-route tools, whose input is a VHDL or Verilog specification at the structural or register-transfer level (RTL). Direct use of these tools is difficult, for several reasons:

- A structural description is completely different from an usual algorithmic language description, as it is written in term of interconnected basic operators. One may say that it has a spatial orientation, in place of the familiar temporal orientation of algorithmic languages.
- The basic operators are extracted from a library, which poses problems of selection, similar to the instruction selection problem in ordinary compilation.
- Since there is no accepted standard for VHDL synthesis, each tool has its own idiosyncrasies and reports its results in a different format. This makes it difficult to build portable HLS tools.
- HLS tools have trouble handling loops. This is particularly true for logic synthesis systems, where loops are systematically unrolled (or considered as sequential) before synthesis. An efficient treatment of loops needs the polyhedral model. This is where past results from the automatic parallelization community are useful.
- More generally, a VHDL specification is too low level to allow the designer to perform, easily, higher-level code optimizations, especially on multi-dimensional loops and arrays, which are of paramount importance to exploit parallelism, pipelining, and perform communication and memory optimizations.

Some intermediate tools were proposed that generate VHDL from a specification in restricted C, both in academia (such as SPARK, Gaut, UGH, CloogVHDL), and in industry (such as C2H, CatapultC, Pico-Express, Vivado HLS). All these tools use only the most elementary form of parallelization, equivalent to instruction-level parallelism in ordinary compilers, with some limited form of block pipelining, and communication through FIFOs. Targeting one of these tools for low-level code generation, while we concentrate on exploiting loop parallelism, might be a more fruitful approach than directly generating VHDL. However, it may be that the restrictions they impose preclude efficient use of the underlying hardware. Our first experiments with these HLS tools reveal two important issues. First, they are, of course, limited to certain types of input programs so as to make their design flows successful, even if, over the years, they become more and more mature. But it remains a painful and tricky task for the user to transform the program so that it fits these constraints and to tune it to get good results. Automatic or semi-automatic program transformations can help the user achieve this task. Second, users, even expert users, have only a very limited understanding of what back-end compilers do and why they do not lead to the expected results. An effort must be done to analyze the different design flows of HLS tools, to explain what to expect from them, and how to use them to get a good quality of results. Our first goal was thus to develop high-level techniques that, used in front of existing HLS tools, improve their utilization. This should also give us directions on how to modify them or to design new tools from scratch.

More generally, HLS has to be considered as a more global parallelization process. So far, no HLS tools is capable of generating designs with communicating *parallel* accelerators, even if, in theory, at least for the scheduling part, a tool such as Pico-Express could have such capabilities. The reason is that it is, for example, very hard to automatically design parallel memories and to decide the distribution of array elements in memory banks to get the desired performances with parallel accesses. Also, how to express communicating processes at the language level? How to express constraints, pipeline behavior, communication media, etc.? To better exploit parallelism, a first solution is to extend the source language with parallel constructs, as in all derivations of the Kahn process networks model, including communicating regular processes (CRP). The other solution is a form of automatic parallelization. However, classical methods, which are mostly based on scheduling, need to be revisited, to pay more attention to locality, process streaming, and low-level pipelining, which are of paramount importance in hardware. Besides, classical methods mostly rely on the runtime system to tailor the parallelism degree to the available resources. Obviously, there is no runtime system in hardware. The real challenge is thus to invent new scheduling algorithms that take resource, locality, and pipelining into account, and then to infer the necessary hardware from the schedule. This is probably possible only for programs that fit into the polyhedral model, or in an incrementally-extended model.

Our research activities on polyhedral code analysis and optimizations directly targeted these HLS challenges. But they are not limited to the automatic generation of hardware as can be seen from our different contributions on X10, OpenStream, parametric tiling, etc. The same underlying concepts also arise when optimizing codes for GPUs and multicores. In this context of polyhedral analysis and optimizations, we focused on three aspects:

- developing high-level transformations, especially for loops and memory/communication optimizations, that can be used in front of HLS tools so as to improve their use, as well as for hardware accelerators;
- developing concepts and techniques in a more global view of high-level synthesis and high-level parallel programming, starting from specification languages down to hardware implementation;
- developing more general code analysis so as to extract more information from codes as well as to extend the programs that can be handled.

3.2. Code Analysis, Code Transformations, Code Optimizations

Embedded systems, as we recalled earlier, generated new problems in code analysis and optimization both for optimizing embedded software (compilation) and hardware (HLS). We now give a bit more details on some general challenges for program analysis, optimizations, and transformations, induced by this context, and on our methodology, in particular our development and use of polyhedral optimizations and its extensions.

3.2.1. Processes, Scheduling, Mapping, Communications, etc.

Before mapping an application to an architecture, one has to decide which execution model is targeted and where to intervene in the design flow. Then one has to solve scheduling, placement, and memory management problems. These three aspects should be handled as a whole, but present state of the art dictates that they be treated separately. One of our aims was to develop more comprehensive solutions. The last task is code generation, both for the processing elements and the interfaces processors/accelerators.

There are basically two execution models for embedded systems: one is the classical accelerator model, in which data is deposited in the memory of the accelerator, which then does its job, and returns the results. In the streaming model, computations are done on the fly, as data items flow from an input channel to the output. Here, the data are never stored in (addressable) memory. Other models are special cases, or sometimes compositions of the basic models. For instance, a systolic array follows the streaming model, and sometimes extends it to higher dimensions. Software radio modems follow the streaming model in the large, and the accelerator model in detail. The use of first-in first-out queues (FIFO) in hardware design is an application of the streaming model. Experience shows that designs based on the streaming model are more efficient that those based on memory, for such applications. One of the point to be investigated is whether it is general enough to handle arbitrary (regular) programs. The answer is probably negative. One possible implementation of the streaming model is as a network of communicating processes either as Kahn process networks (FIFO based) or as our more recent model of communicating regular processes (memory based, such as CRP mentioned hereafter). It is an interesting fact that several researchers have investigated the translation from process networks [12] and to process networks [20], [21]. Streaming languages such as StreamIt and OpenStream are also interesting solutions to explore.

Kahn process networks (KPN) were introduced 30 years ago as a notation for representing parallel programs. Such a network is built from processes that communicate via perfect FIFO channels. Because the channel histories are deterministic, one can define a semantics and talk meaningfully about the equivalence of two implementations. As a bonus, the dataflow diagrams used by signal processing specialists can be translated on-the-fly into process networks. The problem with KPNs is that they rely on an asynchronous execution model, while VLIW processors and FPGAs are synchronous or partially synchronous. Thus, there is a need for a tool for synchronizing KPNs. This can be done by computing a schedule that has to satisfy data dependences within each process, a causality condition for each channel (a message cannot be received before it is sent), and real-time constraints. However, there is a difficulty in writing the channel constraints because one has to count messages in order to establish the send/receive correspondence and, in multi-dimensional loop nests, the counting functions may not be affine. The same situation arises for the OpenStream language (see Section 7.2 .

Recent developments on the theory of polynomials (see Section 7.1) may offer a solution to this problem. One can also define another model, *communicating regular processes* (CRP), in which channels are represented as write-once/read-many arrays. One can then dispense with counting functions and prove that the determinacy property still holds. As an added benefit, a communication system in which the receive operation is not destructive is closer to the expectations of system designers.

The main difficulty with this approach is that ordinary programs are usually not constructed as process networks. One needs automatic or semi-automatic tools for converting sequential programs into process networks. One possibility is to start from array dataflow analysis [15] or variants. Another approach attempts to construct threads, i.e., pieces of sequential code with the smallest possible interactions. In favorable cases, one may even find outermost parallelism, i.e., threads with no interactions whatsoever. Tiling mechanisms can also be used to define atomic processes that can be pipelined as we proposed initially for FPGA [9].

Whatever the chosen solution (FIFO or addressable memory) for communicating between two accelerators or between the host processor and an accelerator, the problems of optimizing communication between processes and of optimizing buffers have to be addressed. Many local memory optimization problems have already been solved theoretically. Some examples are loop fusion and loop alignment for array contraction, techniques for data allocation in scratch-pad memory, or techniques for folding multi-dimensional arrays [11]. Nevertheless, the problem is still largely open. Some questions are: how to schedule a loop sequence (or even a process network) for minimal scratch-pad memory size? How is the problem modified when one introduces unlimited and/or bounded parallelism (same questions for analyzing explicitly-parallel programs)? How does one take into account latency or throughput constraints, bandwidth constraints for input and output channels, memory hierarchies? All loop transformations are useful in this context, in particular loop tiling, and may be applied either as source-to-source transformations (when used in front of HLS or C-level compilers) or to generate directly VHDL or lower-level C-dialects such as OpenCL. One should keep in mind that theory will not be sufficient to solve these problems. Experiments are required to check the relevance of the various models (computation model, memory model, power consumption model) and to select the most important factors according to the architecture. Besides, optimizations do interact: for instance, reducing memory size and increasing parallelism are often antagonistic. Experiments will be needed to find a global compromise between local optimizations. In particular, the design of cost models remain a fundamental challenge.

Finally, there remains the problem of code generation for accelerators. It is a well-known fact that methods for program optimization and parallelization do not generate a new program, but just deliver blueprints for program generation, in the form, e.g., of schedules, placement functions, or new array subscripting functions. A separate code generation phase must be crafted with care, as a too naive implementation may destroy the benefits of high-level optimization. There are two possibilities here as suggested before; one may target another high-level synthesis or compilation tool, or one may target directly VHDL or low-level code. Each approach has its advantages and drawbacks. However, both situations require that the input program respects some strong constraints on the code shape, array accesses, memory accesses, communication protocols, etc. Furthermore, to get the compilers do what the user wants requires a lot of program tuning, i.e., of program rewriting or of program annotations. What can be automated in this rewriting process? Semi-automated?

In other words, we still need to address scheduling, memory, communication, and code generation issues, in the light of the developments of new languages and architectures, pushing the limits of such an automation of program analysis, program optimizations, and code generation.

3.2.2. Beyond Static Control Programs

With the advent of parallelism in supercomputers, the bulk of research in code transformation resulted in (semi-)automatic parallelization, with many techniques (analysis, scheduling, code generation, etc.) based on the description and manipulation of nested loops with polyhedra. Compsys has always taken an active part in the development of these so-called “polyhedral techniques”. Historically, these analysis were (wrongly) understood to be limited to static control programs.

Actually, the polyhedral model is neither a programming language nor an execution model, rather an intermediate representation. As such, it can be generated from imperative sequential languages like C or

Fortran, streaming languages like CRP, or equational languages like Alpha. While the structure of the model is the same in all three cases, it may enjoy different properties, e.g., a schedule always exists in the first case, not in the two others. The import of the polyhedral model is that many questions relative to the analysis of a program and the applicability of transformations can be answered precisely and efficiently by applying well-known mathematical results to the model.

For irregular programs, the basic idea is to construct a polyhedral over-approximation, i.e., a program which has more operations, a larger memory footprint, and more dependences than the original. One can then parallelize the approximated program using polyhedral tools, and then return to the original, either by introducing guards, or by insuring that approximations are harmless. This technique is the standard way of dealing with approximated dependences. We already started to study the impact of approximations in our kernel offloading technique, for optimizing remote communications [10]. It is clear however that this extension method based on over-approximation will apply only to mildly non-polyhedral programs. The restriction to arrays as the only data structure is still present. Its advantage is that it will be able to subsume in a coherent framework many disparate tricks: the extraction of SCoPs, induction variable detection, the omission of non-affine subscripts, or the conversion of control dependences into data dependences. The link with the techniques developed in the PIPS compiler (based on array region analysis) is strong and will have to be explored.

Such over-approximations can be found by mean of abstract interpretation, a general framework to develop static analysis on real-life programs. However, they were designed mainly for verification purposes, thus precision was the main issue before scalability. Although many efforts were made in designing specialized analyses (pointers, data structures, arrays), these approaches still suffer from a lack of experimental evidence concerning their applicability for code optimization. Following our experience and work on termination analysis (that connects the work on back-end CFG-like and front-end polyhedral-like optimizations), and our work on range analysis of numerical variables and on the memory footprint on real-world C programs [18], one of our objectives for the future was to bridge the gap between abstract interpretation and compilation, by designing cheaper analyses that scale well, mainly based on compact representations derived from variants of static single assignment (SSA), with a special focus on complex control, and complex data structures (pointers, lists) that still suffer from complexity issues in the area of optimization.

Another possibility is to rely on application specific knowledge to guide compiler decisions, as it is impossible for a compiler alone to fully exploit such pieces of information. A possible approach to better utilize such knowledge is to put the programmers “in the loop”. Expert parallel programmers often have a good idea about coarse-grain parallelism and locality that they want to use for an application. On the other hand, fine-grain parallelism (e.g., ILP, SIMD) is tedious and specific to each underlying architecture, and is best left to the compiler. Furthermore, approximations will have opportunities to be refined using programmer knowledge. The key challenge is to create a programming environment where compiler techniques and programmer knowledge can be combined effectively. One of the difficulties is to design a common language between the compiler and the programmer. The first step towards this objective is to establish inter-disciplinary collaborations with users, and take the time to analyze and optimize their applications together.M

3.3. Mathematical Tools

All compilers have to deal with *sets* and relations. In classical compilers, these sets are finite: the set of statements of a program, the set of its variables, its abstract syntax tree (AST), its control-flow graph (CFG), and many others. It is only in the first phase of compilation, parsing, that one has to deal with infinite objects, regular and context-free languages, and those are represented by finite grammars, and are processed by a symbolic algorithm, `yacc` or one of its clones.

When tackling parallel programs and parallel compilation, it was soon realized that this position was no longer tenable. Since it makes no sense to ask whether a statement can be executed in parallel with itself, one has to consider sets of operations, which may be so large as to forbid an extensive representation, or even be infinite. The same is true for dependence sets, for memory cells, for communication sets, and for many other objects a parallel compiler has to consider. The representation is to be *symbolic*, and all necessary algorithms have to be promoted to symbolic versions.

Such symbolic representations have to be efficient – the formula representing a set has to be much smaller than the set itself – and effective – the operations one needs, union, intersection, emptiness tests and many others – have to be feasible and fast. As an aside, note that progress in algorithm design has blurred the distinction between polynomially-solvable and NP-complete problems, and between decidable and undecidable questions. For instance SAT, SMT, and ILP software tools solve efficiently many NP-complete problems, and the Z3 tool is able to "solve" many instances of the undecidable Hilbert's 10th problem.

Since the times of Pip and of the Polylib, Compsys has been active in the implementation of basic mathematical tools for program analysis and synthesis. Pip is still developed by Paul Feautrier and Cédric Bastoul, while the Polylib is now taken care of by the Inria Camus project, which introduced Ehrhart polynomials. These tools are still in use world-wide and they also have been reimplemented many times with (sometimes slight) improvements, e.g., as part of the Parma Polylib, of Sven Verdoolaege's Isl and Barvinok libraries, or of the Jollylib of Reservoir Labs. Other groups also made a lot of efforts towards the democratization of the use of polyhedral techniques, in particular the Alchemy Inria project, with Cloog and the development of Graphite in GCC, and Sadayappan's group in the USA, with the development of U. Bondhugula's Pluto prototype compiler. The same effort is made through the PPCG prototype compiler (for GPU) and Pencil (directives-based language on top of PPCG).

After 2009, Compsys continued to focus on the introduction of concepts and techniques to extend the polytope model, with a shift toward tools that may prepare the future. For instance, PoCo and C2fsm are able to parse general programs, not just SCoPs (static control programs), while the efficient handling of Boolean affine formulas [13] is a prerequisite for the construction of non-convex approximations. Euclidean lattices provide an efficient abstraction for the representation of spatial phenomena, and the construction of *critical lattices* as embedded in the tool Cl@k is a first step towards memory optimization in stream languages and may be useful in other situations. Our work on Chuba introduced a new element-wise array reuse analysis and the possibility of handling approximations. Our work on the analysis of while loops is both an extension of the polytope model itself (i.e., beyond SCoPs) and of its applications, here links with program termination and worst-case execution time (WCET) tools.

A recent example of this extension idea is the proposal by Paul Feautrier to use polynomials for program analysis and optimization [14]. The associated tools are based on Handelman and Schweighofer theorems, the polynomial analogue of Farkas lemma. While this is definitely work in progress, with many unsolved questions, it has the potential of greatly enlarging the set of tractable programs.

As a last remark, observe that a common motif of these developments is the transformation of finite algorithms into symbolic algorithms, able to solve very large or even infinite instances. For instance, PIP is a symbolic extension of the Simplex; our work on memory allocation is a symbolic extension of the familiar register allocation problem; loop scheduling extends DAG scheduling. Many other algorithms await their symbolic transformation: a case in point is resource-constrained scheduling.

CONVECS Project-Team

3. Research Program

3.1. New Formal Languages and their Concurrent Implementations

We aim at proposing and implementing new formal languages for the specification, implementation, and verification of concurrent systems. In order to provide a complete, coherent methodological framework, two research directions must be addressed:

- *Model-based specifications*: these are operational (i.e., constructive) descriptions of systems, usually expressed in terms of processes that execute concurrently, synchronize together and communicate. Process calculi are typical examples of model-based specification languages. The approach we promote is based on LOTOS NT (LNT for short), a formal specification language that incorporates most constructs stemming from classical programming languages, which eases its acceptance by students and industry engineers. LNT [29] is derived from the ISO standard E-LOTOS (2001), of which it represents the first successful implementation, based on a source-level translation from LNT to the former ISO standard LOTOS (1989). We are working both on the semantic foundations of LNT (enhancing the language with module interfaces and timed/probabilistic/stochastic features, compiling the m among n synchronization, etc.) and on the generation of efficient parallel and distributed code. Once equipped with these features, LNT will enable formally verified asynchronous concurrent designs to be implemented automatically.
- *Property-based specifications*: these are declarative (i.e., non-constructive) descriptions of systems, which express *what* a system should do rather than *how* the system should do it. Temporal logics and μ-calculi are typical examples of property-based specification languages. The natural models underlying value-passing specification languages, such as LNT, are Labeled Transition Systems (LTSs or simply *graphs*) in which the transitions between states are labeled by actions containing data values exchanged during handshake communications. In order to reason accurately about these LTSs, temporal logics involving data values are necessary. The approach we promote is based on MCL (*Model Checking Language*) [51], which extends the modal μ-calculus with data-handling primitives, fairness operators encoding generalized Büchi automata, and a functional-like language for describing complex transition sequences. We are working both on the semantic foundations of MCL (extending the language with new temporal and hybrid operators, translating these operators into lower-level formalisms, enhancing the type system, etc.) and also on improving the MCL on-the-fly model checking technology (devising new algorithms, enhancing ergonomy by detecting and reporting vacuity, etc.).

We address these two directions simultaneously, yet in a coherent manner, with a particular focus on applicable concurrent code generation and computer-aided verification.

3.2. Parallel and Distributed Verification

Exploiting large-scale high-performance computers is a promising way to augment the capabilities of formal verification. The underlying problems are far from trivial, making the correct design, implementation, fine-tuning, and benchmarking of parallel and distributed verification algorithms long-term and difficult activities. Sequential verification algorithms cannot be reused as such for this task: they are inherently complex, and their existing implementations reflect several years of optimizations and enhancements. To obtain good speedup and scalability, it is necessary to invent new parallel and distributed algorithms rather than to attempt a parallelization of existing sequential ones. We seek to achieve this objective by working along two directions:

- *Rigorous design:* Because of their high complexity, concurrent verification algorithms should themselves be subject to formal modeling and verification, as confirmed by recent trends in the certification of safety-critical applications. To facilitate the development of new parallel and distributed verification algorithms, we promote a rigorous approach based on formal methods and verification. Such algorithms will be first specified formally in LNT, then validated using existing model checking algorithms of the CADP toolbox. Second, parallel or distributed implementations of these algorithms will be generated automatically from the LNT specifications, enabling them to be experimented on large computing infrastructures, such as clusters and grids. As a side-effect, this "bootstrapping" approach would produce new verification tools that can later be used to self-verify their own design.
- *Performance optimization:* In devising parallel and distributed verification algorithms, particular care must be taken to optimize performance. These algorithms will face concurrency issues at several levels: grids of heterogeneous clusters (architecture-independence of data, dynamic load balancing), clusters of homogeneous machines connected by a network (message-passing communication, detection of stable states), and multi-core machines (shared-memory communication, thread synchronization). We will seek to exploit the results achieved in the parallel and distributed computing field to improve performance when using thousands of machines by reducing the number of connections and the messages exchanged between the cooperating processes carrying out the verification task. Another important issue is the generalization of existing LTS representations (explicit, implicit, distributed) in order to make them fully interoperable, such that compilers and verification tools can handle these models transparently.

3.3. Timed, Probabilistic, and Stochastic Extensions

Concurrent systems can be analyzed from a *qualitative* point of view, to check whether certain properties of interest (e.g., safety, liveness, fairness, etc.) are satisfied. This is the role of functional verification, which produces Boolean (yes/no) verdicts. However, it is often useful to analyze such systems from a *quantitative* point of view, to answer non-functional questions regarding performance over the long run, response time, throughput, latency, failure probability, etc. Such questions, which call for numerical (rather than binary) answers, are essential when studying the performance and dependability (e.g., availability, reliability, etc.) of complex systems.

Traditionally, qualitative and quantitative analyzes are performed separately, using different modeling languages and different software tools, often by distinct persons. Unifying these separate processes to form a seamless design flow with common modeling languages and analysis tools is therefore desirable, for both scientific and economic reasons. Technically, the existing modeling languages for concurrent systems need to be enriched with new features for describing quantitative aspects, such as probabilities, weights, and time. Such extensions have been well-studied and, for each of these directions, there exist various kinds of automata, e.g., discrete-time Markov chains for probabilities, weighted automata for weights, timed automata for hard real-time, continuous-time Markov chains for soft real-time with exponential distributions, etc. Nowadays, the next scientific challenge is to combine these individual extensions altogether to provide even more expressive models suitable for advanced applications.

Many such combinations have been proposed in the literature, and there is a large amount of models adding probabilities, weights, and/or time. However, an unfortunate consequence of this diversity is the confuse landscape of software tools supporting such models. Dozens of tools have been developed to implement theoretical ideas about probabilities, weights, and time in concurrent systems. Unfortunately, these tools do not interoperate smoothly, due both to incompatibilities in the underlying semantic models and to the lack of common exchange formats.

To address these issues, CONVECS follows two research directions:

- *Unifying the semantic models*. Firstly, we will perform a systematic survey of the existing semantic models in order to distinguish between their essential and non-essential characteristics, the goal being to propose a unified semantic model that is compatible with process calculi techniques for specifying and verifying concurrent systems. There are already proposals for unification either

theoretical (e.g., Markov automata) or practical (e.g., PRISM and MODEST modeling languages), but these languages focus on quantitative aspects and do not provide high-level control structures and data handling features (as LNT does, for instance). Work is therefore needed to unify process calculi and quantitative models, still retaining the benefits of both worlds.

- *Increasing the interoperability of analysis tools*. Secondly, we will seek to enhance the interoperability of existing tools for timed, probabilistic, and stochastic systems. Based on scientific exchanges with developers of advanced tools for quantitative analysis, we plan to evolve the CADP toolbox as follows: extending its perimeter of functional verification with quantitative aspects; enabling deeper connections with external analysis components for probabilistic, stochastic, and timed models; and introducing architectural principles for the design and integration of future tools, our long-term goal being the construction of a European collaborative platform encompassing both functional and non-functional analyzes.

3.4. Component-Based Architectures for On-the-Fly Verification

On-the-fly verification fights against state explosion by enabling an incremental, demand-driven exploration of LTSs, thus avoiding their entire construction prior to verification. In this approach, LTS models are handled implicitly by means of their *post* function, which computes the transitions going out of given states and thus serves as a basis for any forward exploration algorithm. On-the-fly verification tools are complex software artifacts, which must be designed as modularly as possible to enhance their robustness, reduce their development effort, and facilitate their evolution. To achieve such a modular framework, we undertake research in several directions:

- *New interfaces for on-the-fly LTS manipulation*. The current application programming interface (API) for on-the-fly graph manipulation, named OPEN/CAESAR [35], provides an "opaque" representation of states and actions (transitions labels): states are represented as memory areas of fixed size and actions are character strings. Although appropriate to the pure process algebraic setting, this representation must be generalized to provide additional information supporting an efficient construction of advanced verification features, such as: handling of the types, functions, data values, and parallel structure of the source program under verification, independence of transitions in the LTS, quantitative (timed/probabilistic/stochastic) information, etc.
- *Compositional framework for on-the-fly LTS analysis*. On-the-fly model checkers and equivalence checkers usually perform several operations on graph models (LTSs, Boolean graphs, etc.), such as exploration, parallel composition, partial order reduction, encoding of model checking and equivalence checking in terms of Boolean equation systems, resolution and diagnostic generation for Boolean equation systems, etc. To facilitate the design, implementation, and usage of these functionalities, it is necessary to encapsulate them in software components that could be freely combined and replaced. Such components would act as graph transformers, that would execute (on a sequential machine) in a way similar to coroutines and to the composition of lazy functions in functional programming languages. Besides its obvious benefits in modularity, such a component-based architecture will also make it possible to take advantage of multi-core processors.
- *New generic components for on-the-fly verification*. The quest for new on-the-fly components for LTS analysis must be pursued, with the goal of obtaining a rich catalog of interoperable components serving as building blocks for new analysis features. A long-term goal of this approach is to provide an increasingly large catalog of interoperable components covering all verification and analysis functionalities that appear to be useful in practice. It is worth noticing that some components can be very complex pieces of software (e.g., the encapsulation of an on-the-fly model checker for a rich temporal logic). Ideally, it should be possible to build a novel verification or analysis tool by assembling on-the-fly graph manipulation components taken from the catalog. This would provide a flexible means of building new verification and analysis tools by reusing generic, interoperable model manipulation components.

3.5. Real-Life Applications and Case Studies

We believe that theoretical studies and tool developments must be confronted with significant case studies to assess their applicability and to identify new research directions. Therefore, we seek to apply our languages, models, and tools for specifying and verifying formally real-life applications, often in the context of industrial collaborations.

CORSE Project-Team

3. Research Program

3.1. Scientific Foundations

One of the characteristics of CORSE is to base our researches on diverse advanced mathematical tools. Compiler optimization requires the usage of the several tools around discrete mathematics: combinatorial optimization, algorithmic, and graph theory. The aim of CORSE is to tackle optimization not only for regular but also for irregular applications. We believe that new challenges in compiler technology design and in particular for split compilation should also take advantage of graph labeling techniques. In addition to runtime and compiler techniques for program instrumentation, hybrid analysis and compilation advances will be mainly based on polynomial and linear algebra.

The other specificity of CORSE is to address technical challenges related to compiler technology, runtime systems, and hardware characteristics. This implies mastering the details of each. This is especially important as any optimization is based on a reasonably accurate model. Compiler expertise will be used in modeling applications (e.g. through automatic analysis of memory and computational complexity); Runtime expertise will be used in modeling the concurrent activities and overhead due to contention (including memory management); Hardware expertise will be extensively used in modeling physical resources and hardware mechanisms (including synchronization, pipelines, etc.).

The core foundation of the team is related to the combination of static and dynamic techniques, of compilation, and runtime systems. We believe this to be essential in addressing high-performance and low energy challenges in the context of new important changes shown by current application, software, and architecture trends.

Our project is structured along two main directions. The first direction belongs to the area of runtime systems with the objective of developing strong relations with compilers. The second direction belongs to the area of compiler analysis and optimization with the objective of combining dynamic analysis and optimization with static techniques. The aim of CORSE is to ground those two research activities on the development of the end-to-end optimization of some specific domain applications.

CTRL-A Team

3. Research Program

3.1. Modeling and control techniques for autonomic computing

3.1.1. Continuous control

Continuous control was used to control computer systems only very recently and in few occasions, despite the promising results that were obtained. This is probably due to many reasons, but the most important seems to be the difficulty by both communities to transform a computer system problem into an automatic control problem. The aim of the team is to explore how to formalize typical autonomic commuting cases into typical control problems. Many new methodological tools will probably be useful for that, e.g., we can cite the hybrid system approach, predictive control or event-based control approach. Computer systems are not usual for the control system community and they often present non-conventional control aspects like saturation control. New methodological tools are required for an efficient use of continuous-time control in computer science.

3.1.2. Discrete control

Discrete control techniques are explored at long-term, to integrate more control in the BZR language, and adress more general control issues, wider than BZR's limitations. Directions are : expressiveness (taking into account in the LTS models value domains of the variables in the program) ; adaptive control (where the controller itself can dynamically switch between differents modes) ; distributed control (for classes of problems where communicating controllers can be designed) ; optimal control (w.r.t. weight functions, on states, transitions, and paths, with multicriteria techniques) ; timed and hybrid control bringing a new dimension for modeling and control, giving solutions where discrete models fail.

3.2. Design and programming for autonomic computing

3.2.1. Reactive programming

Autonomic systems are intrinsically reconfigurable. To describe, specify or design these systems, there is a need to take into account this reconfigurability, within the programming languages used. We propose to consider the reconfigurability of systems from the angle of two properties: the notion of time, as we want to describe the state and behavior of the system before, and after its reconfiguration; the notion of dynamicity of the system, i.e., considering that the system's possible behaviors throughout execution are not completely known, neither at design-time nor at initial execution state. To describe and design such reactive systems, we propose to use the synchronous paradigm. It has been successfully used, in industry, for the design of embedded systems. It allows the description of behaviors based on a specific model of time (discrete time scale, synchronous parallel composition), providing properties which are important w.r.t. the safety of the described system: reactivity, determinism, preservation of safety properties by parallel composition (with other parts of the system or with its environment). Models and languages for control, proposed in this framework, provide designers, experts of the application domain, with a user-friendly access to highly technical formal methods of DCS, by encapsulating them in the compilation of concrete programming languages, generating concrete executable code. They are based on discrete models, but also support programming of sampled continuous controllers.

3.2.2. Component-based approach and domain-specific languages

For integration of the previous control kernels into wider frameworks of reconfigurable systems, they have to be integrated in a design flow, and connected on the one side with higher-level specification languages (with help of DSLs), and on the other side with the generated code level target execution machines. This calls for the adoption of a component-based approach with necessary features, available typically in Fractal, for explicitly identifying the control interfaces and mechanisms.

Structuring and instrumentation for controllability will involve encapsulation of computations into components, specification of their local control (activation, reconfiguration, suspension, termination), and exporting appropriate interfaces (including behavior abstraction). Modeling the configurations space requires determining the controlled aspects (e.g., heterogenous CPUs loads, fault-tolerance and variability, memory, energy/power consumption, communication/bandwidth, QoS level) and their control points, as well as APIs for monitors and actions. Compilation and execution will integrate this in a complete design flow involving : extraction of a reactive model from components; instrumentation of execution platforms to be controllable; combination with other controllers; general "glue" and wrapper code.

Integration of reactive languages and control techniques in component-based systems brings interesting questions of co-existence w.r.t. other approaches like Event-Condition-Action (ECA) rules, or Complex Event Processing (CPE).

3.3. Infrastructure-level support for autonomic computing

The above general kernel of model-based control techniques can be used in a range of different computing infrastructures, representing complementary targets and abstraction levels, exploring the two axes :

- from hardware, to operating system/virtual machine, to middleware, to applications/service level;
- across different criteria for adaptation: resources and energy, quality of service, dependability.

3.3.1. Software and adaptive systems

Autonomic administration loops at operating systems or middleware level are already very widespread. An open problem remains in design techniques for controllers with predictability and safety, e.g. w.r.t. the reachable states. We want to contribute to the topic of discrete control techniques for these systems, and tackle e.g. problems of coordination of multiple autonomic loops in data-centers, as in the ANR project CtrlGreen. Another target application is the control of clusters in map-reduce applications. The objective is to use continuous time control in order to tune finely the number of required clusters for an application running on a map-reduce server. This will use results of the ANR project MyCloud that enables to simulate clients on a real map-reduce server. On a longer term, we are interested in control problems in administration loops of event-based virtual machines, or in the deployment of massively parallel computation of the Cloud.

3.3.2. Hardware and reconfigurable architectures

Reconfigurable architectures based on Field Programmable Gate Arrays (FPGA) are an active research area, where infrastructures are more and more supportive of reconfiguration, but its correct control remains an important issue. Work has begun in the ANR Famous project on identifying domain-specific control criteria and objectives, monitors and management APIs, and on integrating control techniques in the high-level RecoMARTE environment. On a longer term, we want to work on methods and tools for the programming of **multicore architectures**, exploiting the reconfigurability potentials and issues (because of variability, loss of cores), e.g. in our cooperation with ST Microelectronics, using a Fractal-based programming framework in the P2012 project, and in cooperation with Inria Lille (Adam), or with the CEA and TIMA on integrating control loops in the architecture for a fine control of the energy and of the required nodes for running a given application task.

3.3.3. Applications and autonomic systems

In autonomic systems, control systems remain a lively source of inspiration, partly because the notion of control loop implementation is known and practiced naturally. On a wider scale, we started a cooperation with Orange Labs on "intelligent" building automation and control for the Smart Grid, through modeling and control of appliances w.r.t. their power consumption modes, at home, building, and city levels. Other partners on these topics are CEA LETI/DACLE and Schneider Electric.

We could explore more systems and applications e.g., Human-Machine Interfaces, or the orchestration of services. They can help design more general solutions, and result in a more complete methodology.

DANTE Project-Team

3. Research Program

3.1. Graph-based signal processing

Participants: Christophe Crespelle, Éric Fleury, Paulo Gonçalves Andrade, Márton Karsai, Sarah de Nigris, Sarra Ben Alaya, Hadrien Hours.

Evolving networks can be regarded as "*out of equilibrium*" systems. Indeed, their dynamics is typically characterized by non standard and intricate statistical properties, such as non-stationarity, long range memory effects, intricate space and time correlations.

Analyzing, modeling, and even defining adapted concepts for dynamic graphs is at the heart of DANTE. This is a largely open question that has to be answered by keeping a balance between specificity (solutions triggered by specific data sets) and generality (universal approaches disconnected from social realities). We will tackle this challenge from a graph-based signal processing perspective involving signal analysts and computer scientists, together with experts of the data domain application. One can distinguish two different issues in this challenge, one related to the graph-based organisation of the data and the other to the time dependency that naturally exits in the dynamic graph object. In both cases, a number of contributions can be found in the literature, albeit in different contexts. In our application domain, high-dimensional data "naturally reside" on the vertices of weighted graphs. The emerging field of signal processing on graphs merges algebraic and spectral graph theoretic concepts with computational harmonic analysis to process such signals on graphs [70].

As for the first point, adapting well-founded signal processing techniques to data represented as graphs is an emerging, yet quickly developing field which has already received key contributions. Some of them are very general and delineate ambitious programs aimed at defining universal, generally unsupervised methods for exploring high-dimensional data sets and processing them. This is the case for instance of the Â« diffusion wavelets Â» and Â« diffusion maps Â» pushed forward at Yale and Duke [54]. Others are more traditionally connected with standard signal processing concepts, in the spirit of elaborating new methodologies via some bridging between networks and time series, see, *e.g.*, ([65] and references therein). Other viewpoints can be found as well, including multi-resolution Markov models [73], Bayesian networks or distributed processing over sensor networks [64]. Such approaches can be particularly successful for handling static graphs and unveiling aspects of their organisation in terms of dependencies between nodes, grouping, etc. Incorporating possible time dependencies within the whole picture calls however for the addition of an extra dimension to the problem "as it would be the case when switching from one image to a video sequence", a situation for which one can imagine to take advantage of the whole body of knowledge attached to non-stationary signal processing [55].

3.2. Theory and Structure of dynamic Networks

Participants: Christophe Crespelle, Éric Fleury, Anthony Busson, Márton Karsai.

Characterization of the dynamics of complex networks. We need to focus on intrinsic properties of evolving/dynamic complex networks. New notions (as opposed to classical static graph properties) have to be introduced: rate of vertices or links appearances or disappearances, the duration of link presences or absences. Moreover, more specific properties related to the dynamics have to be defined and are somehow related to the way to model a dynamic graph.

Through the systematic analysis and characterization of static network representations of many different systems, researchers of several disciplines have unveiled complex topologies and heterogeneous structures, with connectivity patterns statistically characterized by heavy-tails and large fluctuations, scale-free properties and non trivial correlations such as high clustering and hierarchical ordering [67]. A large amount of work has been devoted to the development of new tools for statistical characterisation and modelling of networks, in order to identify their most relevant properties, and to understand which growth mechanisms could lead to these properties. Most of those contributions have focused on static graphs or on dynamic process (*e.g.* diffusion) occurring on static graphs. This has called forth a major effort in developing the methodology to characterize the topology and temporal behavior of complex networks [67], [58], [74], [63], to describe the observed structural and temporal heterogeneities [52], [58], [53], to detect and measure emerging community structures [56], [71], [72], to see how the functionality of networks determines their evolving structure [62], and to determine what kinds of correlations play a role in their dynamics [59], [61], [66].

The challenge is now to extend this kind of statistical characterization to dynamical graphs. In other words, links in dynamic networks are temporal events, called contacts, which can be either punctual or last for some period of time. Because of the complexity of this analysis, the temporal dimension of the network is often ignored or only roughly considered. Therefore, fully taking into account the dynamics of the links into a network is a crucial and highly challenging issue.

Another powerful approach to model time-varying graphs is via activity driven network models. In this case, the only assumption relates to the distribution of activity rates of interacting entities. The activity rate is realistically broadly distributed and refers to the probability that an entity becomes active and creates a connection with another entity within a unit time step [69]. Even the generic model is already capable to recover some realistic features of the emerging graph, its main advantage is to provide a general framework to study various types of correlations present in real temporal networks. By synthesizing such correlations (*e.g.* memory effects, preferential attachment, triangular closing mechanisms, ...) from the real data, we are able to extend the general mechanism and build a temporal network model, which shows certain realistic feature in a controlled way. This can be used to study the effect of selected correlations on the evolution of the emerging structure [60] and its co-evolution with ongoing processes like spreading phenomena, synchronisation, evolution of consensus, random walk etc. [60], [68]. This approach allows also to develop control and immunisation strategies by fully considering the temporal nature of the backgrounding network.

3.3. Distributed Algorithms for dynamic networks: regulation, adaptation and interaction

Participants: Thomas Begin, Anthony Busson, Paulo Gonçalves Andrade, Isabelle Guérin Lassous.

Dedicated algorithms for dynamic networks. First, the dynamic network object itself trigger original algorithmic questions. It mainly concerns distributed algorithms that should be designed and deployed to efficiently measure the object itself and get an accurate view of its dynamic behavior. Such distributed measure should be "transparent", that is, it should introduce no bias or at least a bias that is controllable and corrigible. Such problem is encountered in all distributed metrology measures / distributed probes: P2P, sensor network, wireless network, QoS routing... This question raises naturally the intrinsic notion of adaptation and control of the dynamic network itself since it appears that autonomous networks and traffic aware routing are becoming crucial.

Communication networks are dynamic networks that potentially undergo high dynamicity. The dynamicity exhibited by these networks results from several factors including, for instance, changes in the topology and varying workload conditions. Although most implemented protocols and existing solutions in the literature can cope with a dynamic behavior, the evolution of their behavior operates identically whatever the actual properties of the dynamicity. For instance, parameters of the routing protocols (*e.g.* hello packets transmission frequency) or routing methods (*e.g.* reactive / proactive) are commonly hold constant regardless of the nodes mobility. Similarly, the algorithms ruling CSMA/CA (*e.g.* size of the contention window) are tuned identically and they do not change according to the actual workload and observed topology.

Dynamicity in computer networks tends to affect a large number of performance parameters (if not all) coming from various layers (viz. physical, link, routing and transport). To find out which ones matter the most for our intended purpose, we expect to rely on the tools developed by the two former axes. These quantities should capture and characterize the actual network dynamicity. Our goal is to take advantage of this latter information in order to refine existing protocols, or even to propose new solutions. More precisely, we will attempt to associate "fundamental" changes occurring in the underlying graph of a network (reported through graph-based signal tools) to quantitative performance that are matter of interests for networking applications and the end-users. We expect to rely on available testbeds such as Senslab and FIT to experiment our solutions and ultimately validate our approach.

DATAMOVE Team

3. Research Program

3.1. Motivation

Today's largest supercomputers [0] are composed of few millions of cores, with performances almost reaching 100 PetaFlops [0] for the largest machine. Moving data in such large supercomputers is becoming a major performance bottleneck, and the situation is expected to worsen even more at exascale and beyond. The data transfer capabilities are growing at a slower rate than processing power ones. The profusion of available flops will very likely be underused due to constrained communication capabilities. It is commonly admitted that data movements account for 50% to 70% of the global power consumption [0]. Thus, data movements are potentially one of the most important source of savings for enabling supercomputers to stay in the commonly adopted energy barrier of 20 MegaWatts. In the mid to long term, non volatile memory (NVRAM) is expected to deeply change the machine I/Os. Data distribution will shift from disk arrays with an access time often considered as uniform, towards permanent storage capabilities at each node of the machine, making data locality an even more prevalent paradigm.

The DataMove team works on **optimizing data movements for large scale computing** mainly at two related levels:

- Resource allocation
- Integration of numerical simulation and data analysis

The resource and job management system (also called batch scheduler or RJMS) is in charge of allocating resources upon user requests for executing their parallel applications. The growing cost of data movements requires adapted scheduling policies able to take into account the influence of intra-application communications, I/Os as well as contention caused by data traffic generated by other concurrent applications. Modelling the application behavior to anticipate its actual resource usage on such architecture is known to be challenging, but it becomes critical for improving performances (execution time, energy, or any other relevant objective). The job management system also needs to handle new types of workloads: high performance platforms now need to execute more and more often data intensive processing tasks like data analysis in addition to traditional computation intensive numerical simulations. In particular, the ever growing amount of data generated by numerical simulation calls for a tighter integration between the simulation and the data analysis. The challenge here is to reduce data traffic and to speed-up result analysis by performing result processing (compression, indexation, analysis, visualization, etc.) as closely as possible to the locus and time of data generation. This emerging trend called *in situ analytics* requires to revisit the traditional workflow (loop of batch processing followed by postmortem analysis). The application becomes a whole including the simulation, in situ processing and I/Os. This motivates the development of new well-adapted resource sharing strategies, data structures and parallel analytics schemes to efficiently interleave the different components of the application and globally improve the performance.

3.2. Strategy

DataMove targets HPC (High Performance Computing) at Exascale. But such machines and the associated applications are expected to be available only in 5 to 10 years. Meanwhile, we expect to see a growing number of petaflop machines to answer the needs for advanced numerical simulations. A sustainable exploitation of these petaflop machines is a real and hard challenge that we address. We may also see in the coming years a convergence between HPC and Big Data, HPC platforms becoming more elastic and supporting Big Data

[0] Top500 Ranking, http://www.top500.org
[0] 10^{15} floating point operations per second
[0] SciDAC Review, 2010, http://www.scidacreview.org/1001/pdf/hardware.pdf

jobs, or HPC applications being more commonly executed on cloud like architectures. This is the second top objective of the 2015 US Strategic Computing Initiative [0]: *Increasing coherence between the technology base used for modelling and simulation and that used for data analytic computing*. We contribute to that convergence at our level, considering more dynamic and versatile target platforms and types of workloads.

Our approaches should entail minimal modifications on the code of numerical simulations. Often large scale numerical simulations are complex domain specific codes with a long life span. We assume these codes as being sufficiently optimized. We influence the behavior of numerical simulations through resource allocation at the job management system level or when interleaving them with analytics code.

To tackle these issues, we propose to intertwine theoretical research and practical developments in an agile mode. Algorithms with performance guarantees are designed and experimented on large scale platforms with realistic usage scenarios developed with partner scientists or based on logs of the biggest available computing platforms (national supercomputers like Curie, or the BlueWaters machine accessible through our collaboration with Argonne National Lab). Conversely, a strong experimental expertise enables to feed theoretical models with sound hypotheses, to twist proven algorithms with practical heuristics that could be further retro-feeded into adequate theoretical models.

A central scientific question is to make the relevant choices for optimizing performance (in a broad sense) in a reasonable time. HPC architectures and applications are increasingly complex systems (heterogeneity, dynamicity, uncertainties), which leads to consider the **optimization of resource allocation based on multiple objectives**, often contradictory (like energy and run-time for instance). Focusing on the optimization of one particular objective usually leads to worsen the others. The historical positioning of some members of the team who are specialists in multi-objective optimization is to generate a (limited) set of trade-off configurations, called *Pareto points*, and choose when required the most suitable trade-off between all the objectives. This methodology differs from the classical approaches, which simplify the problem into a single objective one (focus on a particular objective, combining the various objectives or agglomerate them). The real challenge is thus to combine algorithmic techniques to account for this diversity while guaranteeing a target efficiency for all the various objectives.

The DataMove team aims to elaborate generic and effective solutions of practical interest. We make our new algorithms accessible through the team flagship software tools, **the OAR batch scheduler and the in situ processing framework FlowVR**. We maintain and enforce strong links with teams closely connected with large architecture design and operation, as well as scientists of other disciplines, in particular computational biologists, with whom we elaborate and validate new usage scenarios.

3.3. Research Directions

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[0] https://www.whitehouse.gov/the-press-office/2015/07/29/executive-order-creating-national-strategic-computing-initiative
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DICE Team

3. Research Program

3.1. Introduction

Our goal is to address technological issues as well as investigate their impact on society. We believe that addressing both directions simultaneously is essential. More precisely, we focus on the following two objectives:

- Technologies for global intermediation platforms, at reach for unbounded number of users;
- Trans-disciplinary investigations on the global impact of the new intermediation means.

We focus on intermediation platforms, for their increasingly fundamental role in our societies. Intermediation platforms are online systems which offer services to their users, which are well-tuned with their expectation, thanks to the knowledge the platform has accumulated on usage. Search engines and social networks are fundamental examples of intermediation platforms. More generally, intermediation platforms intermediate between producers of services and consumers of services in two-sided markets, with generally one side subsidizing the other. Intermediation will generalise beyond people to things, such as producers or consumers of energy for instance. The capacity to intermediate "in the cloud" with no presence in the physical world in which the market is deployed, by working purely on data with algorithms and in particular learning techniques, is at the heart of the revolution which reshapes our societies.

Platforms ensure a gatekeeping function, always in direct contact with their users, providing them with the most relevant information or contact. They also generate an ecosystem. To do so, platforms allow existing industries as well as new applications proposed by developers to build new services on top of their API. Their impact goes far beyond the Web, while they disrupt step by step all sectors of the economy, transportation, press, education, to name a few.

So far as computer science is concerned, we focus on the technologies used for intermediation, which are at the basis of the largest existing online systems. For the transdisciplinary questions, we focus mostly on the new equilibria that is resulting from the evolution of power balances due mostly to intermediation platforms.

3.2. Intermediation technologies

DICE focuses on intermediation platforms because of the central role they play in the emerging economy.

Intermediation platforms connect users to one another, or users to services with a very high accuracy. They rely on both technological and social innovations. These innovations were unthinkable only a decade ago, when platforms such as Facebook started. They allow communication and interaction between billions of users, gathered in the same digital space, both producers and consumers of data and services. State-of-the-art intermediation platforms include Facebook, Google, Twitter, GitHub, as well as Wikipedia, StackOverflow or Quora. These systems share a common design and their market penetration follows the same pattern. They are built around an initial minimal viable product based on a somehow naive low-tech implementation, which evolves after a few years of improvement to Web giants. Their domination now contributes to standardize the web industry, that means in particular:

- Gatekeeping, a direct relation with users together with services satisfying users' needs;
- Continuous data flows mapped to users' profiles;
- Search engines associating, in a relevant manner, producers, consumers and services.

These common characteristics lead to new software architectural standards, which are shared by all these systems, and used in the peripheral services developed in the ecosystem on top of their API:

- Authentication systems: openId, OAuth, ...
- Object graphs: opengraph, follower/followee scheme, ...
- DataFlow engines: Twitter storm, Google millwheel, ...
- Databases: noSql, keyValues stores, ...
- Application development: javascript, dart, MEAN (Mongo, Express, Angular, Node),...

These architectural components impact the whole digital world. DICE targets systems that use standard architecture services but preserve some aspects we consider as disruptive ones: *data concentration, data symmetry* and *computational subsidiarity*. Our current research activity includes the following directions:

- Peer-to-peer design for preserving users' primary data;
- Third parties based organic systems providing subsidiary data computation hosted at peer sites;
- In-Browser applications that impact mobile device and demonstrate instantaneous usability;
- Flow-based computing enabling a stream based exchange of information between peers at runtime.

3.3. Economy of intermediation

The recent neologism *uberization* coined after the name of *Uber*, a young intermediation platform, may summarize the effects of the digital revolution. This revolution is impacting all sectors of our societies such as organizations, education, energy, transportation and health, to name a few. This revolution results in a serie of what Schumpeter calls *creative destruction*. As traditional sectors disappear, new ones are created. Our societies, which did not anticipate the depth of the changes, have to struggle to adapt to the pace of the development of the industry. Legal reforms in various important sectors including taxation are at stake. Some countries, more reactive than others, are clearly leading the changes, exploiting the benefits for businesses and the capacity to generate information and value, while others are trying to catch up with the global trends.

Data form the bricks of the information society, and their flows between users and services constitute the blood of the industry. We focus in DICE on the strategic role of data in this revolution, and in particular on the systems that harvest the data and concentrate it. In particular, we focus on *intermediation platforms*. Doing so, we investigate the issues they raise and the disruptions they entail.

We are especially interested in the global political impact of intermediation platforms. The settlement of the *right to be forgotten* in Europe, for instance, examplifies the new roles platforms are playing: they are both targets of complaints from institutions and mandatory partners in the governance of the world in the digital era. Indeed, they deeply revolutionize the relations between governments and citizens. If privacy is the focus of considerable attention, together with the state surveillance, in Europe in particular, it is only one aspect of the new knowledge made available. Social media produce considerable knowledge not only on individuals, but on populations as well, their economic fate, their political orientation, etc. On the other hand, open data from governments allow citizens to monitor the action of their governments, as well as to contribute to it. The digital revolution, with the capacity to access information in ways unthinkable in the recent past, modifies completely the balance of powers between citizens, states and corporations.

We investigate the digital world, and more precisely the power relations, from an interdisciplinary perspective. We simultaneously quantify power relations by studying data flows and the rise of intermediation platforms and produce an economical, political and ethical analysis of this new state of affairs. Namely, we show that areas such as the US or China dominate the digital world when others, such as Europe, do not succeed in proposing widely used intermediation platforms. This situation generates several conflicts between countries and companies and prevents *weak* countries from promoting their values and policies.

A new trend is emerging in the humanities, around in particular the digital studies, which promote the cooperation between computer scientists and specialists of social sciences. Among them, the Berkman center for Internet and Society in Harvard, the Medialab at MIT, or the Web Science Institute in the UK have gained strong visibility. They address positive as well as negative externalities of IT for societies, that is the new potentials offered as well as their risks. The Center for Information Technology Research in the Interest of Society in Berkeley also addresses fundamental political impacts on democracy, which can be enhanced by open data as well as another philosophy of political power as currently implemented in the State of California for instance. The Open Data Institute in the UK is also a leading center for political issues in Europe. France should catch up on these research trends, at the intersection of different scientific fields.

DRACULA Project-Team

3. Research Program

3.1. Cell dynamics

We model dynamics of cell populations with two approaches, dissipative particle dynamics (DPD) and partial differential equations (PDE) of continuum mechanics. DPD is a relatively new method developed from molecular dynamics approach largely used in statistical physics. Particles in DPD do not necessarily correspond to atoms or molecules as in molecular dynamics. These can be mesoscopic particles. Thus, we describe in this approach a system of particles. In the simplest case where each particle is a sphere, they are characterized by their positions and velocities. The motion of particles is determined by Newton's second law (see Figure 1).

In our case, particles correspond to biological cells. The specific feature of this case in comparison with the conventional DPD is that cells can divide (proliferation), change their type (differentiation) and die by apoptosis or necrosis. Moreover, they interact with each other and with the extra-cellular matrix not only mechanically but also chemically. They can exchange signals, they can be influenced by various substances (growth factors, hormones, nutrients) coming from the extra-cellular matrix and, eventually, from other organs.

Distribution of the concentrations of bio-chemical substances in the extra-cellular matrix will be described by the diffusion equation with or without convective terms and with source and/or sink terms describing their production or consumption by cells. Thus we arrive to a coupled DPD-PDE model.

Cell behaviour (proliferation, differentiation, apoptosis) is determined by intra-cellular regulatory networks, which can be influenced by external signals. Intra-cellular regulatory networks (proteins controlling the cell cycle) can be described by systems of ordinary differential equations (ODE). Hence we obtain DPD-PDE-ODE models describing different levels of cell dynamics (see Figure 1). It is important to emphasize that the ODE systems are associated to each cell and they can depend on the cell environment (extra-cellular matrix and surrounding cells).

3.2. From particle dynamics to continuum mechanics

DPD is well adapted to describe biological cells. However, it is a very time consuming method which becomes difficult to use if the number of particles exceeds the order of 10^5-10^6 (unless distributed computing is used). On the other hand, PDEs of continuum mechanics are essentially more efficient for numerical simulations. Moreover, they can be studied by analytical methods which have a crucial importance for the understanding of relatively simple test cases. Thus we need to address the question about the relation between DPD and PDE. The difficulty follows already from the fact that molecular dynamics with the Lennard-Jones potential can describe very different media, including fluids (compressible, incompressible, non-Newtonian, and so on) and solids (elastic, elasto-plastic, and so on). Introduction of dissipative terms in the DPD models can help to justify the transition to a continuous medium because each medium has a specific to it law of dissipation. Our first results [33] show the correspondence between a DPD model and Darcy's law describing fluid motion in a porous medium. However, we cannot expect a rigorous justification in the general case and we will have to carry out numerical comparison of the two approaches.

An interesting approach is related to hybrid models where PDEs of continuum mechanics are considered in the most part of the domain, where we do not need a microscopical description, while DPD in some particular regions are required to consider individual cells.

3.3. PDE models

If we consider cell populations as a continuous medium, then cell concentrations can be described by reaction-diffusion systems of equations with convective terms. The diffusion terms correspond to a random cell motion and the reaction terms to cell proliferation, differentiation and death. These are more traditional models [36] with properties that depend on the particular problem under consideration and with many open questions, both from the point of view of their mathematical properties and for applications. In particular we are interested in the spreading of cell populations which describes the development of leukemia in the bone marrow and many other biological phenomena (solid tumors, morphogenesis, atherosclerosis, and so on). From the mathematical point of view, these are reaction-diffusion waves, intensively studied in relation with various biological problems. We will continue our studies of wave speed, stability, nonlinear dynamics and pattern formation. From the mathematical point of view, these are elliptic and parabolic problems in bounded or unbounded domains, and integro-differential equations. We will investigate the properties of the corresponding linear and nonlinear operators (Fredholm property, solvability conditions, spectrum, and so on). Theoretical investigations of reaction-diffusion-convection models will be accompanied by numerical simulations and will be applied to study hematopoiesis.

Hyperbolic problems are also of importance when describing cell population dynamics ([42], [46]), and they proved effective in hematopoiesis modelling ([28], [29], [31]). They are structured transport partial differential equations, in which the structure is a characteristic of the considered population, for instance age, size, maturity, protein concentration, etc. The transport, or movement in the structure space, simulates the progression of the structure variable, growth, maturation, protein synthesis, etc. Several questions are still open in the study of transport PDE, yet we will continue our analysis of these equations by focusing in particular on the asymptotic behaviour of the system (stability, bifurcation, oscillations) and numerical simulations of nonlocal transport PDE.

The use of age structure often leads to a reduction (by integration over the age variable) to nonlocal problems [46]. The nonlocality can be either in the structure variable or in the time variable [28]. In particular, when coefficients of an age-structured PDE are not supposed to depend on the age variable, this reduction leads to delay differential equations.

3.4. Delay differential Equations

Delay differential equations (DDEs) are particularly useful for situations where the processes are controlled through feedback loops acting after a certain time. For example, in the evolution of cell populations the transmission of control signals can be related to some processes as division, differentiation, maturation, apoptosis, etc. Because these processes can take a certain time, the system depends on an essential way of its past state, and can be modelled by DDEs.

We explain hereafter how delays can appear in hematopoietic models. Based on biological aspects, we can divide hematopoietic cell populations into many compartments. We basically consider two different cell populations, one composed with immature cells, and the other one made of mature cells. Immature cells are separated in many stages (primitive stem cells, progenitors and precursors, for example) and each stage is composed with two sub-populations, resting (G0) and proliferating cells. On the opposite, mature cells are known to proliferate without going into the resting compartment. Usually, to describe the dynamic of these multi-compartment cell populations, transport equations (hyperbolic PDEs) are used. Structure variables are age and discrete maturity. In each proliferating compartment, cell count is controlled by apoptosis (programmed cell death), and in the other compartments, cells can be eliminated only by necrosis (accidental cell death). Transitions between the compartments are modelled through boundary conditions. In order to reduce the complexity of the system and due to some lack of information, no dependence of the coefficients on cell age is assumed. Hence, the system can be integrated over the age variable and thus, by using the method of characteristics and the boundary conditions, the model reduces to a system of DDEs, with several delays.

Leaving all continuous structures, DDEs appear well adapted to us to describe the dynamics of cell populations. They offer good tools to study the behaviour of the systems. The main investigation of DDEs are the effect of perturbations of the parameters, as cell cycle duration, apoptosis, differentiation, self-renewal, and re-introduction from quiescent to proliferating phase, on the behaviour of the system, in relation for instance with some hematological disorders [38].

ERABLE Project-Team

3. Research Program

3.1. Two main goals

ERABLE has two main goals, one related to biology and the other to methodology (algorithms, combinatorics, statistics). In relation to biology, the main goal of ERABLE is to contribute, through the use of mathematical models and algorithms, to a better understanding of close and often persistent interactions between "collections of genetically identical or distinct self-replicating cells" which will correspond to organisms/species or to actual cells. The first will cover the case of what has been called symbiosis, meaning when the interaction involves different species, while the second will cover the case of a (cancerous) tumour which may be seen as a collection of cells which suddenly disrupts its interaction with the other (collections of) cells in an organism by starting to grow uncontrollably.

Such interactions are being explored initially at the molecular level. Although we rely as much as possible on already available data, we intend to also continue contributing to the identification and analysis of the main genomic and systemic (regulatory, metabolic, signalling) elements involved or impacted by an interaction, and how they are impacted. We started going to the populational and ecological levels by modelling and analysing the way such interactions influence, and are or can be influenced by the ecosystem of which the "collections of cells" are a part. The key steps are:

- identifying the molecular elements based on so-called omics data (genomics, transcriptomics, metabolomics, proteomics, etc.): such elements may be gene/proteins, genetic variations, (DNA/RNA/protein) binding sites, (small and long non coding) RNAs, etc.
- simultaneously inferring and analysing the network that models how these molecular elements are physically and functionally linked together for a given goal, or find themselves associated in a response to some change in the environment;
- modelling and analysing the populational and ecological network formed by the "collections of cells in interaction", meaning modelling a network of networks (previously inferred or as already available in the literature);
- analysing how the behaviour and dynamics of such a network of networks might be controlled by modifying it, including by substracting some of its components from the network or by adding new ones.

In relation to methodology, the main goal is to provide those enabling to address our main biological objective as stated above that lead to the best possible interpretation of the results within a given pre-established model and a well defined question. Ideally, given such a model and question, the method is exact and also exhaustive if more than one answer is possible. Three aspects are thus involved here: establishing the model within which questions can and will be put; clearly defining such questions; exactly answering to them or providing some guarantee on the proximity of the answer given to the "correct" one. We intend to continue contributing to these three aspects:

- at the modelling level, by exploring better models that at a same time are richer in terms of the information they contain (as an example, in the case of metabolism, using hypergraphs as models for it instead of graphs) and are susceptible to an easier treatment:
  - these two objectives (rich models that are at the same time easy to treat) might in many cases be contradictory and our intention is then to contribute to a fuller characterisation of the frontiers between the two;
  - even when feasible, the richer models may lack a full formal characterisation (this is for instance the case of hypergraphs) and our intention is then to contribute to such a characterisation;

- at the question level, by providing clear formalisations of those that will be raised by our biological concerns;
- at the answer level:
  - to extend the area of application of exact algorithms by: (i) a better exploration of the combinatorial properties of the models, (ii) the development of more efficient data structures, (iii) a smarter traversal of the space of solutions when more than one exists;
  - when exact algorithms are not possible, or when there is uncertainty in the input data to an algorithm, to improve the quality of the results given by a deeper exploration of the links between different algorithmic approaches: combinatorial, randomised, stochastic.

3.2. Different research axes

The goals of the team are biological and methodological, the two being intrinsically linked. Any division into axes along one or the other aspect or a combination of both is thus somewhat artificial. Our choice is based more on the biological questions as these are a main (but not unique) driver for the methodological developments. However, since another main objective is to contribute to the fields of exact enumeration algorithms and of combinatorics, we also defined an axis that is exclusively oriented towards some of the more theoretical aspects of such objective in as much as these can be abstracted from the biological motivation. This will concern improving theory and deeply exploring the links between different algorithmic approaches: combinatorial, randomised, stochastic. The first four axes thus fall in the first category, and the fifth one in the second. As concerns the first four axes, the model organisms or systems chosen will be those studied by the biologists among our permanent members or among our close collaborators. Currently these include the following cases:

- Arthropods, notably insects, and their parasites;
- Symbiont-harbouring trypanosomatids and trypanosomas more in general;
- The bacterial communities inside the respiratory tract of mammals (swine, bovine);
- Human in general, and the human microbiota in particular also for its possible relation to cancer.

Notice however that: (1) new model organisms or systems may be considered as the opportunity for new collaborations appears, indeed such collaborations will be actively searched for; and (2) we will always attempt to explore mathematical and computational models and to develop algorithmic methods that are as much as possible generic.

Axis 1: Identifying the molecular elements
Intra and inter-cellular interactions involve molecular elements whose identification is crucial to understand what governs, and also what might enable to control such interactions. For the sake of clarity, the elements may be classified in two main classes, one corresponding to the elements that allow the interactions to happen by moving around or across the cells, and another that are the genomic regions where contact is established. Examples of the first are non coding RNAs, proteins, and mobile genetic elements such as (DNA) transposons, retro-transposons, insertion sequences, etc. Examples of the second are DNA/RNA/protein binding sites and targets. Furthermore, both types (effectors and targets) are subject to variation across individuals of a population, or even within a single (diploid) individual. Identification of these variations is yet another topic that we wish to cover. Variations are understood in the broad sense and cover single nucleotide polymorphisms (SNPs), copy-number variants (CNVs), repeats other than mobile elements, genomic rearrangements (deletions, duplications, insertions, inversions, translocations) and alternative splicings (ASs). All three classes of identification problems (effectors, targets, variations) may be put under the general umbrella of genomic functional annotation.

Axis 2: Inferring and analysing the networks of molecular elements

As increasingly more data about the interaction of molecular elements (among which those described above) becomes available, these should then be modelled in a subsequent step in the form of genetic, metabolic, protein-protein interaction and signalling networks. This raises two main classes of problems. The first is to accurately infer such networks. Reconstructing, by analogy, the metabolic network of an organism is often considered, rightly or wrongly, to be easier than inferring a gene regulatory network, also because in the latter case, identifying all the elements participating in the network is in itself a complex and far from solved issue, as we saw in Axis 1. Moreover, the difficulty varies depending on whether only the structure or also the dynamics of the network is of interest, assuming that the latter may be studied (kinetics data are often missing even with the increasingly more sophisticated and performing technologies we have nowadays). A more complete picture of the functioning of a cell would further require that ever more layers of network and molecular profile data, when available, are integrated together, which raises the problem of how to model together information that is heterogeneous at different levels. Modelling together metabolic and gene regulation for instance is already a hard problem given that the two happen at very different time-scales: fast for metabolic regulation, slow for gene regulation.

Even assuming such a network, integrated or "simple", has been inferred for a given organism or set of organisms, the second problem is then to develop the appropriate mathematical models and methods to extract further biological information from such networks. The difficulty of this differs of course again depending on whether only the structure of the network is of interest, or also its dynamics. We are addressing various questions related to one or the other of the above aspects – inference and analysis.

Axis 3: Modelling and analysing a network of individuals, or a network of individuals' networks
As mentioned, at its extreme, life can be seen as one collection, or a collection of collections of genetically identical or distinct self-replicating cells who interact, sometimes closely and for long periods of evolutionary time, with a same or with distinct functional objectives. One striking example is human, who is composed of cells which are both native and extraneous; in fact, a surprising 90% is believed to belong to the second category, mostly bacteria, including one which lost its identity to become a "mere" human organelle, the mitochondrion. Bacteria on the other hand group into colonies of genetically identical individuals which may sometimes acquire the ability to become specialised for different tasks. Which is the "individual", a single bacterium or a group thereof is difficult to say. To understand human or bacteria, or to understand any other organism, it appears therefore essential to better comprehend the interactions in which they are involved. Methodologically speaking, we must therefore move towards modelling and analysing not a single individual anymore but a network of individuals. Ultimately, we should move towards investigating a network of individuals' networks. Moreover, since organisms interact not only with others but also with their abiotic environment, there is a need to model full ecosystems, at a static but also at a dynamic level, that is by taking into account the fact that individuals or populations move in space. Our intention at a longer term is to address all such different levels. We started with the molecular and static one that we are treating from different perspectives for a large number of species at the genomic level (Baudet *et al.*, Syst Biol, 64(3), 2015) and for a small number at the network level (Cottret *et al.*, PLoS Comput Biol, 6(9), 2010). We intend in a near future to slowly move towards a populational and ecological approach that is dynamic in both time and space.

Axis 4: Going towards control
What was described in the Axes 2 and 3 above concerned modelling and analysing a molecular network, or network of networks, but not attempting to control the network at either level for bio-technological, environmental or health purposes.

In the bio-technological case, the objective can be briefly described as involving the manipulation of a species, in general a bacterium, in order for it to produce more of a given chemical compound it already synthetises (for instance, ethanol) but not in enough quantity, or to produce a metabolite it normally is not able to synthetise. The motivation for transplanting its production in a bacterium is, again, to be able to make it more effective.

As concerns control for environmental or health purposes, this could be achieved at least in some cases by manipulating the symbionts with which an organism, insect pest for instance, or humans leave. In the environmental case, this has gone under the name of "biological control" (see for instance Flint & Dreistat, "Natural Enemies Handbook: The Illustrated Guide to Biological Pest Control", University of California Press, 1998) and involves the use of "natural enemies" of a pest organism. This idea has a long history: the ancient Chinese, observing that ants were effective predators of many citrus pests, decided to increase the ants population by displacing their nests from the surrounding habitats and placing them inside their orchards to protect them. More recently, there has been growing evidence that some endosymbiotic bacteria, that is bacteria that live within the cells of their hosts, could become efficient biocontrol agents. This is in particular the case of *Wolbachia*, a bacterium much studied in ERABLE (Ahantarig & Kittayapong, J Appl Entomology, 135(7):479-486, 2011).

The connection between disease and the disruption of homeostatic interactions between the host and its microbiota is on the other hand now well established. Microbiota-targeted therapies involve altering the community composition by eliminating individual strains of a single species (for example, with antibiotics) or replacing the entire community with a new intact microbiota. Secondary infections linked to antibiotic use provide however a cautionary tale of the possible consequences of perturbing a microbial species network.

Besides the biotechnological aspects on which we are already working in the context of two European projects (BacHBerry, and to a lesser extent, MicroWine), our main goal in this case is to try to formalise such type of control. There are two objectives here. One is methodological and concerns attempting to provide a single formal framework for the diverse ways of controlling a network, or a network of networks. Our attention has concentrated initially on metabolism, and will at a mid to longer term include regulation. Our intention notably as concerns the incorporation of regulation is to collaborate with other Inria teams, most notably IBIS with whom we are already in discussion. The second objective is biological and concerns control for environmental and health purposes. The originality we are seeking in this case is to attempt such control not by eliminating species, which is done mainly through the use of antibiotics that may then create resistance, a phenomenon that is becoming a major clinical and public health problem, but by manipulating the species or their environment, or by changing the composition of the community by adding or displacing some other species in such a way that new equilibria may be reached which enable all the species living in a same niche to survive. The idea is not new: the areas of prebiotics (non-digestible food ingredients that stimulate the growth and/or activity of bacteria in the digestive system in beneficial ways) and probiotics (micro-organisms claimed to provide benefits when consumed) indeed cover similar concerns in relation to health. Other novel approaches propose to work at the level of bacterial communication (quorum sensing) to control for pathogenicity (Rutherford & Bassler, Cold Spring Harbor Perspectives in Medicine, 2012). Small RNAs in particular are believed to play an important role in quorum sensing.

Axis 5: Cross-fertilising different computational approaches

In computer science and in optimisation, different approaches and techniques have been proposed to cope with hardness results. It is clear that none of them is dominant: there are classes of problems for which approach A is better than approach B, and vice-versa. Moreover, there is no satisfactory understanding of the conditions that favour one approach with respect to another one.

As an example, the team that gave birth to ERABLE, BAMBOO, had expertise more in the area of combinatorial algorithms for strings (sequences), trees and graphs. Many such algorithms addressed an enumeration problem: given a certain description of the object(s) searched for or definition of a function to be optimised, the method was supposed to list all the solutions. In many real life situations, notably in biology, a majority of the problems treated, of whatever kind, enumeration or else, are however hard. Although combinatorics remains crucial to better understand the structure of such problems and delimit the conditions that could render them easy or at least tractable in practice, often other types of approaches have to be attempted.

Although all approaches may be valid and valuable, in many cases one only is explored. More in general, there appears to be relatively little cross-talk and cross-fertilisation being attempted between these different approaches. Guided by problems from computational biology, the goal of this axis is to add to the growing insights on how well such problems can be solved theoretically.

EXMO Project-Team

3. Research Program

3.1. Knowledge representation semantics

We work with semantically defined knowledge representation languages (like description logics, conceptual graphs and object-based languages). Their semantics is usually defined within model theory initially developed for logics. The languages dedicated to the semantic web (RDF and OWL) follow that approach. RDF is a knowledge representation language dedicated to the description of resources; OWL is designed for expressing ontologies: it describes concepts and relations that can be used within RDF.

We consider a language L as a set of syntactically defined expressions (often inductively defined by applying constructors over other expressions). A representation ($o \subseteq L$) is a set of such expressions. It is also called an ontology. An interpretation function (I) is inductively defined over the structure of the language to a structure called interpretation domain (D). This expresses the construction of the "meaning" of an expression in function of its components. A formula is satisfied by an interpretation if it fulfills a condition (in general being interpreted over a particular subset of the domain). A model of a set of expressions is an interpretation satisfying all these expressions. An expression (δ) is then a consequence of a set of expressions (o) if it is satisfied by all of their models (noted $o \models \delta$).

A computer must determine if a particular expression (taken as a query, for instance) is the consequence of a set of axioms (a knowledge base). For that purpose, it uses programs, called provers, that can be based on the processing of a set of inference rules, on the construction of models or on procedural programming. These programs are able to deduce theorems (noted $o \vdash \delta$). They are said to be sound if they only find theorems which are indeed consequences and to be complete if they find all the consequences as theorems. However, depending on the language and its semantics, the decidability, i.e., the ability to create sound and complete provers, is not warranted. Even for decidable languages, the algorithmic complexity of provers may prohibit their exploitation.

To solve this problem a trade-off between the expressivity of the language and the complexity of its provers has to be found. These considerations have led to the definition of languages with limited complexity – like conceptual graphs and object-based representations – or of modular families of languages with associated modular prover algorithms – like description logics.

EXMO mainly considers languages with well-defined semantics (such as RDF and OWL that we contributed to define), and defines the semantics of some languages such as the SPARQL query language and alignment languages, in order to establish the properties of computer manipulations of the representations.

3.2. Ontology matching and alignments

When different representations are used, it is necessary to identify their correspondences. This task is called ontology matching and its result is an alignment [4]. It can be described as follows: given two ontologies, each describing a set of discrete entities (which can be classes, properties, rules, predicates, etc.), find the relationships, if any, holding between these entities.

An alignment between two ontologies o and o' is a set of correspondences $\langle e, e', r \rangle$ such that:

- e and e' are the entities between which a relation is asserted by the correspondence, e.g., formulas, terms, classes, individuals;
- r is the relation asserted to hold between e and e'. This relation can be any relation applying to these entities, e.g., equivalence, subsumption.

In addition, a correspondence may support various types of metadata, in particular measures of the confidence in a correspondence.

Given the semantics of the two ontologies provided by their consequence relation, we define an interpretation of two aligned ontologies as a pair of interpretations $\langle m, m' \rangle$, one for each ontology. Such a pair of interpretations is a model of the aligned ontologies o and o' if and only if each respective interpretation is a model of the ontology and they satisfy all correspondences of the alignment.

This definition is extended to networks of ontologies: a collection of ontologies and associated alignments. A model of such an ontology network is a tuple of local models such that each alignment is valid for the models involved in the tuple. In such a system, alignments play the role of model filters which select the local models that are compatible with all alignments. So, given an ontology network, it is possible to interpret it.

However, given a set of ontologies, it is necessary to find the alignments between them and the semantics does not tell which ones they are. Ontology matching aims at finding these alignments. A variety of methods is used for this task. They perform pairwise comparisons of entities from each of the ontologies and select the most similar pairs. Most matching algorithms provide correspondences between named entities, more rarely between compound terms. The relationships are generally equivalence between these entities. Some systems are able to provide subsumption relations as well as other relations in the support language (like incompatibility or instantiation). Confidence measures are usually given a value between 0 and 1 and are used for expressing preferences between two correspondences.

3.3. Data interlinking

Links are important for the publication of RDF data on the web. We call data interlinking the process of generating links identifying the same resource described in two data sets. Data interlinking parallels ontology matching: from two datasets (d and d') it generates a set of links (also called a link set, L).

We have extended the notion of database keys in a way which is more adapted to the context of description logics and the openness of the semantic web. We have introduced the notion of a link key [4], [1] which is a combination of such keys with alignments. More precisely, a link key is a structure $\langle K^{eq}, K^{in}, C \rangle$ such that:

- K^{eq} is a set of pairs of property expressions;
- K^{in} is a set of pairs of property expressions;
- C is a correspondence between classes.

Such a link key holds if and only if for any pair of resources belonging to the classes in correspondence such that the values of their property in K^{eq} are pairwise equal and the values of those in K^{in} pairwise intersect, the resources are the same.

As can be seen, link key validity is only relying on pairs of objects in two different data sets. We further qualify link keys as weak, plain and strong depending on them satisfying further constraints: a weak link key is only valid on pairs of individuals of different data sets, a plain link key has to apply in addition to pairs of individuals of the same data set as soon as one of them is identified with another individual of the other data set, a strong link key is a link key which is also a key for each data set, it can be though of as a link key which is made of two keys.

Link keys can then be used for finding equal individuals across two data sets and generating the corresponding owl:sameAs links.

IBIS Project-Team

3. Research Program

3.1. Analysis of qualitative dynamics of gene regulatory networks

Participants: Hidde de Jong [Correspondent], Michel Page.

The dynamics of gene regulatory networks can be modeled by means of ordinary differential equations (ODEs), describing the rate of synthesis and degradation of the gene products as well as regulatory interactions between gene products and metabolites. In practice, such models are not easy to construct though, as the parameters are often only constrained to within a range spanning several orders of magnitude for most systems of biological interest. Moreover, the models usually consist of a large number of variables, are strongly nonlinear, and include different time-scales, which makes them difficult to handle both mathematically and computationally. This has motivated the interest in qualitative models which, from incomplete knowledge of the system, are able to provide a coarse-grained picture of its dynamics.

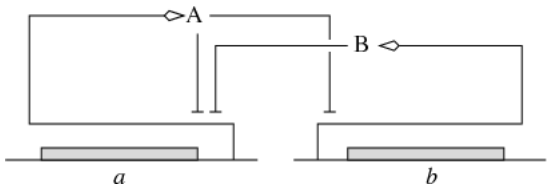
A variety of qualitative modeling formalisms have been introduced over the past decades. Boolean or logical models, which describe gene regulatory and signalling networks as discrete-time finite-state transition systems, are probably most widely used. The dynamics of these systems are governed by logical functions representing the regulatory interactions between the genes and other components of the system. IBIS has focused on a related, hybrid formalism that embeds the logical functions describing regulatory interactions into an ODE formalism, giving rise to so-called piecewise-linear differential equations (PLDEs, Figure 2). The use of logical functions allows the qualitative dynamics of the PLDE models to be analyzed, even in high-dimensional systems. In particular, the qualitative dynamics can be represented by means of a so-called state transition graph, where the states correspond to (hyperrectangular) regions in the state space and transitions between states arise from solutions entering one region from another.

First proposed by Leon Glass and Stuart Kauffman in the early seventies, the mathematical analysis of PLDE models has been the subject of active research for more than four decades. IBIS has made contributions on the mathematical level, in collaboration with the BIOCORE and BIPOP project-teams, notably for solving problems induced by discontinuities in the dynamics of the system at the boundaries between regions, where the logical functions may abruptly switch from one discrete value to another, corresponding to the (in)activation of a gene. In addition, many efforts have gone into the development of the computer tool GENETIC NETWORK ANALYZER (GNA) and its applications to the analysis of the qualitative dynamics of a variety of regulatory networks in microorganisms. Some of the methodological work underlying GNA, notably the development of analysis tools based on temporal logics and model checking, which was carried out with the Inria project-teams CONVEX (ex-VASY) and POP-ART, has implications beyond PLDE models as they apply to logical and other qualitative models as well.

3.2. Inference of gene regulatory networks from time-series data

Participants: Eugenio Cinquemani [Correspondent], Johannes Geiselmann, Hidde de Jong, Cyril Dutrieux, Stephan Lacour, Yannick Martin, Michel Page, Corinne Pinel, Delphine Ropers.

Measurements of the transcriptome of a bacterial cell by means of DNA microarrays, RNA sequencing, and other technologies have yielded huge amounts of data on the state of the transcriptional program in different growth conditions and genetic backgrounds, across different time-points in an experiment. The information on the time-varying state of the cell thus obtained has fueled the development of methods for inferring regulatory interactions between genes. In essence, these methods try to explain the observed variation in the activity of one gene in terms of the variation in activity of other genes. A large number of inference methods have been proposed in the literature and have been successful in a variety of applications, although a number of difficult problems remain.



$$\dot{x}_a = \kappa_a \, s^-(x_a, \theta_a^2) \, s^-(x_b, \theta_b) - \gamma_a \, x_a$$
$$\dot{x}_b = \kappa_b \, s^-(x_a, \theta_a^1) - \gamma_b \, x_b$$
$$s^+(x, \theta) = \begin{cases} 1, & \text{if } x > \theta \\ 0, & \text{if } x < \theta \end{cases}$$
$$s^-(x, \theta) = 1 - s^+(x, \theta)$$

Figure 2. (Left) Example of a gene regulatory network of two genes (a and b), each coding for a regulatory protein (A and B). Protein B inhibits the expression of gene a, while protein A inhibits the expression of gene b and its own gene. (Right) PLDE model corresponding to the network in (a). Protein A is synthesized at a rate κ_a, if and only if the concentration of protein A is below its threshold θ_a^2 ($x_a < \theta_a^2$) and the concentration of protein B below its threshold θ_b ($x_b < \theta_b$). The degradation of protein A occurs at a rate proportional to the concentration of the protein itself ($\gamma_a \, x_a$).

Current reporter gene technologies, based on Green Fluorescent Proteins (GFPs) and other fluorescent and luminescent reporter proteins, provide an excellent means to measure the activity of a gene *in vivo* and in real time (Figure 3). The underlying principle of the technology is to fuse the promoter region and possibly (part of) the coding region of a gene of interest to a reporter gene. The expression of the reporter gene generates a visible signal (fluorescence or luminescence) that is easy to capture and reflects the expression of a gene of interest. The interest of the reporter systems is further enhanced when they are applied in mutant strains or combined with expression vectors that allow the controlled induction of any particular gene, or the degradation of its product, at a precise moment during the time-course of the experiment. This makes it possible to perturb the network dynamics in a variety of ways, thus obtaining precious information for network inference.

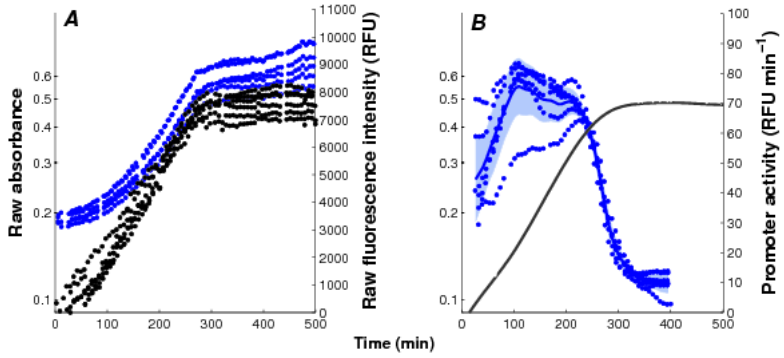


Figure 3. Monitoring of bacterial gene expression in vivo using fluorescent reporter genes (Stefan et al., PLoS Computational Biology, 11(1):e1004028, 2015). The plots show the primary data obtained in a kinetic experiment with E. coli cells, focusing on the expression of the motility gene tar in a mutant background. A: Absorbance (•, black) and fluorescence (•, blue) data, corrected for background intensities, obtained with the ΔcpxR strain transformed with the ptar-gfp reporter plasmid and grown in M9 with glucose. B: Activity of the tar promoter, computed from the primary data. The solid black line corresponds to the mean of 6 replicate absorbance measurements and the shaded blue region to the mean of the promoter activities ± twice the standard error of the mean.

The specific niche of IBIS in the field of network inference has been the development and application of genome engineering techniques for constructing the reporter and perturbation systems described above, as well as the use of reporter gene data for the reconstruction of gene regulation functions. We have developed an experimental pipeline that resolves most technical difficulties in the generation of reproducible time-series measurements on the population level. The pipeline comes with data analysis software that converts the primary data into measurements of time-varying promoter activities (Sections 5.4 and 5.3). In addition, for measuring gene expression on the single-cell level by means of microfluidics and time-lapse fluorescence microscopy, we have established collaborations with groups in Grenoble and Paris. The data thus obtained can be exploited for the structural and parametric identification of gene regulatory networks, for which methods with a solid mathematical foundation are developed, in collaboration with colleagues at ETH Zürich and EPF Lausanne (Switzerland). The vertical integration of the network inference process, from the construction of the biological material to the data analysis and inference methods, has the advantage that it allows the experimental design to be precisely tuned to the identification requirements.

3.3. Analysis of integrated metabolic and gene regulatory networks

Participants: Eugenio Cinquemani, Hidde de Jong, Thibault Etienne, Johannes Geiselmann, Stephan Lacour, Yves Markowicz, Aline Métris, Michel Page, Corinne Pinel, Delphine Ropers [Correspondent].

The response of bacteria to changes in their environment involves responses on several different levels, from the redistribution of metabolic fluxes and the adjustment of metabolic pools to changes in gene expression. In order to fully understand the mechanisms driving the adaptive response of bacteria, as mentioned above, we need to analyze the interactions between metabolism and gene expression. While often studied in isolation, gene regulatory networks and metabolic networks are closely intertwined. Genes code for enzymes which control metabolic fluxes, while the accumulation or depletion of metabolites may affect the activity of transcription factors and thus the expression of enzyme-encoding genes.

The fundamental principles underlying the interactions between gene expressions and metabolism are far from being understood today. From a biological point of view, the problem is quite challenging, as metabolism and gene expression are dynamic processes evolving on different time-scales and governed by different types of kinetics. Moreover, gene expression and metabolism are measured by different experimental methods generating heterogeneous, and often noisy and incomplete data sets. From a modeling point of view, difficult methodological problems concerned with the reduction and calibration of complex nonlinear models need to be addressed.

Most of the work carried out within the IBIS project-team specifically addressed the analysis of integrated metabolic and gene regulatory networks in the context of *E. coli* carbon metabolism (Figure 4). While an enormous amount of data has accumulated on this model system, the complexity of the regulatory mechanisms and the difficulty to precisely control experimental conditions during growth transitions leave many essential questions open, such as the physiological role and the relative importance of mechanisms on different levels of regulation (transcription factors, metabolic effectors, global physiological parameters, ...). We are interested in the elaboration of novel biological concepts and accompanying mathematical methods to grasp the nature of the interactions between metabolism and gene expression, and thus better understand the overall functioning of the system. Moreover, we have worked on the development of methods for solving what is probably the hardest problem when quantifying the interactions between metabolism and gene expression: the estimation of parameters from hetereogeneous and noisy high-throughput data. These problems are tackled in collaboration with experimental groups at Inra/INSA Toulouse and CEA Grenoble, which have complementary experimental competences (proteomics, metabolomics) and biological expertise.

3.4. Natural and engineered control of growth and gene expression

Participants: Célia Boyat, Eugenio Cinquemani, Cyril Dutrieux, Johannes Geiselmann [Correspondent], Nils Giordano, Hidde de Jong, Stephan Lacour, Ludowic Lancelot, Delphine Ropers, Alberto Soria-Lopéz.

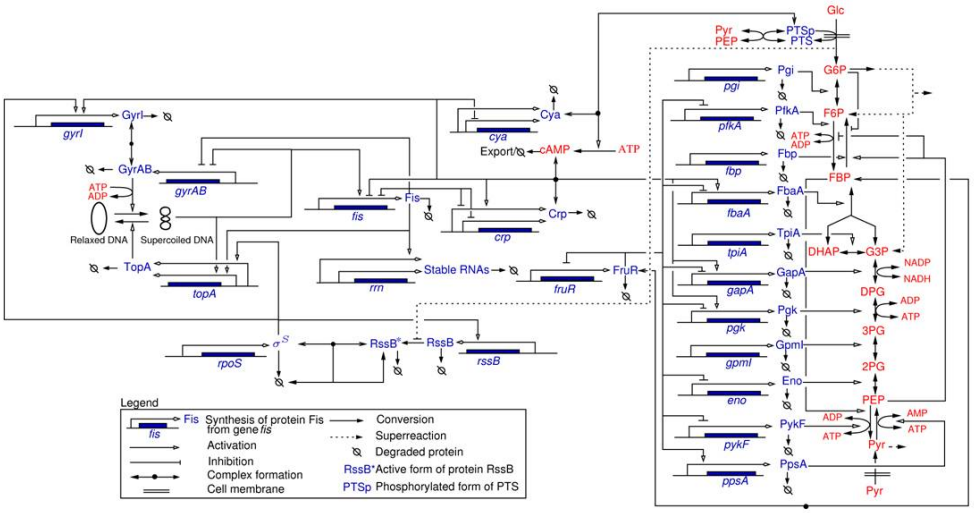


Figure 4. Network of key genes, proteins, and regulatory interactions involved in the carbon assimilation network in E. coli (Baldazzi et al., PLoS Computational Biology, 6(6):e1000812, 2010). The metabolic part includes the glycolysis/gluconeogenesis pathways as well as a simplified description of the PTS system, via the phosphorylated and non-phosphorylated form of its enzymes (represented by PTSp and PTS, respectively). The pentose-phosphate pathway (PPP) is not explicitly described but we take into account that a small pool of G6P escapes the upper part of glycolysis. At the level of the global regulators the network includes the control of the DNA supercoiling level, the accumulation of the sigma factor RpoS and the Crp·cAMP complex, and the regulatory role exerted by the fructose repressor FruR.

The adaptation of bacterial physiology to changes in the environment, involving changes in the growth rate and a reorganization of gene expression, is fundamentally a resource allocation problem. It notably poses the question how microorganisms redistribute their protein synthesis capacity over different cellular functions when confronted with an environmental challenge. Assuming that resource allocation in microorganisms has been optimized through evolution, for example to allow maximal growth in a variety of environments, this question can be fruitfully formulated as an optimal control problem. We have developed such an optimal control perspective, focusing on the dynamical adaptation of growth and gene expression in response to envrionmental changes, in close collaboration with the BIOCORE project-team.

A complementary perspective consists in the use of control-theoretical approaches to modify the functioning of a bacterial cell towards a user-defined objective, by rewiring and selectively perturbing its regulatory networks. The question how regulatory networks in microorganisms can be externally controlled using engineering approaches has a long history in biotechnology and is receiving much attention in the emerging field of synthetic biology. Within a number of on-going projects, IBIS is focusing on two different questions. The first concerns the development of open-loop and closed-loop growth-rate controllers of bacterial cells for both fundamental research and biotechnological applications (Figure 5). Second, we are working on the development of methods for the real-time control of gene expression. These methods are obviously capital for the above-mentioned design of growth-rate controllers, but they have also been applied in the context of a platform for real-time control of gene expression in cell population and single cells, developed by the Inria project-team LIFEWARE, in collaboration with a biophysics group at Université Paris Descartes.

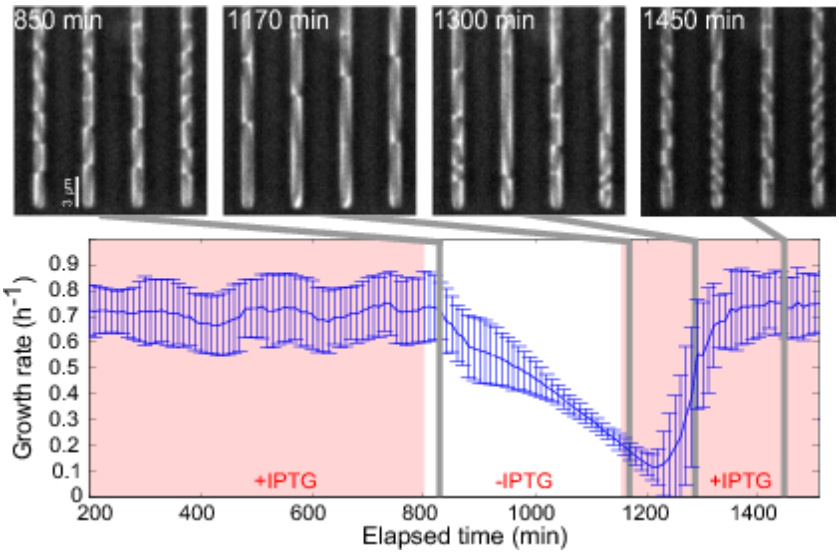


Figure 5. Growth arrest by external control of the gene expression machinery (Izard, Gomez Balderas et al., Molecular Systems Biology, 11:840, 2015). An E. coli strain in which an essential component of the gene expression machinery, the $\beta\beta'$ subunits of RNA polymerase, was put under the control of an externally-supplied inducer (IPTG), was grown in a microfluidics device and phase-contrast images were acquired every 10 min. The cells were grown in minimal medium with glucose, initially in the presence of 1 mM IPTG. 6 h after removing IPTG from the medium, the growth rate slows down and cells are elongated. About 100 min after adding back 1 mM IPTG into the medium, the elongated cells divide and resume normal growth. The growth rates in the plot are the (weighted) mean of the growth rates of 100 individual cells. The error bars correspond to $\pm$ one standard deviation. The results of the experiment show that the growth rate of a bacterial can be switched off in a reversible manner by an external inducer, based on the reengineering of the natural control of the expression of RNA polymerase.

IMAGINE Project-Team

3. Research Program

3.1. Methodology

As already stressed, thinking of future digital modeling technologies as an Expressive Virtual Pen enabling to seamlessly design, refine and convey animated 3D content, leads to revisit models for shapes, motions and stories from a user-centered perspective. More specifically, inspiring from the user-centered interfaces developed in the Human Computer Interaction domain, we introduced the new concept of user-centered graphical models. Ideally, such models should be designed to behave, under any user action, the way a human user would have predicted. In our case, user's actions may include creation gestures such as sketching to draft a shape or direct a motion, deformation gestures such as stretching a shape in space or a motion in time, or copy-paste gestures to transfer some of the features from existing models to other ones. User-centered graphical models need to incorporate knowledge in order to seamlessly generate the appropriate content from such actions. We are using the following methodology to advance towards these goals:

- Develop high-level models for shapes, motion and stories that embed the necessary knowledge to respond as expected to user actions. These models should provide the appropriate handles for conveying the user's intent while embedding procedural methods that seamlessly take care of the appropriate details and constraints.
- Combine these models with expressive design and control tools such as gesture-based control through sketching, sculpting, or acting, towards interactive environments where users can create a new virtual scene, play with it, edit or refine it, and semi-automatically convey it through a video.

3.2. Validation

Validation is a major challenge when developing digital creation tools: there is no ideal result to compare with, in contrast with more standard problems such as reconstructing existing shapes or motions. Therefore, we had to think ahead about our validation strategy: new models for geometry or animation can be validated, as usually done in Computer Graphics, by showing that they solve a problem never tackled before or that they provide a more general or more efficient solution than previous methods. The interaction methods we are developing for content creation and editing rely as much as possible on existing interaction design principles already validated within the HCI community. We also occasionally develop new interaction tools, most often in collaboration with this community, and validate them through user studies. Lastly, we work with expert users from various application domains through our collaborations with professional artists, scientists from other domains, and industrial partners: these expert users validate the use of our new tools compared to their usual pipeline.

3.3. Application Domains

This research can be applied to any situation where users need to create new, imaginary, 3D content. Our work should be instrumental, in the long term, for the visual arts, from the creation of 3D films and games to the development of new digital planning tools for theater or cinema directors. Our models can also be used in interactive prototyping environments for engineering. They can help promoting interactive digital design to scientists, as a tool to quickly express, test and refine models, as well as an efficient way for conveying them to other people. Lastly, we expect our new methodology to put digital modeling within the reach of the general public, enabling educators, media and other practitioners to author their own 3D content.

Our current application domains are:

- Visual arts
  - Modeling and animation for 3D films and games.
  - Virtual cinematography and tools for theater directors.
- Engineering
  - Industrial design.
  - Mechanical & civil engineering.
- Natural Sciences
  - Virtual functional anatomy.
  - Virtual plants.
- Education and Creative tools
  - Sketch-based teaching.
  - Creative environments for novice users.

The diversity of users these domains bring, from digital experts to other professionals and novices, gives us excellent opportunities to validate our general methodology with different categories of users. Our ongoing projects in these various application domains are listed in Section 6.

MAVERICK Project-Team

3. Research Program

3.1. Introduction

The Maverick project-team aims at producing representations and algorithms for efficient, high-quality computer generation of pictures and animations through the study of four **research problems**:

- *Computer Visualization* where we take as input a large localized dataset and represent it in a way that will let an observer understand its key properties. Visualization can be used for data analysis, for the results of a simulation, for medical imaging data...
- *Expressive Rendering*, where we create an artistic representation of a virtual world. Expressive rendering corresponds to the generation of drawings or paintings of a virtual scene, but also to some areas of computational photography, where the picture is simplified in specific areas to focus the attention.
- *Illumination Simulation*, where we model the interaction of light with the objects in the scene, resulting in a photorealistic picture of the scene. Research include improving the quality and photorealism of pictures, including more complex effects such as depth-of-field or motion-blur. We are also working on accelerating the computations, both for real-time photorealistic rendering and offline, high-quality rendering.
- *Complex Scenes*, where we generate, manage, animate and render highly complex scenes, such as natural scenes with forests, rivers and oceans, but also large datasets for visualization. We are especially interested in interactive visualization of complex scenes, with all the associated challenges in terms of processing and memory bandwidth.

The fundamental research interest of Maverick is first, *understanding* what makes a picture useful, powerful and interesting for the user, and second *designing* algorithms to create and improve these pictures.

3.2. Research approaches

We will address these research problems through three interconnected research approaches:

3.2.1. Picture Impact

Our first research axis deals with the *impact* pictures have on the viewer, and how we can improve this impact. Our research here will target:

- *evaluating user response:* we need to evaluate how the viewers respond to the pictures and animations generated by our algorithms, through user studies, either asking the viewer about what he perceives in a picture or measuring how his body reacts (eye tracking, position tracking).
- *removing artefacts and discontinuities:* temporal and spatial discontinuities perturb viewer attention, distracting the viewer from the main message. These discontinuities occur during the picture creation process; finding and removing them is a difficult process.

3.2.2. Data Representation

The data we receive as input for picture generation is often unsuitable for interactive high-quality rendering: too many details, no spatial organisation... Similarly the pictures we produce or get as input for other algorithms can contain superfluous details.

One of our goals is to develop new data representations, adapted to our requirements for rendering. This includes fast access to the relevant information, but also access to the specific hierarchical level of information needed: we want to organize the data in hierarchical levels, pre-filter it so that sampling at a given level also gives information about the underlying levels. Our research for this axis include filtering, data abstraction, simplification and stylization.

The input data can be of any kind: geometric data, such as the model of an object, scientific data before visualization, pictures and photographs. It can be time-dependent or not; time-dependent data bring an additional level of challenge on the algorithm for fast updates.

3.2.3. Prediction and simulation

Our algorithms for generating pictures require computations: sampling, integration, simulation... These computations can be optimized if we already know the characteristics of the final picture. Our recent research has shown that it is possible to predict the local characteristics of a picture by studying the phenomena involved: the local complexity, the spatial variations, their direction...

Our goal is to develop new techniques for predicting the properties of a picture, and to adapt our image-generation algorithms to these properties, for example by sampling less in areas of low variation.

Our research problems and approaches are all cross-connected. Research on the *impact* of pictures is of interest in three different research problems: *Computer Visualization*, *Expressive rendering* and *Illumination Simulation*. Similarly, our research on *Illumination simulation* will use all three research approaches: impact, representations and prediction.

3.3. Cross-cutting research issues

Beyond the connections between our problems and research approaches, we are interested in several issues, which are present throughout all our research:

sampling is an ubiquitous process occurring in all our application domains, whether photorealistic rendering (*e.g.* photon mapping), expressive rendering (*e.g.* brush strokes), texturing, fluid simulation (Lagrangian methods), etc. When sampling and reconstructing a signal for picture generation, we have to ensure both coherence and homogeneity. By *coherence*, we mean not introducing spatial or temporal discontinuities in the reconstructed signal. By *homogeneity*, we mean that samples should be placed regularly in space and time. For a time-dependent signal, these requirements are conflicting with each other, opening new areas of research.

filtering is another ubiquitous process, occuring in all our application domains, whether in realistic rendering (*e.g.* for integrating height fields, normals, material properties), expressive rendering (*e.g.* for simplifying strokes), textures (through non-linearity and discontinuities). It is especially relevant when we are replacing a signal or data with a lower resolution (for hierarchical representation); this involves filtering the data with a reconstruction kernel, representing the transition between levels.

performance and scalability are also a common requirement for all our applications. We want our algorithms to be usable, which implies that they can be used on large and complex scenes, placing a great importance on scalability. For some applications, we target interactive and real-time applications, with an update frequency between 10 Hz and 120 Hz.

coherence and continuity in space and time is also a common requirement of realistic as well as expressive models which must be ensured despite contradictory requirements. We want to avoid flickering and aliasing.

animation: our input data is likely to be time-varying (*e.g.* animated geometry, physical simulation, time-dependent dataset). A common requirement for all our algorithms and data representation is that they must be compatible with animated data (fast updates for data structures, low latency algorithms...).

3.4. Methodology

Our research is guided by several methodological principles:

Experimentation: to find solutions and phenomenological models, we use experimentation, performing statistical measurements of how a system behaves. We then extract a model from the experimental data.

Validation: for each algorithm we develop, we look for experimental validation: measuring the behavior of the algorithm, how it scales, how it improves over the state-of-the-art... We also compare our algorithms to the exact solution. Validation is harder for some of our research domains, but it remains a key principle for us.

Reducing the complexity of the problem: the equations describing certain behaviors in image synthesis can have a large degree of complexity, precluding computations, especially in real time. This is true for physical simulation of fluids, tree growth, illumination simulation... We are looking for *emerging phenomena* and *phenomenological models* to describe them (see framed box "Emerging phenomena"). Using these, we simplify the theoretical models in a controlled way, to improve user interaction and accelerate the computations.

Transferring ideas from other domains: Computer Graphics is, by nature, at the interface of many research domains: physics for the behavior of light, applied mathematics for numerical simulation, biology, algorithmics... We import tools from all these domains, and keep looking for new tools and ideas.

Develop new fondamental tools: In situations where specific tools are required for a problem, we will proceed from a theoretical framework to develop them. These tools may in return have applications in other domains, and we are ready to disseminate them.

Collaborate with industrial partners: we have a long experiment of collaboration with industrial partners. These collaborations bring us new problems to solve, with short-term or medium-term transfert opportunities. When we cooperate with these partners, we have to find *what they need*, which can be very different from *what they want*, their expressed need.

MISTIS Project-Team

3. Research Program

3.1. Mixture models

Participants: Alexis Arnaud, Jean-Baptiste Durand, Florence Forbes, Aina Frau Pascual, Alessandro Chiancone, Stephane Girard, Julyan Arbel, Gildas Mazo, Jean-Michel Becu.

Key-words: mixture of distributions, EM algorithm, missing data, conditional independence, statistical pattern recognition, clustering, unsupervised and partially supervised learning.

In a first approach, we consider statistical parametric models, θ being the parameter, possibly multidimensional, usually unknown and to be estimated. We consider cases where the data naturally divides into observed data $y = \{y_1, ..., y_n\}$ and unobserved or missing data $z = \{z_1, ..., z_n\}$. The missing data z_i represents for instance the memberships of one of a set of K alternative categories. The distribution of an observed y_i can be written as a finite mixture of distributions,

$$f(y_i; \theta) = \sum_{k=1}^{K} P(z_i = k; \theta) f(y_i \mid z_i; \theta) \ . \tag{2}$$

These models are interesting in that they may point out hidden variables responsible for most of the observed variability and so that the observed variables are *conditionally* independent. Their estimation is often difficult due to the missing data. The Expectation-Maximization (EM) algorithm is a general and now standard approach to maximization of the likelihood in missing data problems. It provides parameter estimation but also values for missing data.

Mixture models correspond to independent z_i's. They have been increasingly used in statistical pattern recognition. They enable a formal (model-based) approach to (unsupervised) clustering.

3.2. Markov models

Participants: Brice Olivier, Thibaud Rahier, Jean-Baptiste Durand, Florence Forbes, Karina Ashurbekova.

Key-words: graphical models, Markov properties, hidden Markov models, clustering, missing data, mixture of distributions, EM algorithm, image analysis, Bayesian inference.

Graphical modelling provides a diagrammatic representation of the dependency structure of a joint probability distribution, in the form of a network or graph depicting the local relations among variables. The graph can have directed or undirected links or edges between the nodes, which represent the individual variables. Associated with the graph are various Markov properties that specify how the graph encodes conditional independence assumptions.

It is the conditional independence assumptions that give graphical models their fundamental modular structure, enabling computation of globally interesting quantities from local specifications. In this way graphical models form an essential basis for our methodologies based on structures.

The graphs can be either directed, e.g. Bayesian Networks, or undirected, e.g. Markov Random Fields. The specificity of Markovian models is that the dependencies between the nodes are limited to the nearest neighbor nodes. The neighborhood definition can vary and be adapted to the problem of interest. When parts of the variables (nodes) are not observed or missing, we refer to these models as Hidden Markov Models (HMM). Hidden Markov chains or hidden Markov fields correspond to cases where the z_i's in (1) are distributed according to a Markov chain or a Markov field. They are a natural extension of mixture models. They are widely used in signal processing (speech recognition, genome sequence analysis) and in image processing (remote sensing, MRI, etc.). Such models are very flexible in practice and can naturally account for the phenomena to be studied.

Hidden Markov models are very useful in modelling spatial dependencies but these dependencies and the possible existence of hidden variables are also responsible for a typically large amount of computation. It follows that the statistical analysis may not be straightforward. Typical issues are related to the neighborhood structure to be chosen when not dictated by the context and the possible high dimensionality of the observations. This also requires a good understanding of the role of each parameter and methods to tune them depending on the goal in mind. Regarding estimation algorithms, they correspond to an energy minimization problem which is NP-hard and usually performed through approximation. We focus on a certain type of methods based on variational approximations and propose effective algorithms which show good performance in practice and for which we also study theoretical properties. We also propose some tools for model selection. Eventually we investigate ways to extend the standard Hidden Markov Field model to increase its modelling power.

3.3. Functional Inference, semi- and non-parametric methods

Participants: Clement Albert, Alessandro Chiancone, Stephane Girard, Seydou Nourou Sylla, Pablo Mesejo Santiago, Florence Forbes, Emeline Perthame, Jean-Michel Becu.

Key-words: dimension reduction, extreme value analysis, functional estimation.

We also consider methods which do not assume a parametric model. The approaches are non-parametric in the sense that they do not require the assumption of a prior model on the unknown quantities. This property is important since, for image applications for instance, it is very difficult to introduce sufficiently general parametric models because of the wide variety of image contents. Projection methods are then a way to decompose the unknown quantity on a set of functions (*e.g.* wavelets). Kernel methods which rely on smoothing the data using a set of kernels (usually probability distributions) are other examples. Relationships exist between these methods and learning techniques using Support Vector Machine (SVM) as this appears in the context of *level-sets estimation* (see section 3.3.2). Such non-parametric methods have become the cornerstone when dealing with functional data [77]. This is the case, for instance, when observations are curves. They enable us to model the data without a discretization step. More generally, these techniques are of great use for *dimension reduction* purposes (section 3.3.3). They enable reduction of the dimension of the functional or multivariate data without assumptions on the observations distribution. Semi-parametric methods refer to methods that include both parametric and non-parametric aspects. Examples include the Sliced Inverse Regression (SIR) method [80] which combines non-parametric regression techniques with parametric dimension reduction aspects. This is also the case in *extreme value analysis* [76], which is based on the modelling of distribution tails (see section 3.3.1). It differs from traditional statistics which focuses on the central part of distributions, *i.e.* on the most probable events. Extreme value theory shows that distribution tails can be modelled by both a functional part and a real parameter, the extreme value index.

3.3.1. Modelling extremal events

Extreme value theory is a branch of statistics dealing with the extreme deviations from the bulk of probability distributions. More specifically, it focuses on the limiting distributions for the minimum or the maximum of a large collection of random observations from the same arbitrary distribution. Let $X_{1,n} \leq ... \leq X_{n,n}$ denote n ordered observations from a random variable X representing some quantity of interest. A p_n-quantile of X is the value x_{p_n} such that the probability that X is greater than x_{p_n} is p_n, *i.e.*$P(X > x_{p_n}) = p_n$. When $p_n < 1/n$, such a quantile is said to be extreme since it is usually greater than the maximum observation $X_{n,n}$ (see Figure 1).

To estimate such quantiles therefore requires dedicated methods to extrapolate information beyond the observed values of X. Those methods are based on Extreme value theory. This kind of issue appeared in hydrology. One objective was to assess risk for highly unusual events, such as 100-year floods, starting from flows measured over 50 years. To this end, semi-parametric models of the tail are considered:

$$P(X > x) = x^{-1/\theta}\ell(x),\ x > x_0 > 0, \tag{3}$$

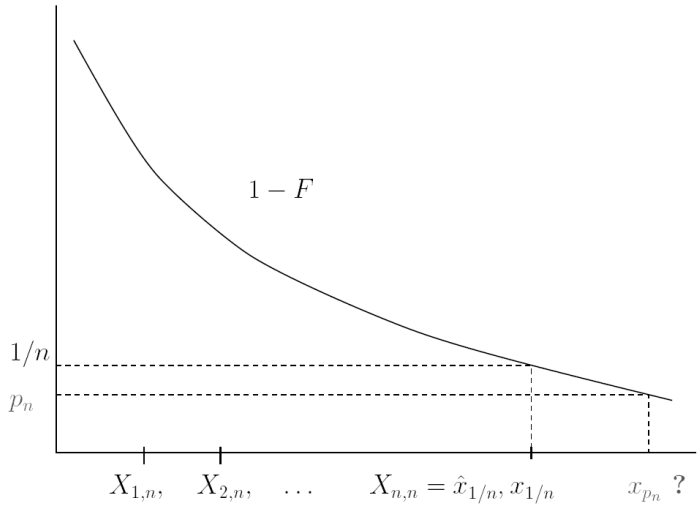


Figure 1. The curve represents the survival function $x \to P(X > x)$. The $1/n$-quantile is estimated by the maximum observation so that $\widehat{x}_{1/n} = X_{n,n}$. As illustrated in the figure, to estimate p_n-quantiles with $p_n < 1/n$, it is necessary to extrapolate beyond the maximum observation.

where both the extreme-value index $\theta > 0$ and the function $\ell(x)$ are unknown. The function ℓ is a slowly varying function *i.e.* such that

$$\frac{\ell(tx)}{\ell(x)} \to 1 \text{ as } x \to \infty \tag{4}$$

for all $t > 0$. The function $\ell(x)$ acts as a nuisance parameter which yields a bias in the classical extreme-value estimators developed so far. Such models are often referred to as heavy-tail models since the probability of extreme events decreases at a polynomial rate to zero. It may be necessary to refine the model (2 ,3) by specifying a precise rate of convergence in (3). To this end, a second order condition is introduced involving an additional parameter $\rho \leq 0$. The larger ρ is, the slower the convergence in (3) and the more difficult the estimation of extreme quantiles.
More generally, the problems that we address are part of the risk management theory. For instance, in reliability, the distributions of interest are included in a semi-parametric family whose tails are decreasing exponentially fast. These so-called Weibull-tail distributions [9] are defined by their survival distribution function:

$$P(X > x) = \exp\{-x^{\theta}\ell(x)\},\ x > x_0 > 0. \tag{5}$$

Gaussian, gamma, exponential and Weibull distributions, among others, are included in this family. An important part of our work consists in establishing links between models (2) and (4) in order to propose new estimation methods. We also consider the case where the observations were recorded with a covariate information. In this case, the extreme-value index and the p_n-quantile are functions of the covariate. We propose estimators of these functions by using moving window approaches, nearest neighbor methods, or kernel estimators.

3.3.2. Level sets estimation

Level sets estimation is a recurrent problem in statistics which is linked to outlier detection. In biology, one is interested in estimating reference curves, that is to say curves which bound 90% (for example) of the population. Points outside this bound are considered as outliers compared to the reference population. Level sets estimation can be looked at as a conditional quantile estimation problem which benefits from a non-parametric statistical framework. In particular, boundary estimation, arising in image segmentation as well as in supervised learning, is interpreted as an extreme level set estimation problem. Level sets estimation can also be formulated as a linear programming problem. In this context, estimates are sparse since they involve only a small fraction of the dataset, called the set of support vectors.

3.3.3. Dimension reduction

Our work on high dimensional data requires that we face the curse of dimensionality phenomenon. Indeed, the modelling of high dimensional data requires complex models and thus the estimation of high number of parameters compared to the sample size. In this framework, dimension reduction methods aim at replacing the original variables by a small number of linear combinations with as small as a possible loss of information. Principal Component Analysis (PCA) is the most widely used method to reduce dimension in data. However, standard linear PCA can be quite inefficient on image data where even simple image distorsions can lead to highly non-linear data. Two directions are investigated. First, non-linear PCAs can be proposed, leading to semi-parametric dimension reduction methods [78]. Another field of investigation is to take into account the application goal in the dimension reduction step. One of our approaches is therefore to develop new Gaussian models of high dimensional data for parametric inference [74]. Such models can then be used in a Mixtures or Markov framework for classification purposes. Another approach consists in combining dimension reduction, regularization techniques, and regression techniques to improve the Sliced Inverse Regression method [80].

MORPHEO Project-Team

3. Research Program

3.1. Shape Acquisition

Multiple camera setups allow to acquire shapes, i.e. geometry, as well as their appearances, i.e. photometry, with a reasonable level of precision. However fundamental limitations still exist, in particular today's state-of-the-art approaches do not fully exploit the redundancy of information over temporal sequences of visual observations. Despite an increasing interest of the computer vision communities in the past years, the problem is still far from solved other than in specific situations with restrictive assumptions and configurations. Our goal in this research axis is to fully leverage temporal aspects of the acquisition process and to open the acquisition process to different modalities, in particular Xrays.

3.2. Generative / discriminative inference

Acquisition of 4D Models can often be conveniently formulated as an estimation or learning problem. Various generative models can be proposed for the problems of shape and appearance modeling over time sequences, and motion segmentation. The idea of these generative models is to predict the noisy measurements (e.g. pixel values, measured 3D points or speed quantities) from a set of parameters describing the unobserved scene state (e.g. shape and appearance), which in turn can be inverted with various inference algorithms. The advantages of this type of modeling are numerous to deal with noisy measurements, explicitly model dependencies between model parameters, hidden variables and observed quantities, and relevant priors over parameters; sensor models for different modalities can also easily be seamlessly integrated and jointly used, which remains central to our goals. A limitation of such algorithms is that classical algorithms to solve them rely on local iterative convergence schemes subject to local minima, or global restart schemes which avert this problem but with a significant computational penalty. This is why we also consider discriminative and deep learning approaches, which allow to formulate the parameter estimation as a direct regression from input quantities or pixel values, whose parameters are learned given a training set. This has the advantage of directly computing a solution from inputs, with robustness and speed benefits, as a standalone estimation algorithm or to initialize local convergence schemes based on generative modeling. A number of the approaches we propose thus leverage the advantages of both generative and such discriminative approaches.

3.3. Shape Analysis

Shape analysis has received much attention from the scientific community and recovering the intrinsic nature of shapes is currently an active research domain. Of particular interest is the study of human and animal shapes and their associated articulated underlying structures, i.e. skeletons, since applications are numerous, either in the entertainment industry or for medical applications, among others. Our main goals in this research axis are : the understanding of a shape's global structure, and a pose-independent classification of shapes.

3.4. Shape Tracking

Recovering the temporal evolution of a deformable surface is a fundamental task in computer vision, with a large variety of applications ranging from the motion capture of articulated shapes, such as human bodies, to the deformation of complex surfaces such as clothes. Methods that solve for this problem usually infer surface evolutions from motion or geometric cues. This information can be provided by motion capture systems or one of the numerous available static 3D acquisition modalities. In this inference, methods are faced with the challenging estimation of the time-consistent deformation of a surface from cues that can be sparse and noisy. Such an estimation is an ill posed problem that requires prior knowledge on the deformation to be introduced in order to limit the range of possible solutions. Our goal is to devise robust and accurate solutions based on new deformation models that fully exploit the geometric and photometric information available.

3.5. Dynamic Motion Modeling

Multiple views systems can significantly change the paradigm of motion capture. Traditional motion capture systems provide 3D trajectories of a sparse set of markers fixed on the subject. These trajectories can be transformed into motion parameters on articulated limbs with the help of prior models of the skeletal structure. However, such skeletal models are mainly robotical abstractions that do not describe the true morphology and anatomical motions of humans and animals. On the other hand, 4D models (temporally consistent mesh sequences) provide dense motion information on body's shape while requiring less prior assumption. They represent therefore a new rich source of information on human and animal shape movements. The analysis of such data has already received some attention but most existing works model motion through static poses and do not consider yet dynamic information. Such information (e.g. trajectories and speed) is anyway required to analyse walking or running sequences. We will investigate this research direction with the aim to propose and study new dynamic models.

3.6. Shape Animation

3D animation is a crucial part of digital media production with numerous applications, in particular in the game and motion picture industry. Recent evolutions in computer animation consider real videos for both the creation and the animation of characters. The advantage of this strategy is twofold: it reduces the creation cost and increases realism by considering only real data. Furthermore, it allows to create new motions, for real characters, by recombining recorded elementary movements. In addition to enable new media contents to be produced, it also allows to automatically extend moving shape datasets with fully controllable new motions. This ability appears to be of great importance with the recent advent of deep learning techniques and the associated need for large learning datasets. In this research direction, we will investigate how to create new dynamic scenes using recorded events.

NANO-D Project-Team

3. Research Program

3.1. The need for practical design of nanosystems

Computing has long been an essential tool of engineering. During the twentieth century, the development of macroscopic engineering has been largely stimulated by progress in numerical design and prototyping. Cars, planes, boats, and many other manufactured objects are nowadays, for the most part, designed and tested on computers. Digital prototypes have progressively replaced actual ones, and effective computer-aided engineering tools (e.g., CATIA, SolidWorks, T-FLEX CAD, Alibre Design, TopSolid, etc.) have helped cut costs and reduce production cycles of macroscopic systems [66].

The twenty-first century is most likely to see a similar development at the atomic scale. Indeed, the recent years have seen tremendous progress in nanotechnology. The magazine Science, for example, recently featured a paper demonstrating an example of DNA nanotechnology, where DNA strands are stacked together through programmable self-assembly [35]. In February 2007, the cover of Nature Nanotechnology showed a "nano-wheel" composed of a few atoms only. Several nanosystems have already been demonstrated, including a *de-novo* computationally designed protein interface [37], a wheelbarrow molecule [44], a nano-car [70], a Morse molecule [18], etc. Typically, these designs are optimized using semi-empirical quantum mechanics calculations, such as the semi-empirical ASED+ calculation technique [19].

While impressive, these are but two examples of the nanoscience revolution already impacting numerous fields, including electronics and semiconductors [53], textiles [52], [40], energy [55], food [29], drug delivery [39], [72], chemicals [41], materials [30], the automotive industry [16], aerospace and defense [38], medical devices and therapeutics [33], medical diagnostics [73], etc. According to some estimates, the world market for nanotechnology-related products and services will reach one trillion dollars by 2015 [65]. Nano-engineering groups are multiplying throughout the world, both in academia and in the industry: in the USA, the MIT has a "NanoEngineering" research group, Sandia National Laboratories created a "National Institute for Nano Engineering", to name a few; China founded a "National Center for Nano Engineering" in 2003, etc. Europe is also a significant force in public funding of nanoscience and nanotechnology and, in Europe, Grenoble and the Rhone-Alpes area gather numerous institutions and organizations related to nanoscience.

Of course, not all small systems that currently fall under the label "nano" have mechanical, electronic, optical properties similar to the examples given above. Furthermore, current construction capabilities lack behind some of the theoretical designs which have been proposed, such as the planetary gear designed by Eric Drexler at Nanorex. However, the trend is clearly for adding more and more functionality to nanosystems. While designing nanosystems is still very much an art mostly performed by physicists, chemists and biologists in labs throughout the world, there is absolutely no doubt that fundamental engineering practices will progressively emerge, and that these practices will be turned into quantitative rules and methods. Similar to what has happened with macroscopic engineering, powerful and generic software will then be employed to engineer complex nanosystems.

3.2. Challenges of practical nanosystem design

As with macrosystems, designing nanosystems will involve modeling and simulation within software applications: modeling, especially structural modeling, will be concerned with the creation of potentially complex chemical structures such as the examples above, using a graphical user interface, parsers, scripts, builders, etc.; simulation will be employed to predict some properties of the constructed models, including mechanical properties, electronic properties, chemical properties, etc.

In general, design may be considered as an "inverse simulation problem". Indeed, designed systems often need to be optimized so that their properties — predicted by simulation — satisfy specific objectives and constraints (e.g. a car should have a low drag coefficient, a drug should have a high affinity and selectivity to a target protein, a nano-wheel should roll when pushed, etc.). Being the main technique employed to predict properties, simulation is essential to the design process. At the nanoscale, simulation is even more important. Indeed, physics significantly constrains atomic structures (e.g. arbitrary inter-atomic distances cannot exist), so that a tentative atomic shape should be checked for plausibility much earlier in the design process (e.g. remove atomic clashes, prevent unrealistic, high-energy configurations, etc.). For nanosystems, thus, efficient simulation algorithms are required both when modeling structures and when predicting systems properties. Precisely, an effective software tool to design nanosystems should (a) allow for interactive physically-based modeling, where all user actions (e.g. displacing atoms, modifying the system's topology, etc.) are automatically followed by a few steps of energy minimization to help the user build plausible structures, even for large number of atoms, and (b) be able to predict systems properties, through a series of increasingly complex simulations.

3.3. Current simulation approaches

Even though the growing need for effective nanosystem design will still increase the demand for simulation, a lot of research has already gone into the development of efficient simulation algorithms. Typically, two approaches are used: (a) increasing the computational resources (use super-computers, computer clusters, grids, develop parallel computing approaches, etc.), or (b) simulating simplified physics and/or models. Even though the first strategy is sometimes favored, it is expensive and, it could be argued, inefficient: only a few supercomputers exist, not everyone is willing to share idle time from their personal computer, etc. Surely, we would see much less creativity in cars, planes, and manufactured objects all around if they had to be designed on one of these scarce super-resources.

The second strategy has received a lot of attention. Typical approaches to speed up molecular mechanics simulation include lattice simulations [75], removing some degrees of freedom (e.g. keeping torsion angles only [51], [71]), coarse-graining [74], [68], [20], [69], multiple time step methods [61], [62], fast multipole methods [34], parallelization [46], averaging [28], multi-scale modeling [27], [24], reactive force fields [26], [78], interactive multiplayer games for predicting protein structures [32], etc. Until recently, quantum mechanics methods, as well as mixed quantum / molecular mechanics methods were still extremely slow. One breakthrough has consisted in the discovery of linear-scaling, divide-and-conquer quantum mechanics methods [76], [77].

Overall, the computational community has already produced a variety of sophisticated simulation packages, for both classical and quantum simulation: ABINIT, AMBER, CHARMM, Desmond, GROMOS and GROMACS, LAMMPS, NAMD, ROSETTA, SIESTA, TINKER, VASP, YASARA, etc. Some of these tools are open source, while some others are available commercially, sometimes via integrating applications: Ascalaph Designer, BOSS, Discovery Studio, Materials Studio, Maestro, MedeA, MOE, NanoEngineer-1, Spartan, etc. Other tools are mostly concerned with visualization, but may sometimes be connected to simulation packages: Avogadro, PyMol, VMD, Zodiac, etc. The nanoHUB network also includes a rich set of tools related to computational nanoscience.

To the best of our knowledge, however, all methods which attempt to speed up dynamics simulations perform a priori simplification assumptions, which might bias the study of the simulated phenomenon. A few recent, interesting approaches have managed to combine several levels of description (e.g. atomistic and coarse-grained) into a single simulation, and have molecules switch between levels during simulation, including the adaptive resolution method [57], [58], [59], [60], the adaptive multiscale method [54], and the adaptive partitioning of the Lagrangian method [42]. Although these approaches have demonstrated some convincing applications, they all suffer from a number of limitations stemming from the fact that they are either ad hoc methods tuned to fix specific problems (e.g. fix density problems in regions where the level of description changes), or mathematically founded methods that necessitate to "calibrate" potentials so that they can be mixed (i.e. all potentials have to agree on a reference point). In general, multi-scale methods, even when

they do not allow molecules to switch between levels of detail during simulation, have to solve the problem of rigorously combining multiple levels of description (i.e. preserve statistics, etc.), of assigning appropriate levels to different parts of the simulated system ("simplify as much as possible, but not too much"), and of determining computable mappings between levels of description (especially, adding back detail when going from coarse-grained descriptions to fine-grained descriptions).

3.4. Research axes

The goal of the NANO-D group is to help current and future designers of *nanosystems*, i.e. systems studied or designed at the atomic scale (whether natural or artificial, independently of the application domain, including structural biology, material science, chemistry, etc.) by developing the **foundations of a software application which will run on a desktop computer, and will allow for efficient analysis, design, modeling and simulation of nanosystems**.

To achieve this, we will be developing a series of **adaptive methods and algorithms** that allow users to focus computational resources on the parts of the models that they want to simulate, and that allow to finely trade between speed and precision.

In parallel, we will develop the architecture of a new desktop application for virtual prototyping of nanosystems, and will integrate all our algorithms into this application. Furthermore, the architecture of this platform will be open, so that independent developers may add modules, for **multiple application domains** (physics, biology, chemistry, materials, electronics, etc.). With this open platform, we will attempt to federate the research performed in computational nanoscience throughout the world.

This application is called **SAMSON: "Software for Adaptive Modeling and Simulation Of Nanosystems"**.

Our two research axes are:

1. **Developing adaptive algorithms for simulating nanosystems**
   - **Defining adaptive Hamiltonians**: In order to be able to perform simulations with good mathematical properties, we are expanding on our recent work on *adaptively restrained Hamiltonians*[22], *i.e.* modified Hamiltonian representations of molecular systems that are able to switch degrees of freedom on and off during a simulation. These will allow us to finely trade between precision and computational performance, by choosing arbitrarily the number of degrees of freedom. Even though we have already obtained some promising results in this domain, our goal is to develop several different simplification methods.
   - **Developing algorithms for incremental potential update**: In order to benefit from performing adaptive particle simulations, we need to develop a series of algorithms that will take advantage of the fact that some (potentially relative) atomic positions are frozen. We have already demonstrated how this is possible for torsion-angle quasi-static simulation of classical bio-molecular force-fields [67], for neighbor search between large rigid molecules [21], and for bond-order reactive force-fields [25]. We are developing new algorithms for incremental neighbor search, energy and force updates corresponding to the adaptive Hamiltonians that we are defining.
2. **Developing algorithms for modeling molecular interactions**
   - **Developing knowledge-driven methods, potentials and algorithms**: Over time, more and more experimental information becomes available. One can use this information to predict and discover new types of molecular interactions and various mechanisms or molecular organization. For example, currently there are more than 50,000 protein structures of a high resolution stored in the Protein Data Bank [23] and over 500,000 structures of small molecules stored in the Cambridge Structural Database [17]. We are developing algorithms for protein-protein interactions and protein-ligand interactions.

- **Developing parametrization algorithms for interaction potentials**: Molecular models typically require their own potential energy function (or a *forcefield*) to be assigned. However, the development of a new potential function is a very difficult and sometimes challenging task [43]. Therefore, we are developing algorithms for automatic parametrization of new potential functions for some particular representations of a molecular system.
- **Developing algorithms for exhaustive sampling**: Some application domains, such as computational docking, cryo-EM rigid-body fitting, etc., require sampling in a low-dimensional space. For such applications it is advantageous to perform an exhaustive search rather than accelerated sampling [64]. Therefore, we are developing fast search methods to perform exhaustive search.

NECS Project-Team

3. Research Program

3.1. Introduction

NECS team deals with Networked Control Systems. Since its foundation in 2007, the team has been addressing issues of control under imperfections and constraints deriving from the network (limited computation resources of the embedded systems, delays and errors due to communication, limited energy resources), proposing co-design strategies. The team has recently moved its focus towards general problems on *control of network systems*, which involve the analysis and control of dynamical systems with a network structure or whose operation is supported by networks. This is a research domain with substantial growth and is now recognized as a priority sector by the IEEE Control Systems Society: IEEE has started a new journal, IEEE Transactions on Control of Network Systems, whose first issue appeared in 2014.

More in detail, the research program of NECS team is along lines described in the following sections.

3.2. Distributed estimation and data fusion in network systems

This research topic concerns distributed data combination from multiple sources (sensors) and related information fusion, to achieve more specific inference than could be achieved by using a single source (sensor). It plays an essential role in many networked applications, such as communication, networked control, monitoring, and surveillance. Distributed estimation has already been considered in the team. We wish to capitalize and strengthen these activities by focusing on integration of heterogeneous, multidimensional, and large data sets:

- Heterogeneity and large data sets. This issue constitutes a clearly identified challenge for the future. Indeed, heterogeneity comes from the fact that data are given in many forms, refer to different scales, and carry different information. Therefore, data fusion and integration will be achieved by developing new multi-perception mathematical models that can allow tracking continuous (macroscopic) and discrete (microscopic) dynamics under a unified framework while making different scales interact with each other. More precisely, many scales are considered at the same time, and they evolve following a unique fully-integrated dynamics generated by the interactions of the scales. The new multi-perception models will be integrated to forecast, estimate and broadcast useful system states in a distributed way. Targeted applications include traffic networks and navigation, and concern recent grant proposals that team has elaborated, among which the SPEEDD EU FP7 project, which has started in February 2014.
- Multidimensionality. This issue concerns the analysis and the processing of multidimensional data, organized in multiway array, in a distributed way. Robustness of previously-developed algorithms will be studied. In particular, the issue of missing data will be taken into account. In addition, since the considered multidimensional data are generated by dynamic systems, dynamic analysis of multiway array (or tensors) will be considered. The targeted applications concern distributed detection in complex networks and distributed signal processing for collaborative networks. This topic is developed in strong collaboration with UFC (Brazil).

3.3. Network systems and graph analysis

This is a research topic at the boundaries between graph theory and dynamical systems theory.

A first main line of research will be to study complex systems whose interactions are modeled with graphs, and to unveil the effect of the graph topology on system-theoretic properties such as observability or controllability. In particular, on-going work concerns observability of graph-based systems: after preliminary results concerning consensus systems over distance-regular graphs, the aim is to extend results to more general networks. A special focus will be on the notion of 'generic properties', namely properties which depend only on the underlying graph describing the sparsity pattern, and hold true almost surely with a random choice of the non-zero coefficients. Further work will be to explore situations in which there is the need for new notions different from the classical observability or controllability. For example, in opinion-forming in social networks or in formation of birds flocks, the potential leader might have a goal different from classical controllability. On the one hand, his goal might be much less ambitious than the classical one of driving the system to any possible state (e.g., he might want to drive everybody near its own opinion, only, and not to any combination of different individual opinions), and on the other hand he might have much weaker tools to construct his control input (e.g., he might not know the whole system's dynamics, but only some local partial information). Another example is the question of detectability of an unknown input under the assumption that such an input has a sparsity constraint, a question arising from the fact that a cyber-physical attack might be modeled as an input aiming at controlling the system's state, and that limitations in the capabilities of the attacker might be modeled as a sparsity constraint on the input.

A second line of research will concern graph discovery, namely algorithms aiming at reconstructing some properties of the graph (such as the number of vertices, the diameter, the degree distribution, or spectral properties such as the eigenvalues of the graph Laplacian), using some measurements of quantities related to a dynamical system associated with the graph. It will be particularly challenging to consider directed graphs, and to impose that the algorithm is anonymous, i.e., that it does not makes use of labels identifying the different agents associated with vertices.

3.4. Collaborative and distributed network control

This research line deals with the problem of designing controllers with a limited use of the network information (i.e. with restricted feedback), and with the aim to reach a pre-specified global behavior. This is in contrast to centralized controllers that use the whole system information and compute the control law at some central node. Collaborative control has already been explored in the team in connection with the underwater robot fleet, and to some extent with the source seeking problem. It remains however a certain number of challenging problems that the team wishes to address:

- Design of control with limited information, able to lead to desired global behaviors. Here the graph structure is imposed by the problem, and we aim to design the "best" possible control under such a graph constraint [0]. The team would like to explore further this research line, targeting a better understanding of possible metrics to be used as a target for optimal control design. In particular, and in connection with the traffic application, the long-standing open problem of ramp metering control under minimum information will be addressed.
- Clustering control for large networks. For large and complex systems composed of several sub-networks, feedback design is usually treated at the sub-network level, and most of the times without taking into account natural interconnections between sub-networks. The team is exploring new control strategies, exploiting the emergent behaviors resulting from new interconnections between the network components. This requires first to build network models operating in aggregated clusters, and then to re-formulate problems where the control can be designed using the cluster boundaries rather than individual control loops inside of each network. Examples can be found in the transportation application domain, where a significant challenge will be to obtain dynamic partitioning and clustering of heterogeneous networks in homogeneous sub-networks, and then to control the perimeter flows of the clusters to optimize the network operation. This topic is at the core of the Advanced ERC project Scale-FreeBack.

[0] Such a problem has been previously addressed in some specific applications, particularly robot fleets, and only few recent theoretical works have initiated a more systematic system-theoretic study of sparsity-constrained system realization theory and of sparsity-constrained feedback control.

3.5. Transportation networks

This is currently the main application domain of the NECS team. Several interesting problems in this area capture many of the generic networks problems described above. For example, distributed collaborative algorithms can be devised for ramp-metering control and traffic-density balancing can be achieved using consensus concepts. The team is already strongly involved in this field, both this theoretical works on traffic modeling, prediction and control, and with the Grenoble Traffic Lab platform. These activities will be continued and strengthened, also thanks to the contributions from the new staff member M.L. Delle Monache.

NUMED Project-Team

3. Research Program

3.1. Multiscale propagation phenomena in biology

3.1.1. Project team positioning

The originality of our work is the quantitative description of propagation phenomena accounting for several time and spatial scales. Here, propagation has to be understood in a broad sense. This includes propagation of invasive species, chemotactic waves of bacteira, evoluation of age structures populations ... Our main objectives are the quantitative calculation of macroscopic quantities as the rate of propagation, and microscopic distributions at the edge and the back of the front. These are essential features of propagation which are intimately linked in the long time dynamics.

Multiscale modeling of propagation phenomena raises a lot of interest in several fields of application. This ranges from shock waves in kinetic equations (Boltzmann, BGK, etc...), bacterial chemotactic waves, selection-mutation models with spatial heterogeneities, evolution in age-structured population or subdiffusive processes.

Earlier works generally focused on numerical simulations, hydrodynamic limits to average over the microscopic variable, or specific models with only local features, not suitable for most of the relevant biological situations. Our contribution enables to derive the relevant features of propagation analytically, and far from the hydrodynamic regime for a wide range of models including nonlocal interaction terms.

Our recent understanding is closely related to the analysis of large deviations in multiscale dispersion equations (e.g. PDMP), for which we gave important contributions too in collaboration with E. Bouin (CEREMADE Dauphine), E. Grenier (Inria NUMED) and G. Nadin (Univ. Paris 6).

These advances are linked to the work of other Inria teams (MAMBA, DRACULA, BEAGLE), and collaborators in mathematics, physics and theoretical biology in France, Austria and UK.

3.1.2. Recent results

Vincent Calvez has focused on the modelling and analysis of propagation phenomena in structured populations. This includes chemotactic concentration waves, transport-reaction equations, coupling between ecological processes (reaction-diffusion) and evolutionary processes (selection of the fittest trait, adaptation), evolution of age structured poulations, and anomalous diffusion. As a main result, he could establish the existence of concentration waves of chemotactic bacteria E. coli in a fully coupled kinetic/reaction-diffusion system previously validated on experimental data.

In collaboration with a group of theoretical biologists at ISEM Montpellier (O. Ronce and O. Cotto), and J. Garnier (Univ. Savoie), Th. Lepoutre (Inria DRACULA), Th. Bourgeron (Inria NUMED) he has investigated quantitatively the maladaptation of an age-structured population in a changing environment. He has unravelled a striking phenomenon of severe maladaptation specific to age structure. This was observed on numerical simulations by biologists, but it has now a systematic mathematical comprehension.

He has also continued his work on the optimal control of monotone linear dynamical systems, using the Hamilton-Jacobi framework, and the weak KAM theory, in collaboration with P. Gabriel (UVSQ) and S. Gaubert (Inria MAXPLUS).

Alvaro Mateos Gonzalez has started his PhD on September 2014 under the supervision of Vincent Calvez, and Hugues Berry (BEAGLE), . He has already collaborated fruitfully with Thomas Lepoutre (DRACULA) and Hugues Berry to investigate the long-time asymptotics of a degenerate renewal equation. This is a first step towards the mathematical analysis of anomalous diffusion processes. In collaboration with P. Gabriel (UVSQ) and V. Calvez (Inria NUMED) he has investigated large deviations of heterogenous continuous time random walks.

3.1.3. Collaborations

- Mathematical description of bacterial chemotactic waves:
  - **N. Bournaveas** (Univ. Edinburgh), **V. Calvez** (ENS de Lyon, Inria NUMED) **B. Perthame** (Univ. Paris 6, Inria BANG), **Ch. Schmeiser** (Univ. Vienna), **N. Vauchelet**: design of the model, analysis of traveling waves, analysis of optimal strategies for bacterial foraging.
  - **J. Saragosti**, **V. Calvez** (ENS de Lyon, Inria NUMED), **A. Buguin**, **P. Silberzan** (Institut Curie, Paris): experiments, design of the model, identification of parameters.
- Transport-reaction waves and large deviations:
  - **E. Bouin**, **V. Calvez** (ENS de Lyon, Inria NUMED), **E. Grenier** (ENS de Lyon, Inria NUMED), **G. Nadin** (Univ. Paris 6)
- Selection-mutation models of invasive species:
  - **E. Bouin** (ENS de Lyon, Inria NUMED), **V. Calvez** (ENS de Lyon, Inria NUMED), **S. Mirrahimi** (Inst. Math. Toulouse): construction of traveling waves, asymptotic propagation of fronts,
  - **E. Bouin** (ENS de Lyon, Inria NUMED), **V. Calvez** (ENS de Lyon, Inria NUMED), **N. Meunier**, (Univ. Paris 5), **B. Perthame** (Univ. Paris 6, Inria Bang), **G. Raoul** (CEFE, Montpellier), **R. Voituriez** (Univ. Paris 6): formal analysis, derivation of various asymptotic regimes.
- Age-structured equations for anomalous diffusion processes, and evolution
  - **H. Berry** (Inria BEAGLE), **V. Calvez** (ENS de Lyon, Inria NUMED), **Th. Lepoutre** (Inria DRACULA), **P. Gabriel** (Univ. UVSQ), O. Ronce (ISEM Montpellier), O. Cotto (ISEM Montpellier), J. Garnier (Univ. Savoie).

3.2. Growth of biological tissues

3.2.1. Project-team positioning

The originality of our work is the derivation, analysis and numerical simulations of mathematical model for growing cells and tissues. This includes mechanical effects (growth induces a modification of the mechanical stresses) and biological effects (growth is potentially influenced by the mechanical forces).

This leads to innovative models, adapted to specific biological problems (*e.g.* suture formation, cell polarisation), but which share similar features. We perform linear stability analysis, and look for pattern formation issues (at least instability of the homogeneous state).

The biophysical literature of such models is large. We refer to the groups of Ben Amar (ENS Paris), Boudaoud (ENS de Lyon), Mahadevan (Harvard), etc.

Our team combines strong expertise in reaction-diffusion equations (V. Calvez) and mechanical models (P. Vigneaux). We develop linear stability analysis on evolving domains (due to growth) for coupled biomechanical systems.

Another direction of work is the mathematical analysis of classical tumor growth models. These continuous mechanics models are very close to classical equations like Euler or Navier Stokes equations in fluid mechanics. However they bring there own difficulties: Darcy law, multispecies equations, non newtonian dynamics (Bingham flows). Part of our work consist in deriving existence results and designing acute numerical schemes for these equations.

3.2.2. Recent results

We have worked on several biological issues. Cell polarisation is the main one. We first analyzed a nonlinear model proposed by theoretical physicists and biologists to describe spontaneous polarisation of the budding yeast *S. cerevisae*. The model assumes a dynamical transport of molecules in the cytoplasm. It is analogous to the Keller-Segel model for cell chemotaxis, except for the source of the transport flux. We developped nonlinear analysis and entropy methods to investigate pattern formation (Calvez et al 2012). We are currently validating the model on experimental data. The analysis of polarization of a single cell is a preliminary step before the study of mating in a population of yeast cells. In the mating phase, secretion of pheromones induces a dialogue between cells of opposite types.

We also derive realistic models for the growth of the fission yeast *S. pombe*. We proposed two models which couple growth and geometry of the cell. We aim to tackle the issue of pattern formation, and more specifically the instability of the spherical shape, leading to a rod shape. The mechanical coupling involves the distribution of microtubules in the cytoplasm, which bring material to the cell wall.

Over the evaluation period, Paul Vigneaux developped expertise in modelling and design of new numerical schemes for complex fluid models of the viscoplastic type. Associated materials are involved in a broad range of applications ranging from chemical industry to geophysical and biological materials. In the context of NUMED, this expertise is linked to the development of complex constitutive laws for cancer cell tissue. During the period, NUMED used mixed compressible/incompressible fluid model for tumor growth and viscoelastic fluid model. Viscoplastic is one of the other types of complex fluid model which is usable in the field. Mathematically, it involves variational inequalities and the need for specific numerical methods.

3.2.3. Collaborations

- **V. Calvez** (ENS de Lyon, Inria NUMED), **Th. Lepoutre** (Inria DRACULA), **N. Meunier**, (Univ. Paris 5), **N. Muller** (Univ. Paris 5), **P. Vigneaux** (ENS de Lyon, Inria NUMED): mathematical analysis of cell polarisation, numerical simulations
- **V. Calvez** (ENS de Lyon, Inria NUMED), **N. Meunier**, (Univ. Paris 5), **M. Piel**, (Institut Curie, Paris), **R. Voituriez** (Univ. Paris 6): biomechanical modeling of the growth of *S. pombe*
- **D. Bresch** (Univ. Chambéry), **V. Calvez** (ENS de Lyon, Inria NUMED), **R.H. Khonsari** (King's College London, CHU Nantes), **J. Olivier** (Univ. Aix-Marseille), **P. Vigneaux** (ENS de Lyon, Inria NUMED): modeling, analysis and simulations of suture formation.
- **Didier Bresch** (Univ Chambéry), **Benoit Desjardins**(Moma group): petrology.

ANR JCJC project "MODPOL", *Mathematical models for cell polarization*, led by Vincent Calvez (ENS de Lyon, CNRS, Inria NUMED).

3.3. Multiscale models in oncology

3.3.1. Project-team positioning

Since 15 years, the development of mathematical models in oncology has become a significant field of research throughout the world. Several groups of researchers in biomathematics have developed complex and multiscale continuous and discrete models to describe the pathological processes as well as the action of anticancer anti-cancer drugs. Many groups in US (e.g. Alexander Anderson's lab, Kristin Swansson's lab) and in Canada (e.g. Thomas Hillen, Gerda de Vries), quickly developed and published interesting modeling frameworks. The setup of European networks such as the Marie Curie research and training networks managed by Nicolas Bellomo and Luigi Preziosi constituted a solid and fertile ground for the development of new oncology models by teams of biomathematicians and in particular Zvia Agur (Israel), Philip Maini (UK), Helen Byrne (UK), Andreas Deutsch (Germany), or Miguel Herrero (Spain).

3.3.2. Results

We have worked on the development of a multiscale system for modeling the complexity of the cancer disease and generate new hypothesis on the use of anti-cancer drugs. This model relies on a multiscale formalism integrating a subcellular level integrating molecular interactions, a cell level (integrating the regulation of the cell cycle at the levels of individual cells) and a macroscopic level for describing the spatio-temporal dynamics of different types of tumor tissues (proliferating, hypoxic and necrotic). The model is thus composed by a set of partial differential equations (PDEs) integrating molecular network up to tissue dynamics using lax from fluid dynamic. This formalism is useful to investigate theoretically different cancer processes such as the angiogenesis and invasion. We have published several examples and case studies of the use of this model in particular, the action of phase-specific chemotherapies (Ribba, You et al. 2009), the use of anti-angiogenic drugs (Billy, Ribba et al. 2009) and their use in combination with chemotherapies (Lignet, Benzekry et al. 2013). This last work also integrates a model of the VEGF molecular pathway for proliferation and migration of endothelial cells in the context of cancer angiogenesis (Lignet, Calvez et al. 2013).

If these types of models present interesting framework to theoretically investigate biological hypothesis, they however present limitation due to their large number of parameters. In consequence, we decided to stop the development of the multiscale platform until exploration of alternative modeling strategies to deal with real data. We focus our interest on the use of mixed-effect modeling techniques as classically used in the field of pharmacokinetic and pharmacodynamics modeling. The general principal of this approach lies in the integration of several levels of variability in the model thus allowing for the simultaneous analysis of data in several individuals. Nowadays, complex algorithms allow for dealing with this problem when the model is composed by few ordinary differential equations (ODEs). However, no similar parameter estimation method is available for models defined as PDEs. In consequence, we decided: 1. To develop more simple models, based on systems of ODEs, assuming simplistic hypothesis of tumor growth and response to treatment but with a real focus on model ability to predict real data. 2. To work alone the development of parameter estimation methods for PDE models in oncology.

3.4. Parametrization of complex systems

3.4.1. Project-team positioning

We focus on a specific problem: the "population" parametrization of a complex system. More precisely, instead of trying to look for parameters in order to fit the available data for one patient, in many cases it is more pertinent to look for the distribution of the parameters (assuming that it is gaussian or log gaussian) in a population of patients, and to maximize the likelihood of the observations of all patients. It is a very useful strategy when few data per patients are available, but when we have a lot of patients. The number of parameters to find is multiplied by two (average and standard deviation for each parameter) but the number of data is greatly increased.

This strategy, that we will call "population" parametrization has been initiated in the eighties by software like Nonmem. Recently Marc Lavielle (Popix team) made a series of breakthroughs and designed a new powerfull algorithm, leading to Monolix software.

However population parametrization is very costly. It requires several hundred of thousands of model evaluations, which may be very long.

3.4.2. Results

We address the problem of computation time when the complex model is long to evaluate. In simple cases like reaction diffusion equations in one space dimension, the evaluation of the model may take a few seconds of even a few minutes. In more realistic geometries, the computation time would be even larger and can reach the hour or day. It is therefore impossible to run a SAEM algorith on such models, since it would be much too long. Moreover the underlying algorithm can not be parallelized.

We propose a new iterative approach combining a SAEM algorithm together with a kriging. This strategy appears to be very efficient, since we were able to parametrize a PDE model as fast as a simple ODE model.

We are currently developing the corresponding software.

3.5. Models for the analysis of efficacy data in oncology

3.5.1. Project-team positioning

The development of new drugs for oncology patients faces significant issues with a global attrition rate of 95 percents and only 40 percents of drug approval in phase III after successful phase II. As for meteorology, the analysis through modeling and simulation (MS), of time-course data related to anticancer drugs efficacy and/or toxicity constitutes a rational method for predicting drugs efficacy in patients. This approach, now supported by regulatory agencies such as the FDA, is expected to improve the drug development process and in consequence the treatment of cancer patients. A private company, Pharsight, has nowadays the leader team in the development of such modeling frameworks. In 2009, this team published a model describing tumor size time-course in more than one thousand colorectal cancer patients. This model was used in an MS framework to predict the outcome of a phase III clinical trials based on the analysis of phase II data. From 2009 to 2013, 12 published articles address similar analysis of different therapeutic indications such as lung, prostate, thyroid and renal cancer. A similar modeling activity is also proposed for the analysis of data in preclinical experiments, and in particular, experiments in mice. Animal experiments represent critical stages to decide if a drug molecule should be tested in humans. MS methods are considered as tools to better investigate the mechanisms of drug action and to potentially facilitate the transition towards the clinical phases of the drug development process. Our team has worked in the development of two modeling frameworks with application in both preclinical and clinical oncology. For the preclinical context, we have worked on the development of models focusing on the process of tumor angiogenesis, i.e. the formation of intra-tumoral blood vessels. At the clinical level, we have developed a model to predict tumor size dynamics in patients with low-grade glioma.

At Inria, several project-teams have developed similar efforts. The project-team BANG has a solid experience in the development of age-structured models of the cell cycle and tissue regulation of tumors with clinical applications for chronotherapy. BANG is also currently applying these types of partial differential equation (PDE) models to the study of leukemia through collaboration with the project-team DRACULA. Project-team MC2 has recently shown that the analysis, through a simplified PDE model of tumor growth and treatment response, of 3D imaging, could lead to correct prediction of tumor volume evolution in patients with pulmonary metastasis from thyroid cancer. Regarding specifically the modeling of brain tumors, project-team ASCLEPIOS has brought an important contribution towards personalized medicine in analyzing 3D data information from MRI with a multiscale model that describes the evolution of high grade gliomas in the brain. Their framework relies on the cancer physiopathological model that was mainly developed by Kristin Swanson and her group at the university of Washington.

Outside from Inria, we wish to mention here the work of the group of Florence Hubert in Marseille in the development of models with an interesting compromise between mathematical complexity and data availability. A national ANR project led by the team is expected to support the development of an MS methodology for the analysis of tumor size data in patients with metastases.

3.5.2. Results

Regarding our contribution in preclinical modeling, we have developed a model to analyze the dynamics of tumor progression in nude mice xenografted with HT29 or HCT116 colorectal cancer cells. This model, based on a system of ordinary differential equations (ODEs), integrated the different types of tumor tissues, and in particular, the proliferating, hypoxic and necrotic tissues. Practically, in our experiment, tumor size was periodically measured, and percentages of hypoxic and necrotic tissue were assessed using immunohistochemistry techniques on tumor samples after euthanasia. In the proposed model, the peripheral non-hypoxic tissue proliferates according to a generalized-logistic equation where the maximal tumor size is represented by a variable called "carrying capacity". The ratio of the whole tumor size to the carrying capacity was used to define the hypoxic stress. As this stress increases, non-hypoxic tissue turns hypoxic. Hypoxic tissue does not stop proliferating, but hypoxia constitutes a transient stage before the tissue becomes necrotic. As the tumor grows, the carrying capacity increases owing to the process of angiogenesis (Ribba, Watkin et al. 2011). The model

is shown to correctly predict tumor growth dynamics as well as percentages of necrotic and hypoxic tissues within the tumor.

Regarding our contribution in clinical oncology, we developed an ODE model based on the analysis of mean tumor diameter (MTD) time-course in low-grade glioma patients (Ribba, Kaloshi et al. 2012).

In this model, the tumor is composed of proliferative (P) and non-proliferative quiescent tissue (Q) expressed in millimeters. The proportion of proliferative tissue transitioning into quiescence is constant. The treatment directly eliminates proliferative cells by inducing lethal DNA damage while these cells progress through the cell cycle. The quiescent cells are also affected by the treatment and become damaged quiescent cells (k_{PQ}). Damaged quiescent cells, when re-entering the cell cycle, can repair their DNA and become proliferative once again (transition from Q_P to P) or can die due to unrepaired damages. We modeled the pharmacokinetics of the PCV chemotherapy using a kinetic-pharmacodynamic (K-PD) approach, in which drug concentration is assumed to decay according to an exponential function. In this model, we did not consider the three drugs separately. Rather, we assumed the treatment to be represented as a whole by a unique variable (C), which represents the concentration of a virtual drug encompassing the three chemotherapeutic components of the PCV regimen. We modeled the exact number of treatment cycles administered by setting the value of C to 1 (arbitrary unit) at the initiation of each cycle(T_{Treat}): $C(T = T_{Treat}) = 1$.

The resulting model is as follows:

$$\begin{aligned}
\frac{dC}{dt} &= -KDE \times C \\
\frac{dP}{dt} &= \lambda_P P \left(1 - \frac{P^{\bigstar}}{K}\right) + k_{Q_pP} Q_p - k_{PQ} P - \gamma \times C \times KDE \times P \\
\frac{dQ}{dt} &= k_{PQ} P - \gamma \times C \times KDE \times Q \\
\frac{dQ_p}{dt} &= \gamma \times C \times KDE \times Q - k_{Q_pP} Q_p - \delta_{Q_p} Q_p
\end{aligned} \tag{6}$$

We challenged this model with additional patient data. In particular, MTD time-course information from 24 patients treated with TMZ (subset of the 120 patients from SH) and 25 patients treated with radiotherapy (SH). Note that exactly the same K-PD approach was used to model treatment pharmacokinetic (including for radiotherapy). This choice, though not really realistic was adopted for simplicity reasons: the same model can be indifferently applied to the three different treatment modalities of LGG patients.

3.5.3. Collaborations

François Ducray and Jérôme Honnorat (Pierre Wertheimer Hospital in Lyon)

External support: grant INSERM PhysiCancer 2012 and Inria IPL MONICA

3.6. Stroke

3.6.1. Project team positioning

Stroke is a major public health problem since it represents the second leading cause of death worldwide and the first cause of acquired disability in adults.

Numed is currently starting completely new issues with D. Rousseau (INSA) and his team. We have now at hand a large data base of clinical images. Our aim is to develop model which are able to predict the final size of the dead brain area as a function of the first two clinical data.

PERCEPTION Project-Team

3. Research Program

3.1. Audio-Visual Scene Analysis

From 2006 to 2009, R. Horaud was the scientific coordinator of the collaborative European project POP (Perception on Purpose), an interdisciplinary effort to understand visual and auditory perception at the crossroads of several disciplines (computational and biological vision, computational auditory analysis, robotics, and psychophysics). This allowed the PERCEPTION team to launch an interdisciplinary research agenda that has been very active for the last five years. There are very few teams in the world that gather scientific competences spanning computer vision, audio signal processing, machine learning and human-robot interaction. The fusion of several sensorial modalities resides at the heart of the most recent biological theories of perception. Nevertheless, multi-sensor processing is still poorly understood from a computational point of view. In particular and so far, audio-visual fusion has been investigated in the framework of speech processing using close-distance cameras and microphones. The vast majority of these approaches attempt to model the temporal correlation between the auditory signals and the dynamics of lip and facial movements. Our original contribution has been to consider that audio-visual localization and recognition are equally important. We have proposed to take into account the fact that the audio-visual objects of interest live in a three-dimensional physical space and hence we contributed to the emergence of *audio-visual scene analysis* as a scientific topic in its own right. We proposed several novel statistical approaches based on supervised and unsupervised mixture models. The *conjugate mixture model* (CMM) is an unsupervised probabilistic model that allows to cluster observations from different modalities (e.g., vision and audio) living in different mathematical spaces [18], [2]. We thoroughly investigated CMM, provided practical resolution algorithms and studied their convergence properties. We developed several methods for sound localization using two or more microphones [1]. The *Gaussian locally-linear model* (GLLiM) is a partially supervised mixture model that allows to map high-dimensional observations (audio, visual, or concatenations of audio-visual vectors) onto low-dimensional manifolds with a partially known structure [6]. This model is particularly well suited for perception because it encodes both observable and unobservable phenomena. A variant of this model, namely *probabilistic piecewise affine mapping* has also been proposed and successfully applied to the problem of sound-source localization and separation [5]. The European projects HUMAVIPS (2010-2013) coordinated by R. Horaud and EARS (2014-2017), applied audio-visual scene analysis to human-robot interaction.

3.2. Stereoscopic Vision

Stereoscopy is one of the most studied topics in biological and computer vision. Nevertheless, classical approaches of addressing this problem fail to integrate eye/camera vergence. From a geometric point of view, the integration of vergence is difficult because one has to re-estimate the epipolar geometry at every new eye/camera rotation. From an algorithmic point of view, it is not clear how to combine depth maps obtained with different eyes/cameras relative orientations. Therefore, we addressed the more general problem of binocular vision that combines the low-level eye/camera geometry, sensor rotations, and practical algorithms based on global optimization [12], [20]. We studied the link between mathematical and computational approaches to stereo (global optimization and Markov random fields) and the brain plausibility of some of these approaches: indeed, we proposed an original mathematical model for the complex cells in visual-cortex areas V1 and V2 that is based on steering Gaussian filters and that admits simple solutions [13]. This addresses the fundamental issue of how local image structure is represented in the brain/computer and how this structure is used for estimating a dense disparity field. Therefore, the main originality of our work is to address both computational and biological issues within a unifying model of binocular vision. Another equally important problem that still remains to be solved is how to integrate binocular depth maps over time. Recently, we have addressed this problem and proposed a semi-global optimization framework that starts with sparse yet reliable matches and proceeds with propagating them over both space and time. The concept of seed-match propagation has then been extended to TOF-stereo fusion [8].

3.3. Audio Signal Processing

Audio-visual fusion algorithms necessitate that the two modalities are represented in the same mathematical space. Binaural audition allows to extract sound-source localization (SSL) information from the acoustic signals recorded with two microphones. We have developed several methods, that perform sound localization in the temporal and the spectral domains. If a direct path is assumed, one can exploit the *time difference of arrival* (TDOA) between two microphones to recover the position of the sound source with respect to the position of the two microphones. The solution is not unique in this case, the sound source lies onto a 2D manifold. However, if one further assumes that the sound source lies in a horizontal plane, it is then possible to extract the azimuth. We used this approach to predict possible sound locations in order to estimate the direction of a speaker [2]. We also developed a geometric formulation and we showed that with four non-coplanar microphones the azimuth and elevation of a single source can be estimated without ambiguity [1]. We also investigated SSL in the spectral domain. This exploits the filtering effects of the head related transfer function (HRTF): there is a different HRTF for the left and right microphones. The interaural spectral features, namely the ILD (interaural level difference) and IPD (interaural phase difference) can be extracted from the short-time Fourier transforms of the two signals. The sound direction is encoded in these interaural features but it is not clear how to make SSL explicit in this case. We proposed a supervised learning formulation that estimates a mapping from interaural spectral features (ILD and IPD) to source directions using two different setups: audio-motor learning [5] and audio-visual learning [7].

3.4. Visual Reconstruction With Multiple Color and Depth Cameras

For the last decade, one of the most active topics in computer vision has been the visual reconstruction of objects, people, and complex scenes using a multiple-camera setup. The PERCEPTION team has pioneered this field and by 2006 several team members published seminal papers in the field. Recent work has concentrated onto the robustness of the 3D reconstructed data using probabilistic outlier rejection techniques combined with algebraic geometry principles and linear algebra solvers [23]. Subsequently, we proposed to combine 3D representations of shape (meshes) with photometric data [21]. The originality of this work was to represent photometric information as a scalar function over a discrete Riemannian manifold, thus *generalizing image analysis to mesh and graph analysis*. Manifold equivalents of local-structure detectors and descriptors were developed [22]. The outcome of this pioneering work has been twofold: the formulation of a new research topic now addressed by several teams in the world, and allowed us to start a three year collaboration with Samsung Electronics. We developed the novel concept of *mixed camera systems* combining high-resolution color cameras with low-resolution depth cameras [14], [10],[9]. Together with our start-up company 4D Views Solutions and with Samsung, we developed the first practical depth-color multiple-camera multiple-PC system and the first algorithms to reconstruct high-quality 3D content [8].

3.5. Registration, Tracking and Recognition of People and Actions

The analysis of articulated shapes has challenged standard computer vision algorithms for a long time. There are two difficulties associated with this problem, namely how to represent articulated shapes and how to devise robust registration and tracking methods. We addressed both these difficulties and we proposed a novel kinematic representation that integrates concepts from robotics and from the geometry of vision. In 2008 we proposed a method that parameterizes the occluding contours of a shape with its intrinsic kinematic parameters, such that there is a direct mapping between observed image features and joint parameters [19]. This deterministic model has been motivated by the use of 3D data gathered with multiple cameras. However, this method was not robust to various data flaws and could not achieve state-of-the-art results on standard dataset. Subsequently, we addressed the problem using probabilistic generative models. We formulated the problem of articulated-pose estimation as a maximum-likelihood with missing data and we devised several tractable algorithms [17], [16]. We proposed several expectation-maximization procedures applied to various articulated shapes: human bodies, hands, etc. In parallel, we proposed to segment and register articulated shapes represented with graphs by embedding these graphs using the spectral properties of graph Laplacians [4]. This turned out to be a very original approach that has been followed by many other researchers in computer vision and computer graphics.

PERVASIVE INTERACTION Team

3. Research Program

3.1. Situation Models

Situation Modelling, Situation Awareness, Probabilistic Description Logistics

The objectives of this research area are to develop and refine new computational techniques that improve the reliability and performance of situation models, extend the range of possible application domains, and reduce the cost of developing and maintaining situation models. Important research challenges include developing machine-learning techniques to automatically acquire and adapt situation models through interaction, development of techniques to reason and learn about appropriate behaviors, and the development of new algorithms and data structures for representing situation models.

Over the next four years we will address the following research challenges:

Techniques for learning and adapting situation models: Hand crafting of situation models is currently an expensive process requiring extensive trial and error. We will investigate combination of interactive design tools coupled with supervised and semi-supervised learning techniques for constructing initial, simplified prototype situation models in the laboratory. One possible approach is to explore developmental learning to enrich and adapt the range of situations and behaviors through interaction with users.

Reasoning about actions and behaviors: Constructing systems for reasoning about actions and their consequences is an important open challenge. We will explore integration of planning techniques for operationalizing actions sequences within behaviors, and for constructing new action sequences when faced with unexpected difficulties. We will also investigate reasoning techniques within the situation modeling process for anticipating the consequences of actions, events and phenomena.

Algorithms and data structures for situation models: In recent years, we have experimented with an architecture for situated interaction inspired by work in human factors. This model organises perception and interaction as a cyclic process in which directed perception is used to detect and track entities, verify relations between entities, detect trends, anticipate consequences and plan actions. Each phase of this process raises interesting challenges questions algorithms and programming techniques. We will experiment alternative programming techniques representing and reasoning about situation models both in terms of difficulty of specification and development and in terms of efficiency of the resulting implementation. We will also investigate the use of probabilistic graph models as a means to better accommodate uncertain and unreliable information. In particular, we will experiment with using probabilistic predicates for defining situations, and maintaining likelihood scores over multiple situations within a context. Finally, we will investigate the use of simulation as technique for reasoning about consequences of actions and phenomena.

Probabilistic Description Logics: In our work, we will explore the use of probabilistic predicates for representing relations within situation models. As with our earlier work, entities and roles will be recognized using multi-modal perceptual processes constructed with supervised and semi-supervised learning [Brdiczka 07], [Barraquand 12]. However, relations will be expressed with probabilistic predicates. We will explore learning based techniques to probabilistic values for elementary predicates, and propagate these through probabilistic representation for axioms using Probabilistic Graphical Models and/or Bayesian Networks.

The challenges in this research area will be addressed through three specific research actions covering situation modelling in homes, learning on mobile devices, and reasoning in critical situations.

3.1.1. Learning Routine patterns of activity in the home.

The objective of this research action is to develop a scalable approach to learning routine patterns of activity in a home using situation models. Information about user actions is used to construct situation models in which key elements are semantic time, place, social role and actions. Activities are encoded as sequences of situations. Recurrent activities are detected as sequences of activities that occur at a specific time and place each day. Recurrent activities provide routines what can be used to predict future actions and anticipate needs and services. An early demonstration has been to construct an intelligent assistant that can respond to and filter communications.

This research action is carried out as part of the doctoral research of Julian Cumin in cooperation with researchers at Orange labs, Meylan. Results are to be published at Ubicomp, Ambient intelligence, Intelligent Environments and IEEE Transactions on System Man and Cybernetics. Julien Cumin will complete and defend his doctoral thesis in 2018.

3.1.2. Learning Patterns of Activity with Mobile Devices

The objective of this research action is to develop techniques to observe and learn recurrent patterns of activity using the full suite of sensors available on mobile devices such as tablets and smart phones. Most mobile devices include seven or more sensors organized in 4 groups: Positioning Sensors, Environmental Sensors, Communications Subsystems, and Sensors for Human-Computer Interaction. Taken together, these sensors can provide a very rich source of information about individual activity.

In this area we explore techniques to observe activity with mobiles devices in order to learn daily patterns of activity. We will explore supervised and semi-supervised learning to construct systems to recognize places and relevant activities. Location and place information, semantic time of day, communication activities, interpersonal interactions, and travel activities (walking, driving, riding public transportation, etc.) are recognized as probabilistic predicates and used to construct situation models. Recurrent sequences of situations will be detected and recorded to provide an ability to predict upcoming situations and anticipate needs for information and services.

Our goal is to develop a theory for building context aware services that can be deployed as part of the mobile applications that companies such as SNCF and RATP use to interact with clients. For example, a current project concerns systems that observe daily travel routines for the Paris region RATP metro and SNCF commuter trains. This system learns individual travel routines on the mobile device without the need to divulge information about personal travel to a cloud based system. The resulting service will consult train and metro schedules to assure that planned travel is feasible and to suggest alternatives in the case of travel disruptions. Similar applications are under discussion for the SNCF inter-city travel and Air France for air travel.

This research action is conducted in collaboration with the Inria Startup Situ8ed. The current objective is to deploy and evaluate a first prototype App during 2017. Techniques will be used commercially by Situ8ed for products to be deployed as early as 2019.

3.1.3. Observing and Modelling Competence and Awareness in Critical Situations

The aim of this research action is to experimentally evaluate and compare current theories for mental modelling for problem solving and attention in stressful situations, as well as to refine theories and techniques for observing visual fixation, attention and emotion. We are currently investigating differences in visual attention, emotional response and mental states of chess experts and chess novices solving chess problems and participating in chess matches. We observe physiological responses, mental states and visual attention using eye-tracking, long term and instantaneous face-expressions (micro-expressions), skin conductivity, blood flow (BVP), posture and other information extracted from audio-visual recordings of players.

We expect that a high degree of expertise in chess should be reflected in patterns of eye movement and emotional reaction in accordance with the game situation. Information from visual attention will be used to determine and model the degree to which a player understands the game situation in terms of abstract configurations of chess pieces rather than the positions of individual pieces. Information about the emotional reactions of players will be expressed as trajectories in the physiological space of pleasure, arousal and

dominance to determine if a players understanding of the game situation can be observed from emotional reaction to game play.

This work is supported by the ANR project CEEGE in cooperation with the department of NeuroCognition of Univ. Bielefeld, as well as the LIG internal project AirBorne in cooperation with the French Air Force training center at ISTRE. Work in this area includes the Doctoral research of Thomas Guntz to be defended in 2019.

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3.2. Perception of People, Activities and Emotions

Machine perception is fundamental for situated behavior. Work in this area will concern construction of perceptual components using computer vision, acoustic perception, accelerometers and other embedded sensors. These include low-cost accelerometers [Bao 04], gyroscopic sensors and magnetometers, vibration sensors, electromagnetic spectrum and signal strength (wifi, bluetooth, GSM), infrared presence detectors, and bolometric imagers, as well as microphones and cameras. With electrical usage monitoring, every power switch can be used as a sensor [Fogarty 06], [Coutaz 16]. We will develop perceptual components for integrated vision systems that combine a low-cost imaging sensors with on-board image processing and wireless communications in a small, low-cost package. Such devices are increasingly available, with the enabling manufacturing technologies driven by the market for integrated imaging sensors on mobile devices. Such technology enables the use of embedded computer vision as a practical sensor for smart objects.

Research challenges to be addressed in this area include development of practical techniques that can be deployed on smart objects for perception of people and their activities in real world environments, integration and fusion of information from a variety of sensor modalities with different response times and levels of abstraction, and perception of human attention, engagement, and emotion using visual and acoustic sensors.

Work in this research area will focus on three specific Research Actions

3.2.1. Multi-modal perception and modeling of activities

The objective of this research action is to develop techniques for observing and scripting activities for common household tasks such as cooking and cleaning. An important part of this project involves acquiring annotated multi-modal datasets of activity using an extensive suite of visual, acoustic and other sensors. We are interested in real-time on-line techniques that capture and model full body movements, head motion and manipulation actions as 3D articulated motion sequences decorated with semantic labels for individual actions and activities with multiple RGB and RGB-D cameras.

We will explore the integration of 3D articulated models with appearance based recognition approaches and statistical learning for modeling behaviors. Such techniques provide an important enabling technology for context aware services in smart environments [Coutaz 05], [Crowley 15], investigated by Pervasive Interaction team, as well as research on automatic cinematography and film editing investigated by the Imagine team [Gandhi 13] [Gandhi 14] [Ronfard 14] [Galvane 15]. An important challenge is to determine which techniques are most appropriate for detecting, modeling and recognizing a large vocabulary of actions and activities under different observational conditions.

We will explore representations of behavior that encodes both temporal-spatial structure and motion at multiple levels of abstraction. We will further propose parameters to encode temporal constraints between actions in the activity classification model using a combination of higher-level action grammars [Pirsiavash 14] and episodic reasoning [Santofimia 14] [Edwards 14].

Our method will be evaluated using long-term recorded dataset that contains recordings of activities in home environments. This work will be reported in the IEEE Conference on Face and Gesture Recognition, IEEE transactions on Pattern Analysis and Machine Intelligence, (PAMI) et IEEE Transactions on Systems man and Cybernetics. This work is carried out in the doctoral research of Nachwa Abubakr in cooperation with Remi Ronfard of the Imagine Team of Inria.

3.2.2. Perception with low-cost integrated sensors

In this research action, we will continue work on low-cost integrated sensors using visible light, infrared, and acoustic perception. We will continue development of integrated visual sensors that combine micro-cameras and embedded image processing for detecting and recognizing objects in storage areas. We will combine visual and acoustic sensors to monitor activity at work-surfaces. Low cost real-time image analysis procedures will be designed that acquire and process images directly as they are acquired by the sensor.

Bolometric image sensors measure the Far Infrared emissions of surfaces in order to provide an image in which each pixel is an estimate of surface temperature. Within the European MIRTIC project, Grenoble startup, ULIS has created a relatively low-cost Bolometric image sensor (Retina) that provides small images of 80 by 80 pixels taken from the Far-infrared spectrum. Each pixel provides an estimate of surface temperature. Working with Schneider Electric, engineers in the Pervasive Interaction team had developed a small, integrated sensor that combines the MIRTIC Bolometric imager with a microprocessor for on-board image processing. The package has been equipped with a fish-eye lens so that an overhead sensor mounted at a height of 3 meters has a field of view of approximately 5 by 5 meters. Real-time algorithms have been demonstrated for detecting, tracking and counting people, estimating their trajectories and work areas, and estimating posture.

Many of the applications scenarios for Bolometric sensors proposed by Schneider Electric assume a scene model that assigns pixels to surfaces of the floor, walls, windows, desks or other items of furniture. The high cost of providing such models for each installation of the sensor would prohibit most practical applications. We have recently developed a novel automatic calibration algorithm that determines the nature of the surface under each pixel of the sensor.

Work in this area will continue to develop low-cost real time infrared image sensing, as well as explore combinations of far-infrared images with RGB and RGBD images.

3.2.3. Observation of emotion from physiological responses in critical situations

Recent research in Cognitive Science indicates that the human emotions result in physiological manifestations in the heart rate, skin conductance, skin color, body movements and facial expressions. It has been proposed that these manifestations can be measured by observation of skin color, body motions, and facial expressions and modeled as activation levels in three dimensions known as Valence, Arousal and Dominance. The goal if this project is to evaluate the effectiveness of visual and acoustic perception technique for measuring these physiological manifestations.

Experimental data will be collected by observing subjects engaged in playing chess. A special apparatus has been constructed that allows synchronized recording from a color camera, Kinect2 3D camera, and Tobi Eye Tracker of a player seated before a computer generated display of a chess board. The masters student will participate in the definition and recording of scenarios for recording test data, apply recently proposed techniques from the scientific literature for measuring emotions, and provide a comparative performance evaluation of various techniques. The project is expected to reveal the relative effectiveness of computer vision and other techniques for observing human emotions.

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3.3. Sociable Interaction with Smart Objects

Reeves and Nass argue that a social interface may be the truly universal interface [Reeves 98]. Current systems lack ability for social interaction because they are unable to perceive and understand humans or to learn from interaction with humans. One of the goals of the research to be performed in Pervasive Interaction is to provide such abilities.

Work in research area RA3 will demonstrate the use of situation models for sociable interaction with smart objects and companion robots. We will explore the use of situation models as a representation for sociable interaction. Our goal in this research is to develop methods to endow an artificial agent with the ability to acquire social common sense using the implicit feedback obtained from interaction with people. We believe that such methods can provide a foundation for socially polite man-machine interaction, and ultimately for other forms of cognitive abilities. We propose to capture social common sense by training the appropriateness of behaviors in social situations. A key challenge is to employ an adequate representation for social situations.

Knowledge for sociable interaction will be encoded as a network of situations that capture both linguistic and non-verbal interaction cues and proper behavioral responses. Stereotypical social interactions will be represented as trajectories through the situation graph. We will explore methods that start from simple stereotypical situation models and extending a situation graph through the addition of new situations and the splitting of existing situations. An important aspect of social common sense is the ability to act appropriately in social situations. We propose to learn the association between behaviors and social situation using reinforcement learning. Situation models will be used as a structure for learning appropriateness of actions and behaviors that may be chosen in each situation, using reinforcement learning to determine a score for appropriateness based on feedback obtained by observing partners during interaction.

Work in this research area will focus on four specific Research Actions

3.3.1. Moving with people

Our objective in this area is to establish the foundations for robot motions that are aware of human social situation that move in a manner that complies with the social context, social expectations, social conventions and cognitive abilities of humans. Appropriate and socially compliant interactions require the ability for real time perception of the identity, social role, actions, activities and intents of humans. Such perception can

be used to dynamically model the current situation in order to understand the situation and to compute the appropriate course of action for the robot depending on the task at hand.

To reach this objective, we propose to investigate three interacting research areas:

- Modeling the context and situation of human activities for motion planning
- Planning and acting in a social context.
- Identifying and modeling interaction behaviors.

In particular, we will investigate techniques that allow a tele-presence robot, such as the BEAM system, to autonomously navigate in crowds of people as may be found at the entry to a conference room, or in the hallway of a scientific meeting. We will also continue experiments on autonomous motion for personal assistance robots (project PRAMAD). Work in this area includes the doctoral work of Jos,aö¬© da Silva, to be defended in 2019.

3.3.2. Understanding and communicating intentions from motion

This research area concerns the communication through motion. When two or more people move as a group, their motion is regulated by implicit rules that signal a shared sense of social conventions and social roles. For example, moving towards someone while looking directly at them signals an intention for engagement. In certain cultures, subtle rules dictate who passes through a door first or last. When humans move in groups, they implicitly communicate intentions with motion. In this research area, we will explore the scientific literature on proxemics and the social sciences on such movements, in order to encode and evaluate techniques for socially appropriate motion by robots.

3.3.3. Socially aware interaction

This research area concerns socially aware man-machine interaction. Appropriate and socially compliant interaction requires the ability for real time perception of the identity, social role, actions, activities and intents of humans. Such perception can be used to dynamically model the current situation in order to understand the context and to compute the appropriate course of action for the task at hand. Performing such interactions in manner that respects and complies with human social norms and conventions requires models for social roles and norms of behavior as well as the ability to adapt to local social conventions and individual user preferences. In this research area, we will complement research area 3.2 with other forms of communication and interaction, including expression with stylistic face expressions rendered on a tablet, facial gestures, body motions and speech synthesis. We will experiment with use of commercially available tool for spoken language interaction in conjunction with expressive gestures.

3.3.4. Stimulating affection and persuasion with affective devices.

This research area concerns technologies that can stimulate affection and engagement, as well as induce changes in behavior. When acting as a coach or cooking advisor, smart objects must be credible and persuasive. One way to achieve this goal is to express affective feedbacks while interacting. This can be done using sound, light and/or complex moves when the system is composed of actuators.

Research in this area will address 3 questions:

1. How do human perceive affective signals expressed by smart objects (including robots)?
2. How does physical embodiment effect perception of affect by humans?
3. What are the most effective models and tools for animation of affective expression?

Both the physical form and the range of motion have important impact on the ability of a system to inspire affection. We will create new models to propose a generic animation model, and explore the effectiveness of different forms of motion in stimulating affect.

3.3.5. Bibliography

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3.4. Interaction with Pervasive Smart Objects and Displays

Currently, the most effective technologies for new media for sensing, perception and experience are provided by virtual and augmented realities [Van Krevelen 2010]. At the same time, the most effective means to augment human cognitive abilities are provided by access to information spaces such as the world-wide-web using graphical user interfaces. A current challenge is to bring these two media together.

Display technologies continue to decrease exponentially, driven largely by investment in consumer electronics as well as the overall decrease in cost of microelectronics. A consequence has been an increasing deployment of digital displays in both public and private spaces. This trend is likely to accelerate, as new technologies and growth in available communications bandwidth enable ubiquitous low-cost access to information and communications.

The arrival of pervasive displays raises a number of interesting challenges for situated multi-modal interaction. For example:

1. Can we use perception to detect user engagement and identify users in public spaces?
2. Can we replace traditional pointing hardware with gaze and gesture based interaction?
3. Can we tailor information and interaction for truly situated interaction, providing the right information at the right time using the right interaction modality?
4. How can we avoid information overload and unnecessary distraction with pervasive displays?

It is increasingly possible to embed sensors and displays in clothing and ordinary devices, leading to new forms of tangible and wearable interaction with information. This raises challenges such as

1. What are the tradeoffs between large-scale environmental displays and wearable displays using technologies such as e-textiles and pico-projector?
2. How can we manage the tradeoffs between implicit and explicit interaction with both tangible and wearable interaction?
3. How can we determine the appropriate modalities for interaction?
4. How can we make users aware of interaction possibilities without creating distraction?

In addition to display and communications, the continued decrease in microelectronics has also driven an exponential decrease in cost of sensors, actuators, and computing resulting in an exponential growth in the number of smart objects in human environments. Current models for systems organization are based on centralized control, in which a controller or local hub, orchestrates smart objects, generally in connection with cloud computing. This model creates problems with privacy and ownership of information. An alternative is to organize local collections of smart objects to provide distributed services without the use of a centralized controller. The science of ecology can provide an architectural model for such organization.

This approach raises a number of interesting research challenges for pervasive interaction:

1. Can we devise distributed models for multi-modal fusion and interaction with information on heterogeneous devices?
2. Can we devise models for distributed interaction that migrates over available devices as the user changes location and task?
3. Can we manage migration of interaction over devices in a manner that provides seamless immersive interaction with information, services and media?
4. Can we provide models of distributed interaction that conserve the interaction context as services migrate?

Research Actions for Interaction with Pervasive Smart Objects for the period 2017 - 2020 include

3.4.1. Situated interaction with pervasive displays

The emergence of low-cost interactive displays will enable a confluence of virtual and physical environments. Our goal in this area is to go beyond simple graphical user interfaces in such environments to provide immersive multi-sensorial interaction and communication. A primary concern will be interaction technologies that blend visual with haptic/tactile feedback and 3D interaction and computer vision. We will investigate the use of visual-tactile feedback as well as vibratory signals to augment multi-sensorial interaction and communication. The focus will be on the phenomena of immersive interaction in real worlds that can be made possible by the blending of physical and virtual in ordinary environments.

3.4.2. Wearable and tangible interaction with smart textiles and wearable projectors

Opportunities in this area result from the emergence of new forms of interactive media using smart objects. We will explore the use of smart objects as tangible interfaces that make it possible to experience and interact with information and services by grasping and manipulating objects. We will explore the use of sensors and actuators in clothing and wearable devices such as gloves, hats and wrist bands both as a means of unobtrusively sensing human intentions and emotional states and as a means of stimulating human senses through vibration and sound. We will explore the new forms of interaction and immersion made possible by deploying interactive displays over large areas of an environment.

3.4.3. Pervasive interaction with ecologies of smart objects in the home

In this research area, we will explore and evaluate interaction with ecologies of smart objects in home environments. We will explore development of a range of smart objects that provide information services, such as devices for Episodic Memory for work surfaces and storage areas, devices to provide energy efficient control of environmental conditions, and interactive media that collect and display information. We propose to develop a new class of socially aware managers that coordinate smart objects and manage logistics in functional areas such as the kitchen, living rooms, closets, bedrooms, bathroom or office.

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POLARIS Team

3. Research Program

3.1. Sound and Reproducible Experimental Methodology

Participants: Vincent Danjean, Nicolas Gast, Guillaume Huard, Arnaud Legrand, Jean-Marc Vincent.

Experiments in large scale distributed systems are costly, difficult to control and therefore difficult to reproduce. Although many of these digital systems have been built by men, they have reached such a complexity level that we are no longer able to study them like artificial systems and have to deal with the same kind of experimental issues as natural sciences. The development of a sound experimental methodology for the evaluation of resource management solutions is among the most important ways to cope with the growing complexity of computing environments. Although computing environments come with their own specific challenges, we believe such general observation problems should be addressed by borrowing good practices and techniques developed in many other domains of science.

This research theme builds on a transverse activity on *Open science and reproducible research* and is organized into the following two directions: (1) *Experimental design* (2) *Smart monitoring and tracing*. As we will explain in more detail hereafter, these transverse activity and research directions span several research areas and our goal within the POLARIS project is foremost to transfer original ideas from other domains of science to the distributed and high performance computing community.

3.2. Multi-Scale Analysis and Visualization

Participants: Vincent Danjean, Guillaume Huard, Arnaud Legrand, Jean-Marc Vincent, Panayotis Mertikopoulos.

As explained in the previous section, the first difficulty encountered when modeling large scale computer systems is to observe these systems and extract information on the behavior of both the architecture, the middleware, the applications, and the users. The second difficulty is to *visualize* and *analyze* such *multi-level traces to understand how the performance* of the application *can be improved*. While a lot of efforts are put into visualizing scientific data, in comparison little effort have gone into to developing techniques specifically tailored for understanding the behavior of distributed systems. Many visualization tools have been developed by renowned HPC groups since decades (e.g., BSC [87], Jülich and TU Dresden [86], [55], UIUC [74], [90], [77] and ANL [104], Inria Bordeaux [61] and Grenoble [106], ...) but most of these tools build on the classical information visualization mantra [95] that consists in always first presenting an overview of the data, possibly by plotting everything if computing power allows, and then to allow users to zoom and filter, providing details on demand. However in our context, the amount of data comprised in such traces is several orders of magnitude larger than the number of pixels on a screen and displaying even a small fraction of the trace leads to harmful visualization artifacts [82]. Such traces are typically made of events that occur at very different time and space scales, which unfortunately hinders classical approaches. Such visualization tools have focused on easing interaction and navigation in the trace (through gantcharts, intuitive filters, pie charts and kiviats) but they are very difficult to maintain and evolve and they require some significant experience to identify performance bottlenecks.

Therefore many groups have more recently proposed in combination to these tools some techniques to help identifying the structure of the application or regions (applicative, spatial or temporal) of interest. For example, researchers from the SDSC [85] propose some segment matching techniques based on clustering (Euclidean or Manhattan distance) of start and end dates of the segments that enables to reduce the amount of information to display. Researchers from the BSC use clustering, linear regression and Kriging techniques [94], [81], [73] to identify and characterize (in term of performance and resource usage) application phases and present aggregated representations of the trace [93]. Researchers from Jülich and TU Darmstadt have proposed techniques to identify specific communication patterns that incur wait states [101], [48]

3.3. Fast and Faithful Performance Prediction of Very Large Systems

Participants: Vincent Danjean, Bruno Gaujal, Arnaud Legrand, Florence Perronnin, Jean-Marc Vincent.

Evaluating the scalability, robustness, energy consumption and performance of large infrastructures such as exascale platforms and clouds raises severe methodological challenges. The complexity of such platforms mandates empirical evaluation but direct experimentation via an application deployment on a real-world testbed is often limited by the few platforms available at hand and is even sometimes impossible (cost, access, early stages of the infrastructure design, ...). Unlike direct experimentation via an application deployment on a real-world testbed, simulation enables fully repeatable and configurable experiments that can often be conducted quickly for arbitrary hypothetical scenarios. In spite of these promises, current simulation practice is often not conducive to obtaining scientifically sound results. To date, most simulation results in the parallel and distributed computing literature are obtained with simulators that are ad hoc, unavailable, undocumented, and/or no longer maintained. For instance, Naicken et al. [47] point out that out of 125 recent papers they surveyed that study peer-to-peer systems, 52% use simulation and mention a simulator, but 72% of them use a custom simulator. As a result, most published simulation results build on throw-away (short-lived and non validated) simulators that are specifically designed for a particular study, which prevents other researchers from building upon it. There is thus a strong need for recognized simulation frameworks by which simulation results can be reproduced, further analyzed and improved.

The *SimGrid* simulation toolkit [59], whose development is partially supported by POLARIS, is specifically designed for studying large scale distributed computing systems. It has already been successfully used for simulation of grid, volunteer computing, HPC, cloud infrastructures and we have constantly invested on the software quality, the scalability [51] and the validity of the underlying network models [49], [99]. Many simulators of MPI applications have been developed by renowned HPC groups (e.g., at SDSC [97], BSC [45], UIUC [105], Sandia Nat. Lab. [100], ORNL [58] or ETH Zürich [75] for the most prominent ones). Yet, to scale most of them build on restrictive network and application modeling assumptions that make them difficult to extend to more complex architectures and to applications that do not solely build on the MPI API. Furthermore, simplistic modeling assumptions generally prevent to faithfully predict execution times, which limits the use of simulation to indication of gross trends at best. Our goal is to improve the quality of SimGrid to the point where it can be used effectively on a daily basis by practitioners to *reproduce the dynamic of real HPC systems*.

We also develop another simulation software, *PSI* (Perfect SImulator) [63], [56], dedicated to the simulation of very large systems that can be modeled as Markov chains. PSI provides a set of simulation kernels for Markov chains specified by events. It allows one to sample stationary distributions through the Perfect Sampling method (pioneered by Propp and Wilson [88]) or simply to generate trajectories with a forward Monte-Carlo simulation leveraging time parallel simulation (pioneered by Fujimoto [67], Lin and Lazowska [80]). One of the strength of the PSI framework is its expressiveness that allows us to easily study networks with finite and infinite capacity queues [57]. Although PSI already allows to simulate very large and complex systems, our main objective is to push its scalability even further and *improve its capabilities by one or several orders of magnitude*.

3.4. Local Interactions and Transient Analysis in Adaptive Dynamic Systems

Participants: Nicolas Gast, Bruno Gaujal, Florence Perronnin, Jean-Marc Vincent, Panayotis Mertikopoulos.

Many systems can be effectively described by stochastic population models. These systems are composed of a set of n entities interacting together and the resulting stochastic process can be seen as a continuous-time Markov chain with a finite state space. Many numerical techniques exist to study the behavior of Markov chains, to solve stochastic optimal control problems [89] or to perform model-checking [46]. These techniques, however, are limited in their applicability, as they suffer from the *curse of dimensionality*: the state-space grows exponentially with n.

This results in the need for approximation techniques. Mean field analysis offers a viable, and often very accurate, solution for large n. The basic idea of the mean field approximation is to count the number of entities that are in a given state. Hence, the fluctuations due to stochasticity become negligible as the number of entities grows. For large n, the system becomes essentially deterministic. This approximation has been originally developed in statistical mechanics for vary large systems composed of more than 10^{20} particles (called entities here). More recently, it has been claimed that, under some conditions, this approximation can be successfully used for stochastic systems composed of a few tens of entities. The claim is supported by various convergence results [68], [78], [103], and has been successfully applied in various domains: wireless networks [50], computer-based systems [71], [84], [98], epidemic or rumour propagation [60], [76] and bike-sharing systems [64]. It is also used to develop distributed control strategies [102], [83] or to construct approximate solutions of stochastic model checking problems [52], [53], [54].

Within the POLARIS project, we will continue developing both the theory behind these approximation techniques and their applications. Typically, these techniques require a homogeneous population of objects where the dynamics of the entities depend only on their state (the state space of each object must not scale with n the number of objects) but neither on their identity nor on their spatial location. Continuing our work in [68], we would like to be able to handle heterogeneous or uncertain dynamics. Typical applications are caching mechanisms [71] or bike-sharing systems [65]. A second point of interest is the use of mean field or large deviation asymptotics to compute the time between two regimes [92] or to reach an equilibrium state. Last, mean-field methods are mostly descriptive and are used to analyse the performance of a given system. We wish to extend their use to solve optimal control problems. In particular, we would like to implement numerical algorithms that use the framework that we developed in [69] to build distributed control algorithms [62] and optimal pricing mechanisms [70].

3.5. Distributed Learning in Games and Online Optimization

Participants: Nicolas Gast, Bruno Gaujal, Arnaud Legrand, Panayotis Mertikopoulos.

Game theory is a thriving interdisciplinary field that studies the interactions between competing optimizing agents, be they humans, firms, bacteria, or computers. As such, game-theoretic models have met with remarkable success when applied to complex systems consisting of interdependent components with vastly different (and often conflicting) objectives – ranging from latency minimization in packet-switched networks to throughput maximization and power control in mobile wireless networks.

In the context of large-scale, decentralized systems (the core focus of the POLARIS project), it is more relevant to take an inductive, "bottom-up" approach to game theory, because the components of a large system cannot be assumed to perform the numerical calculations required to solve a very-large-scale optimization problem. In view of this, POLARIS' overarching objective in this area is to *develop novel algorithmic frameworks that offer robust performance guarantees when employed by all interacting decision-makers.*

A key challenge here is that most of the literature on learning in games has focused on *static* games with a *finite number of actions* per player [66], [91]. While relatively tractable, such games are ill-suited to practical applications where players pick an action from a continuous space or when their payoff functions evolve over time – this being typically the case in our target applications (e.g., routing in packet-switched networks or energy-efficient throughput maximization in wireless). On the other hand, the framework of online convex optimization typically provides worst-case performance bounds on the learner's *regret* that the agents can attain irrespectively of how their environment varies over time. However, if the agents' environment is determined chiefly by their interactions these bounds are fairly loose, so more sophisticated convergence criteria should be applied.

From an algorithmic standpoint, a further challenge occurs when players can only observe their own payoffs (or a perturbed version thereof). In this bandit-like setting regret-matching or trial-and-error procedures guarantee convergence to an equilibrium in a weak sense in certain classes of games. However, these results apply exclusively to static, finite games: learning in games with continuous action spaces and/or nonlinear payoff functions cannot be studied within this framework. Furthermore, even in the case of finite games,

the complexity of the algorithms described above is not known, so it is impossible to decide a priori which algorithmic scheme can be applied to which application.

PRIVATICS Project-Team (section vide)

ROMA Project-Team

3. Research Program

3.1. Algorithms for probabilistic environments

There are two main research directions under this research theme. In the first one, we consider the problem of the efficient execution of applications in a failure-prone environment. Here, probability distributions are used to describe the potential behavior of computing platforms, namely when hardware components are subject to faults. In the second research direction, probability distributions are used to describe the characteristics and behavior of applications.

3.1.1. Application resilience

An application is resilient if it can successfully produce a correct result in spite of potential faults in the underlying system. Application resilience can involve a broad range of techniques, including fault prediction, error detection, error containment, error correction, checkpointing, replication, migration, recovery, etc. Faults are quite frequent in the most powerful existing supercomputers. The Jaguar platform, which ranked third in the TOP 500 list in November 2011 [59], had an average of 2.33 faults per day during the period from August 2008 to February 2010 [83]. The mean-time between faults of a platform is inversely proportional to its number of components. Progresses will certainly be made in the coming years with respect to the reliability of individual components. However, designing and building high-reliability hardware components is far more expensive than using lower reliability top-of-the-shelf components. Furthermore, low-power components may not be available with high-reliability. Therefore, it is feared that the progresses in reliability will far from compensate the steady projected increase of the number of components in the largest supercomputers. Already, application failures have a huge computational cost. In 2008, the DARPA white paper on "System resilience at extreme scale" [58] stated that high-end systems wasted 20% of their computing capacity on application failure and recovery.

In such a context, any application using a significant fraction of a supercomputer and running for a significant amount of time will have to use some fault-tolerance solution. It would indeed be unacceptable for an application failure to destroy centuries of CPU-time (some of the simulations run on the Blue Waters platform consumed more than 2,700 years of core computing time [54] and lasted over 60 hours; the most time-consuming simulations of the US Department of Energy (DoE) run for weeks to months on the most powerful existing platforms [57]).

Our research on resilience follows two different directions. On the one hand we design new resilience solutions, either generic fault-tolerance solutions or algorithm-based solutions. On the other hand we model and theoretically analyze the performance of existing and future solutions, in order to tune their usage and help determine which solution to use in which context.

3.1.2. Scheduling strategies for applications with a probabilistic behavior

Static scheduling algorithms are algorithms where all decisions are taken before the start of the application execution. On the contrary, in non-static algorithms, decisions may depend on events that happen during the execution. Static scheduling algorithms are known to be superior to dynamic and system-oriented approaches in stable frameworks [65], [71], [72], [82], that is, when all characteristics of platforms and applications are perfectly known, known a priori, and do not evolve during the application execution. In practice, the prediction of application characteristics may be approximative or completely infeasible. For instance, the amount of computations and of communications required to solve a given problem in parallel may strongly depend on some input data that are hard to analyze (this is for instance the case when solving linear systems using full pivoting).

We plan to consider applications whose characteristics change dynamically and are subject to uncertainties. In order to benefit nonetheless from the power of static approaches, we plan to model application uncertainties and variations through probabilistic models, and to design for these applications scheduling strategies that are either static, or partially static and partially dynamic.

3.2. Platform-aware scheduling strategies

In this theme, we study and design scheduling strategies, focusing either on energy consumption or on memory behavior. In other words, when designing and evaluating these strategies, we do not limit our view to the most classical platform characteristics, that is, the computing speed of cores and accelerators, and the bandwidth of communication links.

In most existing studies, a single optimization objective is considered, and the target is some sort of absolute performance. For instance, most optimization problems aim at the minimization of the overall execution time of the application considered. Such an approach can lead to a very significant waste of resources, because it does not take into account any notion of efficiency nor of yield. For instance, it may not be meaningful to use twice as many resources just to decrease by 10% the execution time. In all our work, we plan to look only for algorithmic solutions that make a "clever" usage of resources. However, looking for the solution that optimizes a metric such as the efficiency, the energy consumption, or the memory-peak minimization, is doomed for the type of applications we consider. Indeed, in most cases, any optimal solution for such a metric is a sequential solution, and sequential solutions have prohibitive execution times. Therefore, it becomes mandatory to consider multi-criteria approaches where one looks for trade-offs between some user-oriented metrics that are typically related to notions of Quality of Service—execution time, response time, stretch, throughput, latency, reliability, etc.—and some system-oriented metrics that guarantee that resources are not wasted. In general, we will not look for the Pareto curve, that is, the set of all dominating solutions for the considered metrics. Instead, we will rather look for solutions that minimize some given objective while satisfying some bounds, or "budgets", on all the other objectives.

3.2.1. Energy-aware algorithms

Energy-aware scheduling has proven an important issue in the past decade, both for economical and environmental reasons. Energy issues are obvious for battery-powered systems. They are now also important for traditional computer systems. Indeed, the design specifications of any new computing platform now always include an upper bound on energy consumption. Furthermore, the energy bill of a supercomputer may represent a significant share of its cost over its lifespan.

Technically, a processor running at speed s dissipates s^α watts per unit of time with $2 \leq \alpha \leq 3$ [63], [64], [69]; hence, it consumes $s^\alpha \times d$ joules when operated during d units of time. Therefore, energy consumption can be reduced by using speed scaling techniques. However it was shown in [84] that reducing the speed of a processor increases the rate of transient faults in the system. The probability of faults increases exponentially, and this probability cannot be neglected in large-scale computing [80]. In order to make up for the loss in *reliability* due to the energy efficiency, different models have been proposed for fault tolerance: (i) *re-execution* consists in re-executing a task that does not meet the reliability constraint [84]; (ii) *replication* consists in executing the same task on several processors simultaneously, in order to meet the reliability constraints [62]; and (iii) *checkpointing* consists in "saving" the work done at some certain instants, hence reducing the amount of work lost when a failure occurs [79].

Energy issues must be taken into account at all levels, including the algorithm-design level. We plan to both evaluate the energy consumption of existing algorithms and to design new algorithms that minimize energy consumption using tools such as resource selection, dynamic frequency and voltage scaling, or powering-down of hardware components.

3.2.2. Memory-aware algorithms

For many years, the bandwidth between memories and processors has increased more slowly than the computing power of processors, and the latency of memory accesses has been improved at an even slower

pace. Therefore, in the time needed for a processor to perform a floating point operation, the amount of data transferred between the memory and the processor has been decreasing with each passing year. The risk is for an application to reach a point where the time needed to solve a problem is no longer dictated by the processor computing power but by the memory characteristics, comparable to the *memory wall* that limits CPU performance. In such a case, processors would be greatly under-utilized, and a large part of the computing power of the platform would be wasted. Moreover, with the advent of multicore processors, the amount of memory per core has started to stagnate, if not to decrease. This is especially harmful to memory intensive applications. The problems related to the sizes and the bandwidths of memories are further exacerbated on modern computing platforms because of their deep and highly heterogeneous hierarchies. Such a hierarchy can extend from core private caches to shared memory within a CPU, to disk storage and even tape-based storage systems, like in the Blue Waters supercomputer [55]. It may also be the case that heterogeneous cores are used (such as hybrid CPU and GPU computing), and that each of them has a limited memory.

Because of these trends, it is becoming more and more important to precisely take memory constraints into account when designing algorithms. One must not only take care of the amount of memory required to run an algorithm, but also of the way this memory is accessed. Indeed, in some cases, rather than to minimize the amount of memory required to solve the given problem, one will have to maximize data reuse and, especially, to minimize the amount of data transferred between the different levels of the memory hierarchy (minimization of the volume of memory inputs-outputs). This is, for instance, the case when a problem cannot be solved by just using the in-core memory and that any solution must be out-of-core, that is, must use disks as storage for temporary data.

It is worth noting that the cost of moving data has lead to the development of so called "communication-avoiding algorithms" [76]. Our approach is orthogonal to these efforts: in communication-avoiding algorithms, the application is modified, in particular some redundant work is done, in order to get rid of some communication operations, whereas in our approach, we do not modify the application, which is provided as a task graph, but we minimize the needed memory peak only by carefully scheduling tasks.

3.3. High-performance computing and linear algebra

Our work on high-performance computing and linear algebra is organized along three research directions. The first direction is devoted to direct solvers of sparse linear systems. The second direction is devoted to combinatorial scientific computing, that is, the design of combinatorial algorithms and tools that solve problems encountered in some of the other research themes, like the problems faced in the preprocessing phases of sparse direct solvers. The last direction deals with the adaptation of classical dense linear algebra kernels to the architecture of future computing platforms.

3.3.1. Direct solvers for sparse linear systems

The solution of sparse systems of linear equations (symmetric or unsymmetric, often with an irregular structure, from a few hundred thousand to a few hundred million equations) is at the heart of many scientific applications arising in domains such as geophysics, structural mechanics, chemistry, electromagnetism, numerical optimization, or computational fluid dynamics, to cite a few. The importance and diversity of applications are a main motivation to pursue research on sparse linear solvers. Because of this wide range of applications, any significant progress on solvers will have a significant impact in the world of simulation. Research on sparse direct solvers in general is very active for the following main reasons:

- many applications fields require large-scale simulations that are still too big or too complicated with respect to today's solution methods;
- the current evolution of architectures with massive, hierarchical, multicore parallelism imposes to overhaul all existing solutions, which represents a major challenge for algorithm and software development;
- the evolution of numerical needs and types of simulations increase the importance, frequency, and size of certain classes of matrices, which may benefit from a specialized processing (rather than resort to a generic one).

Our research in the field is strongly related to the software package MUMPS (see Section 6.1). MUMPS is both an experimental platform for academics in the field of sparse linear algebra, and a software package that is widely used in both academia and industry. The software package MUMPS enables us to (i) confront our research to the real world, (ii) develop contacts and collaborations, and (iii) receive continuous feedback from real-life applications, which is extremely critical to validate our research work. The feedback from a large user community also enables us to direct our long-term objectives towards meaningful directions.

In this context, we aim at designing parallel sparse direct methods that will scale to large modern platforms, and that are able to answer new challenges arising from applications, both efficiently—from a resource consumption point of view—and accurately—from a numerical point of view. For that, and even with increasing parallelism, we do not want to sacrifice in any manner numerical stability, based on threshold partial pivoting, one of the main originalities of our approach (our "trademark") in the context of direct solvers for distributed-memory computers; although this makes the parallelization more complicated, applying the same pivoting strategy as in the serial case ensures numerical robustness of our approach, which we generally measure in terms of sparse backward error. In order to solve the hard problems resulting from the always-increasing demands in simulations, special attention must also necessarily be paid to memory usage (and not only execution time). This requires specific algorithmic choices and scheduling techniques. From a complementary point of view, it is also necessary to be aware of the functionality requirements from the applications and from the users, so that robust solutions can be proposed for a wide range of applications.

Among direct methods, we rely on the multifrontal method [73], [74], [78]. This method usually exhibits a good data locality and hence is efficient in cache-based systems. The task graph associated with the multifrontal method is in the form of a tree whose characteristics should be exploited in a parallel implementation.

Our work is organized along two main research directions. In the first one we aim at efficiently addressing new architectures that include massive, hierarchical parallelism. In the second one, we aim at reducing the running time complexity and the memory requirements of direct solvers, while controlling accuracy.

3.3.2. Combinatorial scientific computing

Combinatorial scientific computing (CSC) is a recently coined term (circa 2002) for interdisciplinary research at the intersection of discrete mathematics, computer science, and scientific computing. In particular, it refers to the development, application, and analysis of combinatorial algorithms to enable scientific computing applications. CSC's deepest roots are in the realm of direct methods for solving sparse linear systems of equations where graph theoretical models have been central to the exploitation of sparsity, since the 1960s. The general approach is to identify performance issues in a scientific computing problem, such as memory use, parallel speed up, and/or the rate of convergence of a method, and to develop combinatorial algorithms and models to tackle those issues.

Our target scientific computing applications are (i) the preprocessing phases of direct methods (in particular MUMPS), iterative methods, and hybrid methods for solving linear systems of equations, and tensor decomposition algorithms; and (ii) the mapping of tasks (mostly the sub-tasks of the mentioned solvers) onto modern computing platforms. We focus on the development and use of graph and hypergraph models, and related tools such as hypergraph partitioning algorithms, to solve problems of load balancing and task mapping. We also focus on bipartite graph matching and vertex ordering methods for reducing the memory overhead and computational requirements of solvers. Although we direct our attention on these models and algorithms through the lens of linear system solvers, our solutions are general enough to be applied to some other resource optimization problems.

3.3.3. Dense linear algebra on post-petascale multicore platforms

The quest for efficient, yet portable, implementations of dense linear algebra kernels (QR, LU, Cholesky) has never stopped, fueled in part by each new technological evolution. First, the LAPACK library [67] relied on BLAS level 3 kernels (Basic Linear Algebra Subroutines) that enable to fully harness the computing power of a single CPU. Then the SCALAPACK library [66] built upon LAPACK to provide a coarse-grain parallel version, where processors operate on large block-column panels. Inter-processor communications

occur through highly tuned MPI send and receive primitives. The advent of multi-core processors has led to a major modification in these algorithms [68], [81], [77]. Each processor runs several threads in parallel to keep all cores within that processor busy. Tiled versions of the algorithms have thus been designed: dividing large block-column panels into several tiles allows for a decrease in the granularity down to a level where many smaller-size tasks are spawned. In the current panel, the diagonal tile is used to eliminate all the lower tiles in the panel. Because the factorization of the whole panel is now broken into the elimination of several tiles, the update operations can also be partitioned at the tile level, which generates many tasks to feed all cores.

The number of cores per processor will keep increasing in the following years. It is projected that high-end processors will include at least a few hundreds of cores. This evolution will require to design new versions of libraries. Indeed, existing libraries rely on a static distribution of the work: before the beginning of the execution of a kernel, the location and time of the execution of all of its component is decided. In theory, static solutions enable to precisely optimize executions, by taking parameters like data locality into account. At run time, these solutions proceed at the pace of the slowest of the cores, and they thus require a perfect load-balancing. With a few hundreds, if not a thousand, cores per processor, some tiny differences between the computing times on the different cores ("jitter") are unavoidable and irremediably condemn purely static solutions. Moreover, the increase in the number of cores per processor once again mandates to increase the number of tasks that can be executed in parallel.

We study solutions that are part-static part-dynamic, because such solutions have been shown to outperform purely dynamic ones [70]. On the one hand, the distribution of work among the different nodes will still be statically defined. On the other hand, the mapping and the scheduling of tasks inside a processor will be dynamically defined. The main difficulty when building such a solution will be to design lightweight dynamic schedulers that are able to guarantee both an excellent load-balancing and a very efficient use of data locality.

3.4. Compilers, code optimization and high-level synthesis for FPGA

Christophe Alias and Laure Gonnord asked to join the ROMA team temporarily, starting from September 2015. This was accepted by the team and by Inria. The text below describes their research domain. The results that they have achieved in 2016 are included in this report.

The advent of parallelism in supercomputers, in embedded systems (smartphones, plane controllers), and in more classical end-user computers increases the need for high-level code optimization and improved compilers. Being able to deal with the complexity of the upcoming software and hardware while keeping energy consumption at a reasonnable level is one of the main challenges cited in the Hipeac Roadmap which among others cites the two major issues :

- Enhance the efficiency of the design of embedded systems, and especially the design of optimized specialized hardware.
- Invent techniques to "expose data movement in applications and optimize them at runtime and compile time and to investigate communication-optimized algorithms".

In particular, the rise of embedded systems and high performance computers in the last decade has generated new problems in code optimization, with strong consequences on the research area. The main challenge is to take advantage of the characteristics of the specific hardware (generic hardware, or hardware accelerators). The long-term objective is to provide solutions for the end-user developers to use at their best the huge opportunities of these emerging platforms.

3.4.1. Compiler algorithms for irregular applications

In the last decades, several frameworks has emerged to design efficient compiler algorithms. The efficiency of all the optimizations performed in compilers strongly relies on performant *static analyses* and *intermediate representations*. Among these representations, the polyhedral model [75] focus on regular programs, whose execution trace is predictable statically. The program and the data accessed are represented with a single mathematical object endowed with powerful algorithmic techniques for reasoning about it. Unfortunately, most of the algorithms used in scientific computing do not fit totally in this category.

We plan to explore the extensions of these techniques to handle irregular programs with while loops and complex data structures (such as trees, and lists). This raises many issues. We cannot represent finitely all the possible executions traces. Which approximation/representation to choose? Then, how to adapt existing techniques on approximated traces while preserving the correctness? To address these issues, we plan to incorporate new ideas coming from the abstract interpretation community: control flow, approximations, and also shape analysis; and from the termination community: rewriting is one of the major techniques that are able to handle complex data structures and also recursive programs.

3.4.2. High-level synthesis for FPGA

Energy consumption bounds the performance of supercomputers since the end of Dennard scaling. Hence, reducing the electrical energy spent in a computation is the major challenge raised by Exaflop computing. Novel hardware, software, compilers and operating systems must be designed to increase the energy efficiency (in flops/watt) of data manipulation and computation itself. In the last decade, many specialized hardware accelerators (Xeon Phi, GPGPU) has emerged to overcome the limitations of mainstream processors, by trading the genericity for energy efficiency. However, the best supercomputers can only reach 8 Gflops/watt [61], which is far less than the 50 Gflops/watt required by an Exaflop supercomputer. An extreme solution would be to trade all the genericity by using specialized circuits. However such circuits (application specific integrated circuits, ASIC) are usually too expensive for the HPC market and lacks of flexibility. Once printed, an ASIC cannot be modified. Any algorithm update (or bug fix) would be impossible, which clearly not realistic.

Recently, reconfigurable circuits (Field Programmable Gate Arrays, FPGA) has appeared as a credible alternative for Exaflop computing. Major companies (including Intel, Google, Facebook and Microsoft) show a growing interest to FPGA and promising results has been obtained. For instance, in 2015, Microsoft reaches 40 Gflop/watts on a data-center deep learning algorithm mapped on Intel/Altera Arria 10 FPGAs. We believe that FPGA will become the new building block for HPC and Big Data systems. Unfortunately, programming an FPGA is still a big challenge: the application must be defined at circuit level and use properly the logic cells. Hence, there is a strong need for a compiler technology able to *map complex applications specified in a high-level language*. This compiler technology is usually refered as high-level synthesis (HLS).

We plan to investigate how to extend the models and the algorithms developed by the HPC community to map automatically a complex application to an FPGA. This raises many issues. How to schedule/allocate the computations and the data on the FPGA in order to reduce the data transfers while keeping a high throughput? How to use optimally the resources of the FPGA while keeping a low critical path? To address these issues, we plan to develop novel execution models based on process networks and to extend/cross-fertilize the algorithms developed in both HPC and high-level synthesis communities. The purpose of the XtremLogic start-up company, co-founded by Christophe Alias and Alexandru Plesco is to transfer the results of this research to an industrial level compiler.

SOCRATE Project-Team

3. Research Program

3.1. Research Axes

In order to keep young researchers in an environment close to their background, we have structured the team along the three research axes related to the three main scientific domains spanned by Socrate. However, we insist that a *major objective* of the Socrate team is to *motivate the collaborative research between these axes*, this point is specifically detailed in Section 3.5 . The first one is entitled "Flexible Radio Front-End" and will study new radio front-end research challenges brought up by the arrival of MIMO technologies, and reconfigurable front-ends. The second one, entitled "Multi-user communication", will study how to couple the self-adaptive and distributed signal processing algorithms to cope with the multi-scale dynamics found in cognitive radio systems. The last research axis, entitled "Software Radio Programming Models" is dedicated to embedded software issues related to programming the physical protocols layer on these software radio machines. Figure 3 illustrates the three regions of a transceiver corresponding to the three Socrate axes.

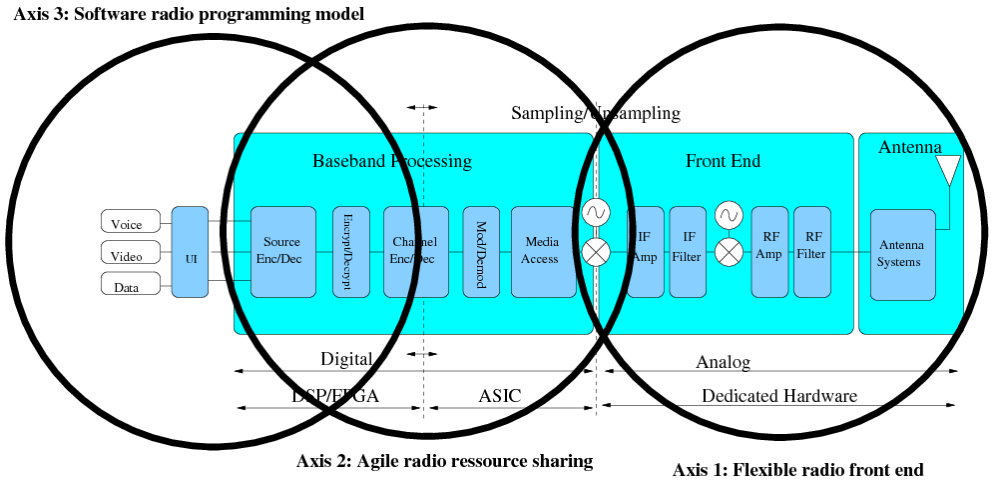

Figure 3. Center of interest for each of the three Socrate research axes with respect to a generic software radio terminal.

3.2. Flexible Radio Front-End

Participants: Guillaume Villemaud, Florin Hutu.

This axis mainly deals with the radio front-end of software radio terminals (right of Fig 3). In order to ensure a high flexibility in a global wireless network, each node is expected to offer as many degrees of freedom as possible. For instance, the choice of the most appropriate communication resource (frequency channel, spreading code, time slot,...), the interface standard or the type of antenna are possible degrees of freedom. The *multi-** paradigm denotes a highly flexible terminal composed of several antennas providing MIMO features to enhance the radio link quality, which is able to deal with several radio standards to offer interoperability and efficient relaying, and can provide multi-channel capability to optimize spectral reuse. On the other hand, increasing degrees of freedom can also increase the global energy consumption, therefore for energy-limited terminals a different approach has to be defined.

In this research axis, we expect to demonstrate optimization of flexible radio front-end by fine grain simulations, and also by the design of home made prototypes. Of course, studying all the components deeply would not be possible given the size of the team, we are currently not working in new technologies for DAC/ADC and power amplifiers which are currently studied by hardware oriented teams. The purpose of this axis is to build system level simulation taking into account the state of the art of each key component.

3.3. Multi-User Communications

Participants: Jean-Marie Gorce, Claire Goursaud, Nikolai Lebedev, Samir Perlaza, Leonardo Sampaio-Cardoso.

While the first and the third research axes deal with the optimization of the cognitive radio nodes themselves from system and programming point of view, an important complementary objective is to consider the radio nodes in their environments. Indeed, cognitive radio does not target the simple optimization of point to point transmissions, but the optimization of simultaneous concurrent transmissions. The tremendous development of new wireless applications and standards currently observed calls for a better management of the radio spectrum with opportunistic radio access, cooperative transmissions and interference management. This challenge has been identified as one of the most important issue for 5G to guarantee a better exploitation of the spectrum. In addition, mobile internet is going to support a new revolution that is the *tactile internet*, with real time interactions between the virtual and the real worlds, requiring new communication objectives to be met such as low latency end to end communications, distributed learning techniques, in-the-network computation, and many more. The future network will be heterogeneous in terms of technologies, type of data flows and QoS requirements. To address this revolution two work directions have naturally formed within the axis. The first direction concerns the theoretical study of fundamental limits in wireless networks. Introduced by Claude Shannon in the 50s and heavily developed up to today, Information Theory has provided a theoretical foundation to study the performance of wireless communications, not from a practical design view point, but using the statistical properties of wireless channels to establish the fundamental trade-offs in wireless communications. Beyond the classical *energy efficiency - spectral efficiency* tradeoff, information theory and its many derivations, i.e., network information theory, may also help to address additional questions such as determining the optimal rates under decentralized policies, asymptotic behavior when the density of nodes increases, latency controled communication with finite block-length theory, etc... In these cases, information theory is often associated to other theoretical tools such as game theory, stochastic geometry, control theory, graph theory and many others.

Our first research direction consists in evaluating specific mulit-user scenarios from a network information theory perspective, inspired by practical scenarios from various applicative frameworks (e.g. 5G, Wifi, sensor networks, IoT, etc...), and to establish fundamental limits for these scenarios. The second research direction is related to algorithmic and protocol design (PHY/MAC), applied to practical scenarios. Exploiting signal processing, linear algebra inspired models and distributed algorithms, we develop and evaluate various distributed algorithms allowing to improve many QoS metrics such as communication rates, reliability, stability, energy efficiency or computational complexity.

It is clear that both research directions are symbiotic with respect to each other, with the former providing theoretical bounds that serves as a reference to the performance of the algorithms created in the later. In the other way around, the later offers target scenarios for the former, through identifying fundamental problems that are interesting to be studied from the fundamental side. Our contributions of the year in these two directions are summarized further in the document.

3.4. Software Radio Programming Model

Participants: Tanguy Risset, Kevin Marquet, Lionel Morel, Guillaume Salagnac, Florent de Dinechin.

Finally the third research axis is concerned with software aspect of the software radio terminal (left of Fig 3). We have currently two actions in this axis, the first one concerns the programming issues in software defined radio devices, the second one focusses on low power devices: how can they be adapted to integrate some reconfigurability.

The expected contributions of Socrate in this research axis are :

- The design and implementation of a "middleware for SDR", probably based on a Virtual Machine.
- Prototype implementations of novel software radio systems, using chips from Leti and/or Lyrtech software radio boards.
- Development of a *smart node*: a low-power Software-Defined Radio node adapted to WSN applications.
- Methodology clues and programming tools to program all these prototypes.

3.5. Inter-Axes Collaboration

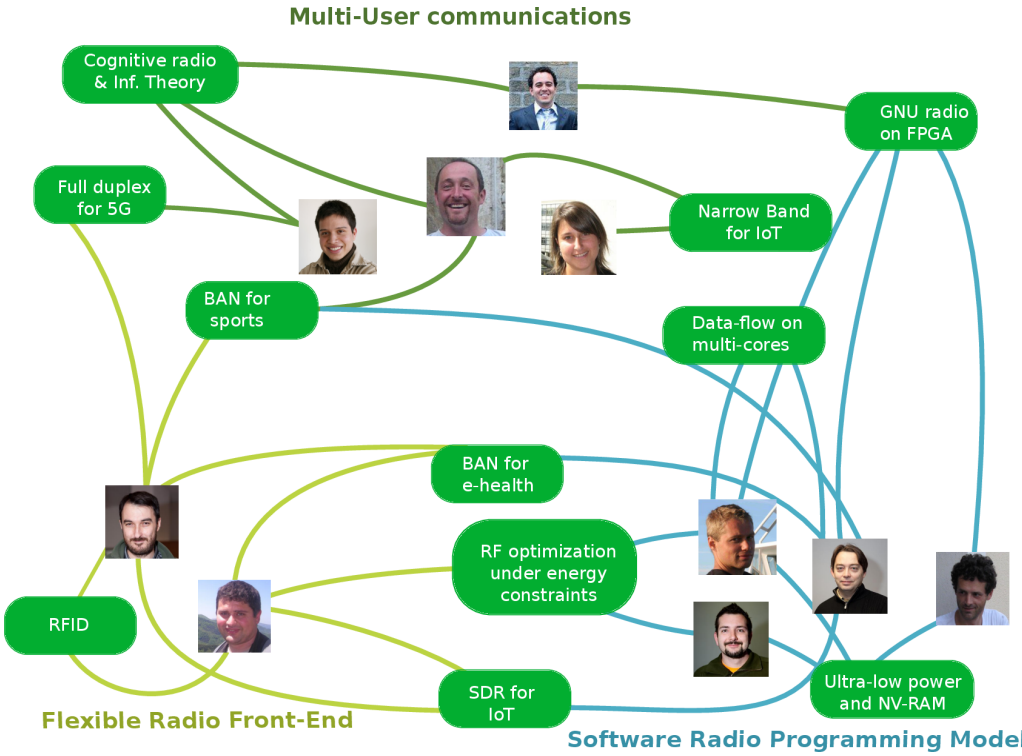

Figure 4. Inter-Axis Collaboration in Socrate: we expect innovative results to come from this pluri-disciplinary research

Innovative results come from collaborations between the three axes. To highlight the fact that this team structure does not limit the ability of inter-axes collaborations between Socrate members, we list below the *on-going* research actions that *already* involve actors from two or more axes, this is also represented on Fig 4 .

- *Optimizing network capacity of very large scale networks*. 2 Phds started in October/November 2011 with Guillaume Villemaud (axis 1) and Claire Goursaud (axis 2), respectively.
- *SDR for sensor networks*. A PhD started in 2012 in collaboration with FT R&D, involving people from axis 3 (Guillaume Salagnac, Tanguy Risset) and axis 1 (Guillaume Villemaud).
- *CorteXlab*. The 3 axes also collaborate on the design and the development of CorteXlab.

- *body area networks applications*. Axis 2 and axis 3 collaborate on the development of body area networks applications in the framework of the FUI Smacs project. Jean-Marie Gorce and Tanguy Risset co-advised Matthieu Lauzier.
- *Wiplan and NS3*. The MobiSim ADT involves Guillaume Villemaud (axis 1) and Jean-Marie Gorce (axis 2).
- *Resource allocation and architecture of low power multi-band front-end*. The EconHome project involves people from axis 2 (Jean-Marie Gorce,Nikolai Lebedev) and axis 1 (Florin Hutu). 1 Phd started in 2011.
- *Virtual machine for SDR*. In collaboration with CEA, a PhD started in October 2011, involving people from axis 3 (Tanguy Risset, Kevin Marquet) and Leti's engineers closer to axis 2.
- *Relay strategy for cognitive radio*. Guillaume Villemaud and Tanguy Risset were together advisers of Cedric Levy-Bencheton PhD Thesis (defense last June).

Finally, we insist on the fact that the *FIT project* will involve each member of Socrate and will provide many more opportunities to perform cross layer SDR experimentations. FIT is already federating all members of the Socrate team.

SPADES Project-Team

3. Research Program

3.1. Introduction

The SPADES research program is organized around three main themes, *Components and contracts*, *Real-time multicore programming*, and *Language-based fault tolerance*, that seek to answer the three key questions identified in Section 2.1 . We plan to do so by developing and/or building on programming languages and techniques based on formal methods and formal semantics (hence the use of *"sound programming"* in the project-team title). In particular, we seek to support design where correctness is obtained by construction, relying on proven tools and verified constructs, with programming languages and programming abstractions designed with verification in mind.

3.2. Components and Contracts

Component-based construction has long been advocated as a key approach to the "correct-by-construction" design of complex embedded systems [65]. Witness component-based toolsets such as UC Berkeley's PTOLEMY [53], Verimag's BIP [36], or the modular architecture frameworks used, for instance, in the automotive industry (AUTOSAR) [28]. For building large, complex systems, a key feature of component-based construction is the ability to associate with components a set of *contracts*, which can be understood as rich behavioral types that can be composed and verified to guarantee a component assemblage will meet desired properties. The goal in this theme is to study the formal foundations of the component-based construction of embedded systems, to develop component and contract theories dealing with real-time, reliability and fault-tolerance aspects of components, and to develop proof-assistant-based tools for the computer-aided design and verification of component-based systems.

Formal models for component-based design are an active area of research (see *e.g.*, [29], [30]). However, we are still missing a comprehensive formal model and its associated behavioral theory able to deal *at the same time* with different forms of composition, dynamic component structures, and quantitative constraints (such as timing, fault-tolerance, or energy consumption). Notions of contracts and interface theories have been proposed to support modular and compositional design of correct-by-construction embedded systems (see *e.g.*, [40], [41] and the references therein), but having a comprehensive theory of contracts that deals with all the above aspects is still an open question [71]. In particular, it is not clear how to accomodate different forms of composition, reliability and fault-tolerance aspects, or to deal with evolving component structures in a theory of contracts.

Dealing in the same component theory with heterogeneous forms of composition, different quantitative aspects, and dynamic configurations, requires to consider together the three elements that comprise a component model: behavior, structure and types. *Behavior* refers to behavioral (interaction and execution) models that characterize the behavior of components and component assemblages (*e.g.*, transition systems and their multiple variants – timed, stochastic, etc.). *Structure* refers to the organization of component assemblages or configurations, and the composition operators they involve. *Types* refer to properties or contracts that can be attached to components and component interfaces to facilitate separate development and ensure the correctness of component configurations with respect to certain properties. Taking into account dynamicity requires to establish an explicit link between behavior and structure, as well as to consider higher-order systems, both of which have a direct impact on types.

We plan to develop our component theory by progressing on two fronts: component calculi, and semantical framework. The work on typed component calculi aims to elicit process calculi that capture the main insights of component-based design and programming and that can serve as a bridge towards actual architecture description and programming language developments. The work on the semantical framework should, in the longer term, provide abstract mathematical models for the more operational and linguistic analysis afforded by component calculi. Our work on component theory will find its application in the development of a Coq-based toolchain for the certified design and construction of dependable embedded systems, which constitutes our third main objective for this axis.

3.3. Real-Time Multicore Programming

Programming real-time systems (*i.e.*, systems whose correct behavior depends on meeting timing constraints) requires appropriate languages (as exemplified by the family of synchronous languages [39]), but also the support of efficient scheduling policies, execution time and schedulability analyses to guarantee real-time constraints (*e.g.*, deadlines) while making the most effective use of available (processing, memory, or networking) resources. Schedulability analysis involves analyzing the worst-case behavior of real-time tasks under a given scheduling algorithm and is crucial to guarantee that time constraints are met in any possible execution of the system. Reactive programming and real-time scheduling and schedulability for multiprocessor systems are old subjects, but they are nowhere as mature as their uniprocessor counterparts, and still feature a number of open research questions [35], [48], in particular in relation with mixed criticality systems. The main goal in this theme is to address several of these open questions.

We intend to focus on two issues: multicriteria scheduling on multiprocessors, and schedulability analysis for real-time multiprocessor systems. Beyond real-time aspects, multiprocessor environments, and multicore ones in particular, are subject to several constraints *in conjunction*, typically involving real-time, reliability and energy-efficiency constraints, making the scheduling problem more complex for both the offline and the online cases. Schedulability analysis for multiprocessor systems, in particular for systems with mixed criticality tasks, is still very much an open research area.

Distributed reactive programming is rightly singled out as a major open issue in the recent, but heavily biased (it essentially ignores recent research in synchronous and dataflow programming), survey by Bainomugisha et al. [35]. For our part, we intend to focus on two questions: devising synchronous programming languages for distributed systems and precision-timed architectures, and devising dataflow languages for multiprocessors supporting dynamicity and parametricity while enjoying effective analyses for meeting real-time, resource and energy constraints in conjunction.

3.4. Language-Based Fault Tolerance

Tolerating faults is a clear and present necessity in networked embedded systems. At the hardware level, modern multicore architectures are manufactured using inherently unreliable technologies [43], [58]. The evolution of embedded systems towards increasingly distributed architectures highlighted in the introductory section means that dealing with partial failures, as in Web-based distributed systems, becomes an important issue. While fault-tolerance is an old and much researched topic, several important questions remain open: automation of fault-tolerance provision, composable abstractions for fault-tolerance, fault diagnosis, and fault isolation.

The first question is related to the old question of "system structure for fault-tolerance" as originally discussed by Randell for software fault tolerance [77], and concerns in part our ability to clearly separate fault-tolerance aspects from the design and programming of purely "functional" aspects of an application. The classical arguments in favor of a clear separation of fault-tolerance concerns from application code revolve around reduced code and maintenance complexity [49]. The second question concerns the definition of appropriate abstractions for the modular construction of fault-tolerant embedded systems. The current set of techniques available for building such systems spans a wide range, including exception handling facilities, transaction management schemes, rollback/recovery schemes, and replication protocols. Unfortunately, these different

techniques do not necessarily compose well – for instance, combining exception handling and transactions is non trivial, witness the flurry of recent work on the topic, see *e.g.*, [64] and the references therein –, they have no common semantical basis, and they suffer from limited programming language support. The third question concerns the identification of causes for faulty behavior in component-based assemblages. It is directly related to the much researched area of fault diagnosis, fault detection and isolation [66].

We intend to address these questions by leveraging programming language techniques (programming constructs, formal semantics, static analyses, program transformations) with the goal to achieve provable fault-tolerance, *i.e.*, the construction of systems whose fault-tolerance can be formally ensured using verification tools and proof assistants. We aim in this axis to address some of the issues raised by the above open questions by using aspect-oriented programming techniques and program transformations to automate the inclusion of fault-tolerance in systems (software as well as hardware), by exploiting reversible programming models to investigate composable recovery abstractions, and by leveraging causality analyses to study fault-ascription in component-based systems. Compared to the huge literature on fault-tolerance in general, in particular in the systems area (see *e.g.*, [59] for an interesting but not so recent survey), we find by comparison much less work exploiting formal language techniques and tools to achieve or support fault-tolerance. The works reported in [42], [44], [47], [54], [67], [76], [81] provide a representative sample of recent such works.

A common theme in this axis is the use and exploitation of causality information. Causality, *i.e.*, the logical dependence of an effect on a cause, has long been studied in disciplines such as philosophy [72], natural sciences, law [73], and statistics [74], but it has only recently emerged as an important focus of research in computer science. The analysis of logical causality has applications in many areas of computer science. For instance, tracking and analyzing logical causality between events in the execution of a concurrent system is required to ensure reversibility [70], to allow the diagnosis of faults in a complex concurrent system [61], or to enforce accountability [69], that is, designing systems in such a way that it can be determined without ambiguity whether a required safety or security property has been violated, and why. More generally, the goal of fault-tolerance can be understood as being to prevent certain causal chains from occurring by designing systems such that each causal chain either has its premises outside of the fault model (*e.g.*, by introducing redundancy [59]), or is broken (*e.g.*, by limiting fault propagation [78]).

STEEP Project-Team

3. Research Program

3.1. Development of numerical systemic models (economy / society /environment) at local scales

The problem we consider is intrinsically interdisciplinary: it draws on social sciences, ecology or science of the planet. The modeling of the considered phenomena must take into account many factors of different nature which interact with varied functional relationships. These heterogeneous dynamics are *a priori* nonlinear and complex: they may have saturation mechanisms, threshold effects, and may be density dependent. The difficulties are compounded by the strong interconnections of the system (presence of important feedback loops) and multi-scale spatial interactions. Environmental and social phenomena are indeed constrained by the geometry of the area in which they occur. Climate and urbanization are typical examples. These spatial processes involve proximity relationships and neighborhoods, like for example, between two adjacent parcels of land, or between several macroscopic levels of a social organization. The multi-scale issues are due to the simultaneous consideration in the modeling of actors of different types and that operate at specific scales (spatial and temporal). For example, to properly address biodiversity issues, the scale at which we must consider the evolution of rurality is probably very different from the one at which we model the biological phenomena.

In this context, to develop flexible integrated systemic models (upgradable, modular, ...) which are efficient, realistic and easy to use (for developers, modelers and end users) is a challenge in itself. What mathematical representations and what computational tools to use? Nowadays many tools are used: for example, cellular automata (e.g. in the LEAM model), agent models (e.g. URBANSIM), system dynamics (e.g. World3), large systems of ordinary equations (e.g. equilibrium models such as TRANUS), and so on. Each of these tools has strengths and weaknesses. Is it necessary to invent other representations? What is the relevant level of modularity? How to get very modular models while keeping them very coherent and easy to calibrate? Is it preferable to use the same modeling tools for the whole system, or can we freely change the representation for each considered subsystem? How to easily and effectively manage different scales? (difficulty appearing in particular during the calibration process). How to get models which automatically adapt to the granularity of the data and which are always numerically stable? (this has also a direct link with the calibration processes and the propagation of uncertainties). How to develop models that can be calibrated with reasonable efforts, consistent with the (human and material) resources of the agencies and consulting firms that use them?

Before describing our research axes, we provide a brief overview of the types of models that we are or will be working with. As for LUTI (Land Use and Transportation Integrated) modeling, we have been using the TRANUS model since the start of our group. It is the most widely used LUTI model, has been developed since 1982 by the company Modelistica, and is distributed *via* Open Source software. TRANUS proceeds by solving a system of deterministic nonlinear equations and inequalities containing a number of economic parameters (e.g. demand elasticity parameters, location dispersion parameters, etc.). The solution of such a system represents an economic equilibrium between supply and demand. A second LUTI model that will be considered in the near future, within the CITiES project, is UrbanSim [0]. Whereas TRANUS aggregates over e.g. entire population or housing categories, UrbanSim takes a micro-simulation approach, modeling and simulating choices made at the level of individual households, businesses, and jobs, for instance, and it operates on a finer geographic scale than TRANUS.

[0] http://www.urbansim.org

On the other hand, the scientific domains related to ecosystem services and ecological accounting are much less mature than the one of urban economy from a modelling point of view (as a consequence of our more limited knowledge of the relevant complex processes and/or more limited available data). Nowadays, the community working on ecological accounting develops statistical models based on the enforcement of the mass conservation constraint for accounting for material fluxes through a territorial unit or a supply chain, relying on more or less simple data correlations when the relevant data is missing; the overall modelling makes heavy use of more or less sophisticated linear algebra and constrained optimization techniques. The ecosystem service community has been using statical models too, but is also developing more sophisticated models based for example on system dynamics, multi-agent type simulations or cellular models. In the ESNET project, STEEP will work in particular on a land use/ land cover change (LUCC) modelling environments (Dinamica [0]) which belongs to the category of spatially explicit statistical models.

In the following, our two main research axes are described, from the point of view of applied mathematical development. The domains of application of this research effort is described in the application section, where some details about the context of each field is given.

3.2. Model calibration and validation

The overall calibration of the parameters that drive the equations implemented in the above models is a vital step. Theoretically, as the implemented equations describe e.g. socio-economic phenomena, some of these parameters should in principle be accurately estimated from past data using econometrics and statistical methods like regressions or maximum likelihood estimates, e.g. for the parameters of logit models describing the residential choices of households. However, this theoretical consideration is often not efficient in practice for at least two main reasons. First, the above models consist of several interacting modules. Currently, these modules are typically calibrated independently; this is clearly sub-optimal as results will differ from those obtained after a global calibration of the interaction system, which is the actual final objective of a calibration procedure. Second, the lack of data is an inherent problem.

As a consequence, models are usually calibrated by hand. The calibration can typically take up to 6 months for a medium size LUTI model (about 100 geographic zones, about 10 sectors including economic sectors, population and employment categories). This clearly emphasizes the need to further investigate and at least semi-automate the calibration process. Yet, in all domains STEEP considers, very few studies have addressed this central issue, not to mention calibration under uncertainty which has largely been ignored (with the exception of a few uncertainty propagation analyses reported in the literature).

Besides uncertainty analysis, another main aspect of calibration is numerical optimization. The general state-of-the-art on optimization procedures is extremely large and mature, covering many different types of optimization problems, in terms of size (number of parameters and data) and type of cost function(s) and constraints. Depending on the characteristics of the considered models in terms of dimension, data availability and quality, deterministic or stochastic methods will be implemented. For the former, due to the presence of non-differentiability, it is likely, depending on their severity, that derivative free control methods will have to be preferred. For the latter, particle-based filtering techniques and/or metamodel-based optimization techniques (also called response surfaces or surrogate models) are good candidates.

These methods will be validated, by performing a series of tests to verify that the optimization algorithms are efficient in the sense that 1) they converge after an acceptable computing time, 2) they are robust and 3) that the algorithms do what they are actually meant to. For the latter, the procedure for this algorithmic validation phase will be to measure the quality of the results obtained after the calibration, i.e. we have to analyze if the calibrated model fits sufficiently well the data according to predetermined criteria.

To summarize, the overall goal of this research axis is to address two major issues related to calibration and validation of models: (a) defining a calibration methodology and developing relevant and efficient algorithms to facilitate the parameter estimation of considered models; (b) defining a validation methodology and developing the related algorithms (this is complemented by sensitivity analysis, see the following section).

[0] http://www.csr.ufmg.br/dinamica/

In both cases, analyzing the uncertainty that may arise either from the data or the underlying equations, and quantifying how these uncertainties propagate in the model, are of major importance. We will work on all those issues for the models of all the applied domains covered by STEEP.

3.3. Sensitivity analysis

A sensitivity analysis (SA) consists, in a nutshell, in studying how the uncertainty in the output of a model can be apportioned to different sources of uncertainty in the model inputs. It is complementary to an uncertainty analysis, which focuses on quantifying uncertainty in model output. SA's can be useful for several purposes, such as guiding model development and identifying the most influential model parameters and critical data items. Identifying influential model parameters may help in divising metamodels (or, surrogate models) that approximate an original model and may be simulated, calibrated, or analyzed more efficiently. As for detecting critical data items, this may indicate for which type of data more effort must be spent in the data collection process in order to eventually improve the model's reliability. Finally, SA can be used as one means for validating models, together with validation based on historical data (or, put simply, using training and test data) and validation of model parameters and outputs by experts in the respective application area. All these uses of SA will be considered in our research.

The first two applications of SA are linked to model calibration, discussed in the previous section. Indeed, prior to the development of the calibration tools, one important step is to select the significant or sensitive parameters and to evaluate the robustness of the calibration results with respect to data noise (stability studies). This may be performed through a global sensitivity analysis, e.g. by computation of Sobol's indices. Many problems will have to be circumvented e.g. difficulties arising from dependencies of input variables, variables that obey a spatial organization, or switch inputs. We will take up on current work in the statistics community on SA for these difficult cases.

As for the third application of SA, model validation, a preliminary task bears on the propagation of uncertainties. Identifying the sources of uncertainties and their nature is crucial to propagate them via Monte Carlo techniques. To make a Monte Carlo approach computationally feasible, it is necessary to develop specific metamodels. Both the identification of the uncertainties and their propagation require a detailed knowledge of the data collection process; these are mandatory steps before a validation procedure based on SA can be implemented. First, we will focus on validating LUTI models, starting with the CITiES ANR project: here, an SA consists in defining various land use policies and transportation scenarios and in using these scenarios to test the integrated land use and transportation model. Current approaches for validation by SA consider several scenarios and propose various indicators to measure the simulated changes. We will work towards using sensitivity indices based on functional analysis of variance, which will allow us to compare the influence of various inputs on the indicators. For example it will allow the comparison of the influences of transportation and land use policies on several indicators.

THOTH Project-Team

3. Research Program

3.1. Designing and learning structured models

The task of understanding image and video content has been interpreted in several ways over the past few decades, namely image classification, detecting objects in a scene, recognizing objects and their spatial extents in an image, estimating human poses, recovering scene geometry, recognizing activities performed by humans. However, addressing all these problems individually provides us with a partial understanding of the scene at best, leaving much of the visual data unexplained.

One of the main goals of this research axis is to go beyond the initial attempts that consider only a subset of tasks jointly, by developing novel models for a more complete understanding of scenes to address all the component tasks. We propose to incorporate the structure in image and video data explicitly into the models. In other words, our models aim to satisfy the complex sets of constraints that exist in natural images and videos. Examples of such constraints include: (i) relations between objects, like signs for shops indicate the presence of buildings, people on a road are usually walking or standing, (ii) higher-level semantic relations involving the type of scene, geographic location, and the plausible actions as a global constraint, e.g., an image taken at a swimming pool is unlikely to contain cars, (iii) relating objects occluded in some of the video frames to content in other frames, where they are more clearly visible as the camera or the object itself move, with the use of long-term trajectories and video object proposals.

This research axis will focus on three topics. The first is developing deep features for video. This involves designing rich features available in the form of long-range temporal interactions among pixels in a video sequence to learn a representation that is truly spatio-temporal in nature. The focus of the second topic is the challenging problem of modeling human activities in video, starting from human activity descriptors to building intermediate spatio-temporal representations of videos, and then learning the interactions among humans, objects and scenes temporally. The last topic is aimed at learning models that capture the relationships among several objects and regions in a single image scene, and additionally, among scenes in the case of an image collection or a video. The main scientific challenges in this topic stem from learning the structure of the probabilistic graphical model as well as the parameters of the cost functions quantifying the relationships among its entities. In the following we will present work related to all these three topics and then elaborate on our research directions.

- **Deep features for vision.** Deep learning models provide a rich representation of complex objects but in return have a large number of parameters. Thus, to work well on difficult tasks, a large amount of data is required. In this context, video presents several advantages: objects are observed from a large range of viewpoints, motion information allows the extraction of moving objects and parts, and objects can be differentiated by their motion patterns. We initially plan to develop deep features for videos that incorporate temporal information at multiple scales. We then plan to further exploit the rich content in video by incorporating additional cues, such as the detection of people and their body-joint locations in video, minimal prior knowledge of the object of interest, with the goal of learning a representation that is more appropriate for video understanding. In other words, a representation that is learned from video data and targeted at specific applications. For the application of recognizing human activities, this involves learning deep features for humans and their body-parts with all their spatiotemporal variations, either directly from raw video data or “pre-processed” videos containing human detections. For the application of object tracking, this task amounts to learning object-specific deep representations, further exploiting the limited annotation provided to identify the object.
- **Modeling human activities in videos.** Humans and their activities are not only one of the most frequent and interesting subjects in videos but also one of the hardest to analyze owing to the

complexity of the human form, clothing and movements. As part of this task, the Thoth project-team plans to build on state-of-the-art approaches for spatio-temporal representation of videos. This will involve using the dominant motion in the scene as well as the local motion of individual parts undergoing a rigid motion. Such motion information also helps in reasoning occlusion relationships among people and objects, and the state of the object. This novel spatio-temporal representation ultimately provides the equivalent of object proposals for videos, and is an important component for learning algorithms using minimal supervision. To take this representation even further, we aim to integrate the proposals and the occlusion relationships with methods for estimating human pose in videos, thus leveraging the interplay among body-joint locations, objects in the scene, and the activity being performed. For example, the locations of shoulder, elbow and wrist of a person drinking coffee are constrained to move in a certain way, which is completely different from the movement observed when a person is typing. In essence, this step will model human activities by dynamics in terms of both low-level movements of body-joint locations and global high-level motion in the scene.

- **Structured models.** The interactions among various elements in a scene, such as, the objects and regions in it, the motion of object parts or entire objects themselves, form a key element for understanding image or video content. These rich cues define the structure of visual data and how it evolves spatio-temporally. We plan to develop a novel graphical model to exploit this structure. The main components in this graphical model are spatio-temporal regions (in the case of video or simply image regions), which can represent object parts or entire objects themselves, and the interactions among several entities. The dependencies among the scene entities are defined with a higher order or a global cost function. A higher order constraint is a generalization of the pairwise interaction term, and is a cost function involving more than two components in the scene, e.g., several regions, whereas a global constraint imposes a cost term over the entire image or video, e.g., a prior on the number of people expected in the scene. The constraints we plan to include generalize several existing methods, which are limited to pairwise interactions or a small restrictive set of higher-order costs. In addition to learning the parameters of these novel functions, we will focus on learning the structure of the graph itself—a challenging problem that is seldom addressed in current approaches. This provides an elegant way to go beyond state-of-the-art deep learning methods, which are limited to learning the high-level interaction among parts of an object, by learning the relationships among objects.

3.2. Learning of visual models from minimal supervision

Today's approaches to visual recognition learn models for a limited and fixed set of visual categories with fully supervised classification techniques. This paradigm has been adopted in the early 2000's, and within it enormous progress has been made over the last decade.

The scale and diversity in today's large and growing image and video collections (such as, e.g., broadcast archives, and personal image/video collections) call for a departure from the current paradigm. This is the case because to answer queries about such data, it is unfeasible to learn the models of visual content by manually and precisely annotating every relevant concept, object, scene, or action category in a representative sample of everyday conditions. For one, it will be difficult, or even impossible to decide a-priori what are the relevant categories and the proper granularity level. Moreover, the cost of such annotations would be prohibitive in most application scenarios. One of the main goals of the Thoth project-team is to develop a new framework for learning visual recognition models by actively exploring large digital image and video sources (off-line archives as well as growing on-line content), and exploiting the weak supervisory signal provided by the accompanying metadata (such as captions, keywords, tags, subtitles, or scripts) and audio signal (from which we can for example extract speech transcripts, or exploit speaker recognition models).

Textual metadata has traditionally been used to index and search for visual content. The information in metadata is, however, typically sparse (e.g., the location and overall topic of newscasts in a video archive [0])

[0]For example at the Dutch national broadcast archive Netherlands Institute of Sound and Vision, with whom we collaborated in the EU FP7 project AXES, typically one or two sentences are used in the metadata to describe a one hour long TV program.

and noisy (e.g., a movie script may tell us that two persons kiss in some scene, but not when, and the kiss may occur off screen or not have survived the final cut). For this reason, metadata search should be complemented by visual content based search, where visual recognition models are used to localize content of interest that is not mentioned in the metadata, to increase the usability and value of image/video archives. *The key insight that we build on in this research axis is that while the metadata for a single image or video is too sparse and noisy to rely on for search, the metadata associated with large video and image databases collectively provide an extremely versatile source of information to learn visual recognition models.* This form of "embedded annotation" is rich, diverse and abundantly available. Mining these correspondences from the web, TV and film archives, and online consumer generated content sites such as Flickr, Facebook, or YouTube, guarantees that the learned models are representative for many different situations, unlike models learned from manually collected fully supervised training data sets which are often biased.

The approach we propose to address the limitations of the fully supervised learning paradigm aligns with "Big Data" approaches developed in other areas: we rely on the orders-of-magnitude-larger training sets that have recently become available with metadata to compensate for less explicit forms of supervision. This will form a sustainable approach to learn visual recognition models for a much larger set of categories with little or no manual intervention. Reducing and ultimately removing the dependency on manual annotations will dramatically reduce the cost of learning visual recognition models. This in turn will allow such models to be used in many more applications, and enable new applications based on visual recognition beyond a fixed set of categories, such as natural language based querying for visual content. This is an ambitious goal, given the sheer volume and intrinsic variability of the every day visual content available on-line, and the lack of a universally accepted formalism for modeling it. Yet, the potential payoff is a breakthrough in visual object recognition and scene understanding capabilities.

This research axis is organized into the following three sub-tasks:

- **Weakly supervised learning.** For object localization we will go beyond current methods that learn one category model at a time and develop methods that learn models for different categories concurrently. This allows "explaining away" effects to be leveraged, i.e., if a certain region in an image has been identified as an instance of one category, it cannot be an instance of another category at the same time. For weakly supervised detection in video we will consider detection proposal methods. While these are effective for still images, recent approaches for the spatio-temporal domain need further improvements to be similarly effective. Furthermore, we will exploit appearance and motion information jointly over a set of videos. In the video domain we will also continue to work on learning recognition models from subtitle and script information. The basis of leveraging the script data which does not have a temporal alignment with the video, is to use matches in the narrative in the script and the subtitles (which do have a temporal alignment with the video). We will go beyond simple correspondences between names and verbs relating to self-motion, and match more complex sentences related to interaction with objects and other people. To deal with the limited amount of occurrences of such actions in a single movie, we will consider approaches that learn action models across a collection of movies.
- **Online learning of visual models.** As a larger number of visual category models is being learned, online learning methods become important, since new training data and categories will arrive over time. We will develop online learning methods that can incorporate new examples for existing category models, and learn new category models from few examples by leveraging similarity to related categories using multi-task learning methods. Here we will develop new distance-based classifiers and attribute and label embedding techniques, and explore the use of NLP techniques such as skipgram models to automatically determine between which classes transfer should occur. Moreover, NLP will be useful in the context of learning models for many categories to identify synonyms, and to determine cases of polysemy (e.g. jaguar car brand v.s. jaguar animal), and merge or refine categories accordingly. Ultimately this will result in methods that are able to learn an"encyclopedia" of visual models.
- **Visual search from unstructured textual queries.** We will build on recent approaches that learn

recognition models on-the-fly (as the query is issued) from generic image search engines such as Google Images. While it is feasible to learn models in this manner in a matter of seconds, it is challenging to use the model to retrieve relevant content in real-time from large video archives of more than a few thousand hours. To achieve this requires feature compression techniques to store visual representations in memory, and cascaded search techniques to avoid exhaustive search. This approach, however, leaves untouched the core problem of how to associate visual material with the textual query in the first place. The second approach we will explore is based on image annotation models. In particular we will go beyond image-text retrieval methods by using recurrent neural networks such as Elman networks or long short-term memory (LSTM) networks to generate natural language sentences to describe images.

3.3. Large-scale learning and optimization

We have entered an era of massive data acquisition, leading to the revival of an old scientific utopia: it should be possible to better understand the world by automatically converting data into knowledge. It is also leading to a new economic paradigm, where data is a valuable asset and a source of activity. Therefore, developing scalable technology to make sense of massive data has become a strategic issue. Computer vision has already started to adapt to these changes.

In particular, very high dimensional models such as deep networks are becoming highly popular and successful for visual recognition. This change is closely related to the advent of big data. On the one hand, these models involve a huge number of parameters and are rich enough to represent well complex objects such as natural images or text corpora. On the other hand, they are prone to overfitting (fitting too closely to training data without being able to generalize to new unseen data) despite regularization; to work well on difficult tasks, they require a large amount of labelled data that has been available only recently. Other cues may explain their success: the deep learning community has made significant engineering efforts, making it possible to learn in a day on a GPU large models that would have required weeks of computations on a traditional CPU, and it has accumulated enough empirical experience to find good hyper-parameters for its networks.

To learn the huge number of parameters of deep hierarchical models requires scalable optimization techniques and large amounts of data to prevent overfitting. This immediately raises two major challenges: how to learn without large amounts of labeled data, or with weakly supervised annotations? How to efficiently learn such huge-dimensional models? To answer the above challenges, we will concentrate on the design and theoretical justifications of deep architectures including our recently proposed deep kernel machines, with a focus on weakly supervised and unsupervised learning, and develop continuous and discrete optimization techniques that push the state of the art in terms of speed and scalability.

This research axis will be developed into three sub-tasks:

- **Deep kernel machines for structured data.** Deep kernel machines combine advantages of kernel methods and deep learning. Both approaches rely on high-dimensional models. Kernels implicitly operate in a space of possibly infinite dimension, whereas deep networks explicitly construct high-dimensional nonlinear data representations. Yet, these approaches are complementary: Kernels can be built with deep learning principles such as hierarchies and convolutions, and approximated by multilayer neural networks. Furthermore, kernels work with structured data and have well understood theoretical principles. Thus, a goal of the Thoth project-team is to design and optimize the training of such deep kernel machines.
- **Large-scale parallel optimization.** Deep kernel machines produce nonlinear representations of input data points. After encoding these data points, a learning task is often formulated as a *large-scale convex optimization problem*; for example, this is the case for linear support vector machines, logistic regression classifiers, or more generally many empirical risk minimization formulations. We intend to pursue recent efforts for making convex optimization techniques that are dedicated to machine learning more scalable. Most existing approaches address scalability issues either in model size (meaning that the function to minimize is defined on a domain of very high dimension), or in the amount of training data (typically, the objective is a large sum of elementary functions). There is

thus a large room for improvements for techniques that jointly take these two criteria into account.

- **Large-scale graphical models.** To represent structured data, we will also investigate graphical models and their optimization. The challenge here is two-fold: designing an adequate cost function and minimizing it. While several cost functions are possible, their utility will be largely determined by the efficiency and the effectiveness of the optimization algorithms for solving them. It is a combinatorial optimization problem involving billions of variables and is NP-hard in general, requiring us to go beyond the classical approximate inference techniques. The main challenges in minimizing cost functions stem from the large number of variables to be inferred, the inherent structure of the graph induced by the interaction terms (e.g., pairwise terms), and the high-arity terms which constrain multiple entities in a graph.

3.4. Datasets and evaluation

Standard benchmarks with associated evaluation measures are becoming increasingly important in computer vision, as they enable an objective comparison of state-of-the-art approaches. Such datasets need to be relevant for real-world application scenarios; challenging for state-of-the-art algorithms; and large enough to produce statistically significant results.

A decade ago, small datasets were used to evaluate relatively simple tasks, such as for example interest point matching and detection. Since then, the size of the datasets and the complexity of the tasks gradually evolved. An example is the Pascal Visual Object Challenge with 20 classes and approximately 10,000 images, which evaluates object classification and detection. Another example is the ImageNet challenge, including thousands of classes and millions of images. In the context of video classification, the TrecVid Multimedia Event Detection challenges, organized by NIST, evaluate activity classification on a dataset of over 200,000 video clips, representing more than 8,000 hours of video, which amounts to 11 months of continuous video.

Almost all of the existing image and video datasets are annotated by hand; it is the case for all of the above cited examples. In some cases, they present limited and unrealistic viewing conditions. For example, many images of the ImageNet dataset depict upright objects with virtually no background clutter, and they may not capture particularly relevant visual concepts: most people would not know the majority of subcategories of snakes cataloged in ImageNet. This holds true for video datasets as well, where in addition a taxonomy of action and event categories is missing.

Our effort on data collection and evaluation will focus on two directions. First, we will design and assemble video datasets, in particular for action and activity recognition. This includes defining relevant taxonomies of actions and activities. Second, we will provide data and define evaluation protocols for weakly supervised learning methods. This does not mean of course that we will forsake human supervision altogether: some amount of ground-truth labeling is necessary for experimental validation and comparison to the state of the art. Particular attention will be payed to the design of efficient annotation tools.

Not only do we plan to collect datasets, but also to provide them to the community, together with accompanying evaluation protocols and software, to enable a comparison of competing approaches for action recognition and large-scale weakly supervised learning. Furthermore, we plan to set up evaluation servers together with leaderboards, to establish an unbiased state of the art on held out test data for which the ground-truth annotations are not distributed. This is crucial to avoid tuning the parameters for a specific dataset and to guarantee a fair evaluation.

- **Action recognition.** We will develop datasets for recognizing human actions and human-object interactions (including multiple persons) with a significant number of actions. Almost all of today's action recognition datasets evaluate classification of short video clips into a number of predefined categories, in many cases a number of different sports, which are relatively easy to identify by their characteristic motion and context. However, in many real-world applications the goal is to identify and localize actions in entire videos, such as movies or surveillance videos of several hours. The actions targeted here are "real-world" and will be defined by compositions of atomic actions into higher-level activities. One essential component is the definition of relevant taxonomies of actions

and activities. We think that such a definition needs to rely on a decomposition of actions into poses, objects and scenes, as determining all possible actions without such a decomposition is not feasible. We plan to provide annotations for spatio-temporal localization of humans as well as relevant objects and scene parts for a large number of actions and videos.

- **Weakly supervised learning.** We will collect weakly labeled images and videos for training. The collection process will be semi-automatic. We will use image or video search engines such as Google Image Search, Flickr or YouTube to find visual data corresponding to the labels. Initial datasets will be obtained by manually correcting whole-image/video labels, i.e., the approach will evaluate how well the object model can be learned if the entire image or video is labeled, but the object model has to be extracted automatically. Subsequent datasets will features noisy and incorrect labels. Testing will be performed on PASCAL VOC'07 and ImageNet, but also on more realistic datasets similar to those used for training, which we develop and manually annotate for evaluation. Our dataset will include both images and videos, the categories represented will include objects, scenes as well as human activities, and the data will be presented in realistic conditions.
- **Joint learning from visual information and text.** Initially, we will use a selection from the large number of movies and TV series for which scripts are available on-line, see for example http://www.dailyscript.com and http://www.weeklyscript.com. These scripts can easily be aligned with the videos by establishing correspondences between script words and (timestamped) spoken ones obtained from the subtitles or audio track. The goal is to jointly learn from visual content and text. To measure the quality of such a joint learning, we will manually annotate some of the videos. Annotations will include the space-time locations of the actions as well as correct parsing of the sentence. While DVDs will, initially, receive most attention, we will also investigate the use of data obtained from web pages, for example images with captions, or images and videos surrounded by text. This data is by nature more noisy than scripts.

TYREX Project-Team

3. Research Program

3.1. Modeling

Modeling consists in capturing various aspects of document and data processing and communication in a unifying model. Our modeling research direction mainly focuses on three aspects.

The first aspect aims at reducing the impedance mismatch. The impedance mismatch refers to the complexity, difficulty and lack of performance induced by various web application layers which require the same piece of information to be represented and processed differently. The mismatch occurs because programming languages use different native data models than those used for documents in browsers and for storage in databases. This results in complex and multi-tier software architectures whose different layers are incompatible in nature. This, in turn, results in expensive, inefficient, and error-prone web development. For reducing the impedance mismatch, we will focus on the design of a unifying software stack and programming framework, backed by generic and solid logical foundations similar in spirit to the NoSQL approach.

The second aspect aims at harnessing heterogeneity. Web applications increasingly use diverse data models: ordered and unordered tree-like structures (such as XML), nested records and arrays (such as JSON), graphs (like RDF), and tables. Furthermore, these data models involve a variety of languages for expressing constraints over data (e.g. XML schema, RelaxNG, and RDFS to name just a few). We believe that this heterogeneity is here to stay and is likely to increase. These differences in representations imply loads of error-prone and costly conversions and transformations. Furthermore, some native formats (e.g. JSON) are repurposed from an internal representation to a format for data exchange. This often results in a loss of information and in errors that need to be tracked and corrected. In this context, it is important to seek methods for reducing risks of information loss during data transformation and exchange. For harnessing heterogeneity, we will focus on the integration of data models through unified formal semantics and in particular logical interpretation. This allows using the same programming language constructs on different data models. At the programming language level, this is similar to languages such as JSonIq for JSON and XML.

Finally, the third aspect aims at making applications and data more compositional. Most web programming technologies are currently limited from a compositional point of view. For example, tree grammars (like schema languages for XML) are monolithic in the sense that they require the full description of the considered structures, instead of allowing the assembly of smaller and reusable building blocks. As a consequence, this translates into monolithic web applications, which makes their automated verification harder by making modular analyses more difficult. The need for compositionality is illustrated in the industry by the increasing development of fragmented W3C specifications organised in ad-hoc modules. For making applications and data more compositional, we will focus on the design of modular schema and programming languages. For this purpose, we will notably rely on succinct yet expressive formalisms (like two-way logics, polymorphic types, session types) that ease the process of expressing modular specifications.

3.2. Analysis, verification and optimization

This research direction aims at guaranteeing two different kinds of properties: safety and efficiency.

The first kind of properties concerns the safety of web applications. Software development was traditionally split between critical and non-critical software. Advanced (and costly) formal verification techniques were reserved to the former whereas non-critical software relied almost exclusively on testing, which only offers a ‘best-effort’ guarantee (removes most bugs but some of them may not be detected). The central idea was that in a non-critical system, the damage a failure may create is not worth the cost of formal verification. However, as web applications grow more pervasive in everyday life and gain momentum in corporates and various social organizations, and touch larger numbers of users, the potential cost of failure is rapidly and

significantly increasing. In that sense, we can consider that web applications are becoming more and more critical. The growing dependency on the web as a tool, combined with the fact that some applications involve very large user bases, is becoming problematic as it seems to increase rapidly but silently. Some errors like crashes and confidential information leaks, if not discovered, can have massive effects and cause significant financial or reputation damage.

The second kind of properties concerns the efficiency of web applications. One particular characteristic of web programming languages is that they are essentially data-manipulation oriented. These manipulations rely on query and transformation languages whose performance is critical. This performance is very sensitive to data size and organization (constraints) and to the execution model (e.g. streaming evaluators). Static analysis can be used to optimize runtime performance by compile-time automated modification of the code (e.g. substitution of queries by more efficient ones). One major scientific difficulty here consists in dealing with problems close to the frontier of decidability, and therefore in finding useful trade-offs between programming ease, expressivity, complexity, succinctness, algorithmic techniques and effective implementations.

3.3. Design of advanced (robust, flexible, rich, novel) web applications

The generalized use of mobile terminals deeply affects the way users perceive and interact with their environment. The ubiquitous use of search engines capable of producing results in fractions of a second raised user expectations to a very high level: users now expect relevant information to be made available to them instantly and directly by context sensitivity to the environment itself. However, the information that needs to be processed is becoming more and more complex compared to the traditional web. In order to unlock the potential introduced by this new generation of the web, a radical rethinking of how web information is produced, organized and processed is necessary.

Until now, content rendering on the web was mainly based on supporting media formats separately. It is still notably the case in HTML5 for example where, for instance, vector graphics, mathematical content, audio and video are supported only as isolated media types. With the increasing use of web content in mobile terminals, we also need to take into account highly dynamic information flowing from sensors (positioning and orientation moves) and cameras. To reach that goal, web development platforms need to ease the manipulation of such content with carefully designed programming interfaces and by developing supporting integrative methods.

More precisely, we will focus on the following aspects: (1) **Build Rich content models**. This requires combining in a single model several content facets such as 3D elements, animations, user interactions, etc. We will focus on feature-compositional methods, which have become a prerequisite for the production of compelling web applications. (2) **Physical environment modeling and integration**. This consists of modeling and representing urban data such as buildings, pathways, points of interest. It requires developing appropriate languages and techniques to represent, process and query such environment models. In particular, we will focus on tracking positional user information and design techniques capable of combining semantic annotations, content, and representation of the physical world. (3) **Native streams support**. This consists of capturing new data flows extracted from various sensors in mobile terminals and various equipments. (4) **Cross-platform abstractions**. We will contribute to the design of appropriate abstractions to make applications run in a uniform way across various devices and environments. Our goal is to provide a viable alternative to current (platform-specific) mobile application development practices.

URBANET Team

3. Research Program

3.1. Capillary networks

The definition of Smart Cities is still constantly redefined and expanded so as to comprehensively describe the future of major urban areas. The Smart City concept mainly refers to granting efficiency and sustainability in densely populated metropolitan areas while enhancing citizens' life and protecting the environment. The Smart City vision can be primarily achieved by a clever integration of ICT in the urban tissue. Indeed, ICTs are enabling an evolution from the current duality between the "real world" and its digitalized counterpart to a continuum in which digital contents and applications are seamlessly interacting with classical infrastructures and services. The general philosophy of smart cities can also be seen as a paradigm shift combining the Internet of Things (IoT) and Machine-to-Machine (M2M) communication with a citizen-centric model, all together leveraging massive data collected by pervasive sensors, connected mobile or fixed devices, and social applications.

The fast expansion of urban digitalization yields new challenges that span from social issues to technical problems. Therefore, there is a significant joint effort by public authorities, academic research communities and industrial companies to understand and address these challenges. Within that context, the application layer, i.e., the novel services that ICT can bring to digital urban environments, have monopolized the attention. Lower-layer network architectures have gone instead quite overlooked. We believe that this might be a fatal error, since the communication network plays a critical role in supporting advanced services and ultimately in making the Smart City vision a reality. The UrbaNet project deals precisely with that aspect, and the study of network solutions for upcoming Smart Cities represents the core of our work.

Most network-related challenges along the road to real-world Smart Cities deal with efficient mobile data communication, both at the backbone and at the radio access levels. It is on the latter that the UrbaNet project is focused. More precisely, the scope of the project maps to that of capillary networks, an original concept we define next.

The capillary networking concept represents a unifying paradigm for wireless last-mile communication in smart cities. The term we use is reminiscent of the pervasive penetration of different technologies for wireless communication in future digital cities. Indeed, capillary networks represent the very last portion of the data distribution and collection network, bringing Internet connectivity to every endpoint of the urban tissue in the same exact way capillary blood vessels bring oxygen and collect carbon dioxide at tissues in the human body. Capillary networks inherit concepts from the self-configuring, autonomous, ad hoc networks so extensively studied in the past decade, but they do so in a holistic way. Specifically, this implies considering multiple technologies and applications at a time, and doing so by accounting for all the specificities of the urban environment.

3.2. Specific issues and new challenges of capillary networks

Capillary networks are not just a collection of independent wireless technologies that can be abstracted from the urban environment and/or studied separately. That approach has been in fact continued over the last decade, as technologies such as sensor, mesh, vehicular, opportunistic, and – generally speaking – M2M networks have been designed and evaluated in isolation and in presence of unrealistic mobility and physical layer, simplistic deployments, random traffic demands, impractical application use cases and non-existent business models. In addition, the physical context of the network has a significant impact on its performances and cannot be reduced to a simple random variable. Moreover, one of the main element of a network never appears in many studies: the user. To summarize, networks issues should be addressed from a user- and context-centric perspective.

Such abstractions and approximations were necessary for understanding the fundamentals of wireless network protocols. However, real world deployments have shown their limits. The finest protocols are often unreliable and hardly applicable to real contexts. That also partially explains the marginal impact of multi-hop wireless technologies on today's production market. Industrial solutions are mostly single-hop, complex to operate, and expensive to maintain.

In the UrbaNet project we consider the capillary network as an ensemble of strongly intertwined wireless networks that are expected to coexist and possibly co-operate in the context of arising digital cities. This has three major implications:

- Each technology contributing to the overall capillary network should not be studied apart. As a matter of fact, mobile devices integrate today a growing number of sensors (e.g., environment sensing, resource consumption metering, movement, health or pollution monitoring) and multiple radio interfaces (e.g., LTE, WiFi, ZigBee,. . .), and this is becoming a trend also in the case of privately owned cars, public transport vehicles, commercial fleets, and even city bikes. Similarly, access network sites tend to implement heterogeneous communication technologies so as to limit capital expenses. Enabling smart-cities needs a dense sensing of its activities, which cannot be achieved without multi-service sensor networks. Moreover, all these devices are expected to inter-operate so as to make the communication more sustainable and reliable. Thus, the technologies that build up the capillary network shall be studied as a whole in the future.
- The capillary network paradigm necessarily accounts for actual urban mobility flows, city land-use layouts, metropolitan deployment constraints, and expected activity of the citizens. Often, these specificities do not arise from purely networking features, but relate to the study of city topologies and road layouts, social acceptability, transportation systems, energy management, or urban economics. Therefore, addressing capillary network scenarios cannot but rely on strong multidisciplinary interactions.
- Digital and smart cities are often characterized by arising M2M applications. However, a city is, before all, the gathering of citizens, who use digital services and mobile Internet for increasing their quality of life, empowerment, and entertainment opportunities. Some data flows should be gathered to, or distributed from, an information system. Some other should be disseminated to a geographically or time constrained perimeter. Future usage may induce peer-to-peer like traffics. Moreover these services are also an enabler of new usages of the urban environment. Solutions built within the capillary network paradigm have to manage this heterogeneity of traffic requirements and user behaviors.

By following these guidelines, the UrbaNet ambition is to go one step beyond traditional approaches discussed above. The capillary network paradigm for Smart Cities is tightly linked to the specificities of the metropolitan context and the citizens' activity. Our proposal is thus to re-think the way capillary network technologies are developed, considering a broader and more practical perspective.

3.3. Characterizing urban networks

Our first objective is to understand and model those properties of real-world urban environments that have an impact on the design, deployment and operation of capillary networks. It means to collect and analyze data from actual deployments and services, as well as testbeds experiments. These data have then to be correlated with urban characteristics, e.g. topography, density of population and activities. The objective is to deduce analytical models, simulations and traces of realistic scenarios that can be leveraged afterward. We structure the axis into three tasks that correspond to the three broad categories of networking aspects affected by the urban context.

- **Topological characteristics**. Nowadays, the way urban wireless network infrastructures are typically represented in the literature is dissatisfying. As an example, wireless links are mostly represented as symmetric, lossless channels whose signal quality depends continuously on the distance between the transmitter and the receiver. No need to say, real-world behaviors are very far from

these simplified representations. Another example, topologies are generally modeled according to deterministic (e.g., regular grids and lattices, or perfect hexagonal cell coverages) or stochastic (e.g., random uniform distributions over unbound surfaces) approaches. These make network problems mathematically tractable and simulations easier to set up, but are hardly representative of the layouts encountered in the real world. Employing simplistic models helps understanding some fundamental principles but risks to lead to unreliable results, both from the viewpoint of the network architecture design and from that of its performance evaluation. It is thus our speculation that the actual operations and the real-world topologies of infrastructured capillary networks are key to the successful deployment of these technologies, and, in this task, we aim at characterizing them. To that end, we leverage existing collaborations with device manufacturers (Alcatel-Lucent, HiKob) and operators (Orange), as well as collaboration such as the Sense City project and testbed experiments, in order to provide models that faithfully mimic the behavior of real world network devices. The goal is to understand the important features of the topologies, including, e.g., their overall connectivity level, spatial density, degree distribution, regularity, etc. Building on these results, we try to define network graph models that reproduce such major features and can be employed for the development and evaluation of capillary network solutions.

- **Mobilities**. We aim at understanding and modeling the mobile portion of capillary networks as well as the impact of the human mobility on the network usage. Our definition of "mobile portion" includes traditional mobile users as well as all communication-enabled devices that autonomously interact with Internet-based servers and among themselves. There have been efforts to collect real-world movement traces, to generate synthetic mobility dataset and to derive mobility models. However, real-world traces remain limited to small scenarios or circumstantial subsets of the users (e.g., cabs instead of the whole road traffic). Synthetic traces are instead limited by their scale and by their level of realism, still insufficient. Finally, even the most advanced models cannot but provide a rough representation of user mobility in urban areas, as they do not consider the street layout or the human activity patterns. In the end, although often deprecated, random or stochastic mobility models (e.g., random walks, exponential inter-arrivals and cell residence times) are still the common practice. We are well aware of the paramount importance of a faithful representation of device and user mobility within capillary networks and, in order to achieve it, we leverage a number of realistic sources, including Call Detail Records (CDR) collected by mobile operators, Open Data initiatives, real-world social network data, and experiments. We collect data and analyze it, so as to infer the critical properties of the underlying mobility patterns.
- **Data traffic patterns**. The characterization of capillary network usages means understanding and modeling when, where and how the wireless access provided by the diverse capillary network technologies is exploited by users and devices. In other words, we are interested in learning which applications are used at different geographical locations and day times, which urban phenomena generate network usage, and which kind of data traffic load they induce on the capillary network. Properly characterizing network usages is as critical as correctly modeling network topology and mobility. Indeed, the capillary networks being the link directly collecting the data from end devices, we cannot count on statistical smoothing which yields regular distributions. Unfortunately, the common practice is to consider, e.g., that each user or device generates a constant data traffic or follows on/off models, that the offered load is uniform over space and does not vary over time, that there is small difference between uplink and downlink behaviors, or that source/destination node pairs are randomly distributed in the network. We plan to go further on the specific scenarios we address, such as smart-parking, floating car data, tele-metering, road traffic management of pollution detection. To that end, we collect real-world data, explore it and derive properties useful to the accurate modeling of content consumption.

3.4. Autonomic networking protocols

While the capillary networks concept covers a large panel of technologies, network architectures, applications and services, common challenges remain, regardless the particular choice of a technology or architecture.

Our record of research on spontaneous and multi-hop networks let us think that autonomic networking appears as the main issue: the connectivity to Internet, to cyber-physical systems, to Information Systems should be transparent for the user, context-aware and location-aware. To address these challenges, a capillary network model is required. Unfortunately, very few specific models fit this task today. However, a number of important, specific capillary networks properties can already be inferred from recent experiments: distributed and localized topologies, very high node degree, dynamic network diameter, unstable / asymmetric / non-transitive radio links, concurrent topologies, heterogeneous capabilities, etc. These properties can already be acknowledged in the design of networking solutions, and they are particularly challenging for the functioning of the MAC layer and QoS support. Clearly, capillary networks provide new research opportunities with regard to networking protocols design.

- **Self-* protocols**. In this regard, self-configuration, self-organization and self-healing are some of the major concerns within the context of capillary networks. Solving such issues would allow spontaneous topologies to appear dynamically in order to provide a service depending of the location and the context, while also adapting to the interactions imposed by the urban environment. Moreover, these mechanisms have the capacity to alleviate the management of the network and the deployment engineering rules, and can provide efficient support to the network dynamics due to user mobility, environment modifications, etc. The designed protocols have to be able to react to traffic requests and local node densities. We address such self-adaptive protocols as a transversal solution to several scenarios, e.g. pollution monitoring, smart-services depending on human activities, vehicle to infrastructure communications, etc. In architectures where self-* mechanisms govern the protocol design, both robustness and energy are more than ever essential challenges at the network layer. Solutions such as energy-harvesting can significantly increase the network lifetime in this case, therefore we investigate their impact on the mechanisms at both MAC and network layers.
- **Quality of service issues**. The capillary networks paradigm implies a simultaneous deployment of multiple wireless technologies, and by different entities (industry, local community, citizens). This means that some applications and services can be provided concurrently by different parts of the capillary network, while others might require the cooperation of multiple parties. The notion of Service Level Agreement (SLA) for traffic differentiation, quality of service support (delay, reliability, etc.) is a requirement in these cases for scalability purposes and resource sharing. We contribute to a proper definition of this notion and the related network mechanisms in the settings of low power wireless devices. Because of the urban context, but also because of the wireless media itself, network connectivity is always temporary, while applications require a delivery ratio close to 100%. We investigate different techniques that can achieve this objective in an urban environment.
- **Data impact**. Capillary networks suffer from low capacity facing the increasing user request. In order to cope with network saturation, a promising strategy is to consider the nature of the transmitted data in the development of the protocols. Data aggregation and data gathering are two concepts with a major role to play in this context of limited capacity. In particular, combining local aggregation and measurement redundancy for improving on data reliability is a promising idea, which can also be important for energy saving purposes. Even if the data flow is well known and regular, e.g. temperature or humidity metering, developing aggregation schemes tailored to the constraints of the urban environment is a challenge we address within the UrbaNet team. Many urban applications generate data which has limited spatial and temporal perimeters of relevance, e.g. smart-parking applications, community information broadcasting, etc. When solely a spatial range of relevance is considered, the underlying mechanisms are denoted “geocasting”. We also address these spatio-temporal constraints, which combine geocasting approaches with real-time techniques.

3.5. Optimizing cellular network usage

The capacity of cellular networks, even those that are now being planned, does not seem able to cope with the increasing demands of data users. Moreover, new applications with high bandwidth requirements are also foreseen, for example in the intelligent transportation area, and an exponential growth in signaling traffic is

expected in order to enable this data growth. Cumulated with the lack of available new spectrum, this leads to an important challenge for mobile operators, who are looking at both licensed and unlicensed technologies for solutions. The usual strategy consists in a dramatic densification of micro-cells coverage, allowing both to minimize the transmission power of cellular networks as well as to increase the network capacity. However, this solution has obvious physical limits, which we work on determining, and we propose exploiting the capillarity of network interfaces as a complementary solution.

- **Green cellular network**. Increasing the density of micro-cells means multiplying the energy consumption issues. Indeed, the energy consumption of actual LTE eNodeBs and relays, whatever their state, idle, transmitting or receiving, is a major and growing part of the access network energy consumption. For a sustainable deployment of such micro-cell infrastructures and for a significative decrease of the overall energy consumption, an operator needs to be able to switch off cells when they are not absolutely needed. The densification of the cells induces the need for an autonomic control of the on/off state of cells. One solution in this sense can be to adapt the WSN mechanisms to the energy models of micro-cells and to the requirements of a cellular network. The main difficulty here is to be able to adapt and assess the proposed solutions in a realistic environment (in terms of radio propagation, deployment of the cells, user mobility and traffic dynamics).
- **Offloading**. Offloading the cellular infrastructure implies taking advantage of the wealth of connectivity provided by capillary networks instead of relying solely on 4G connectivity. Cellular operators usually possess an important ADSL or cable infrastructure for wired services, the development of femtocell solutions thus becomes very popular. However, while femtocells can be an excellent solution in zones with poor coverage, their extensive use in areas with a high density of mobile users leads to serious interference problems that are yet to be solved. Taking advantage of capillarity for offloading cellular data relies on using IEEE 802.11 Wi-Fi (or other similar technologies) access points or direct device-to-device communications. The ubiquity of Wi-Fi access in urban areas makes this solution particularly interesting, and many studies have focused on its potential. However, these studies fail to take into account the usually low quality of Wi-Fi connections in public areas, and they consider that a certain data rate can be sustained by the Wi-Fi network regardless of the number of contending nodes. In reality, most public Wi-Fi networks are optimized for connectivity, but not for capacity, and more research in this area is needed to correctly assess the potential of this technology. Direct opportunistic communication between mobile users can also be used to offload an important amount of data. This solution raises a number of major problems related to the role of social information and multi-hop communication in the achievable offload capacity. Moreover, in this case the business model is not yet clear, as operators would indeed offload traffic, but also lose revenue as direct ad-hoc communication would be difficult to charge and privacy issues may arise. However, combining hotspot connectivity and multi-hop communications is an appealing answer to broadcasting geo-localized informations efficiently.